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(54) Title: OLFACTORY RECEPTOR SEQUENCES

(57) Abstract: The present invention provides polynucleotide sequences which encode polypeptides involved in olfactory sensation. The present invention also provides the polypeptides encoded by these polynucleotide sequences, vectors comprising these polynucleotide sequences and host cells transfected with these polynucleotide sequences. The present invention further provides for functional variants and homologues of these polynucleotide sequences and the polypeptides encoded by these polynucleotides. Libraries of polypeptides are also provided. Also included in the present invention is the use of these polypeptides and libraries of polypeptides in screening odorant molecules to determine the correspondence (scent representation, scent fingerprint or scent profile) between individual odorant receptors (the polypeptides) and particular odorant molecules. Also encompassed by the present invention is the use of the scent representation, scent fingerprint or scent profile to re-create and edit scents.

OLFACTORY RECEPTOR SEQUENCES

CROSS-REFERENCE TO RELATED APPLICATIONS

- 5 This application claims priority benefit of United States Provisional Patent Application Serial No. 60/158,615, filed on October 8, 1999, and United States Provisional Patent Application Serial No. 60/184,809, filed on February 24, 2000. The contents of those applications are hereby incorporated by reference herein in their entirety.

10 **STATEMENT OF RIGHTS TO INVENTIONS MADE UNDER**
FEDERALLY SPONSORED RESEARCH

Not applicable.

15 **TECHNICAL FIELD**

- The present invention is in the field of human olfactory receptors and their use in screening for olfactory agonists and antagonists. The present invention pertains to isolated nucleotide sequences which encode human olfactory receptors and also to the proteins
20 encoded by said nucleotide sequences. The present invention also encompasses vectors comprising the nucleotide sequences of the invention and further, host cells transfected with said vectors. The present invention also allows for the determination of primary scents and the identification of the odor receptors which are encoded to detect these primary scents as well as the determination of secondary scents and the identification of
25 combinations of odor receptors which are encoded to detect such secondary scents.

BACKGROUND ART

Our sense of smell plays an important role not only in our appreciation of our surroundings such as the smell of flowers or new mown grass, but also evolved as a survival skill. Numerous odorant molecules can be detected at extremely low concentrations, providing early warning of danger, such as the smell of smoke or contaminated food. Indeed, a potent example of this is that most pregnant women experience a heightened sense of smell, presumably to protect the fetus from the deleterious effects of food poisoning.

It is estimated that humans can detect millions of different molecular species; however, our nose can discriminate only a fraction of these different chemicals (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320), usually estimated at about 10,000 odorants (Axel, *Scientific American* 1995, October, 154-159). Odorants for terrestrial species such as humans, are volatile (air born) ligands which are detected by the olfactory system. Odorants have vastly different chemical structures and subtle differences can lead to pronounced changes in the perceived odor (Mombaerts, *supra*). For instance, when the hydroxyl group of octanol is replaced by a carboxyl group to give octanoic acid, its perceived odor changes from orange and rose-like to rancid and sweaty (Malnic *et al.*, *Cell* 1999 96, 713-723). The basis for these feats of sensory perception are just beginning to be understood at a cellular and molecular level.

The olfactory system contains millions of olfactory sensory neurons (OSNs) located in the olfactory epithelium of the nasal cavity. In humans, the olfactory epithelium occupies an area of approximately 5 cm². The OSNs are bipolar with one end extending through the supporting cell into the mucosal layer, terminating in hairlike cilia. These cilia are the site of the olfactory receptors (OR) where the odorant ligands are thought to bind (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320, Hildebrand *et al.*, *Annu. Rev. Neurosci.*, 1997, 20, 595-631). The OSNs also have a single unbranched axon which leads to the olfactory bulb, a part of the brain containing approximately 2000 glomeruli where the axons terminate and initial processing of the sensory code takes place. OSNs expressing the same OR are randomly interspersed throughout the olfactory epithelium, but in both the nose and the bulb, information derived from different ORs is strictly segregated; each OSN in the nose and each glomerulus in the olfactory bulb appear to be dedicated to input from one or few OR type(s) (Malnic *et al.*, *Cell* 1999 96, 713-723). It also appears that the location of the glomeruli are conserved across individuals of a species, providing the first spatial processing of particular odorant patterns (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). The domains in the olfactory bulb for

different odors may overlap, but the overall patterns are distinct (Hildebrand *et al.*, *supra*), therefore, it should be possible to identify and reproduce the characteristic pattern of a given odorant. Output neurons project from the olfactory bulb to the primary olfactory cortex and from there to the higher cortical areas of the brain and to the limbic system (Malnic *et al.*,
5 *supra*; Hildebrand *et al.*, *supra*, 20, 595-631).

Until the identification of a large family of genes encoding putative odorant receptors (Buck & Axel *Cell* 1991 65, 175-187), progress towards understanding the process of odor recognition was negligible. In recent years there has been an explosion in this field as more and more putative odor receptors are isolated and cloned. The odorant receptor gene products
10 have thus far been characterized through homology as seven transmembrane domain G protein-coupled receptors (GPCR). It is estimated that there are probably 500-750 OR-like sequences in humans, while there are 500-1000 OR genes in rat and mouse (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). In mice, OR-like sequences make up approximately 1% of their genome, the largest known family in the mammalian genome, surpassing the complexity of
15 even the immunoglobulin and T-cell antigen receptor gene families (Mombaerts, *supra*). The OR are concentrated on the surface of the OSN's mucus coated cilia and it is thought that odorant molecules bind to the OR in the olfactory epithelium and thereby initiate signal transduction. Current interpretation of recent experimental evidence favors the idea that each neuron expresses only one, or very few, ORs. Since mammals can detect at least 10,000 odors and
20 there are approximately 1,000 or fewer ORs, each of the ORs must respond to several odorant molecules, and each odorant molecule must bind to several receptors. It is believed that various receptors respond to discrete parts of an odorant molecule's structure and that an odorant consists of several chemical groups each of which bind a characteristic receptor (Axel *Scientific American* 1995, October, 154-159; Malnic *et al.*, *Cell* 1999 96, 713-723).

25 The main signal transduction pathway mediated by OR homologues in vertebrate species involves G protein-mediated stimulation of adenylyl cyclase activity, resulting in cAMP elevation that opens cyclic-nucleotide gated channels with a non-specific cation selectivity (Mombaerts *Curr. Opin. Genet. Dev.* 1999 9, 315-320). However, there are still numerous unanswered questions and recently it has come to light that 38-76% of the human
30 gene OR sequences that are being reported may be pseudogenes and therefore incapable of expressing the proteins that encode the olfactory receptors. Some of the incidences may be due to the method of extracting the genomic DNA libraries (Mombaerts, *supra*). Few pseudogenes have been found in other vertebrates and their incidence in libraries from testicular DNA is also

rare (Hildebrand *et al.*, *Annu. Rev. Neurosci.*, 1997, 20, 595-631). cDNA should not contain pseudogenes. There are a number of examples of ORs which have been successfully expressed and reactions to certain odorant ligands have been determined (Malnic *et al.*, *Cell* 1999 96, 713-723; Mombaerts, *supra*; Zhao *et al.*, *Science* 1998 279, 237-242).

5 Some attempts to express the ORs in heterologous cell lines resulted in the formation of inclusion bodies rather than the insertion of the proteins into the membrane (Kiefer *et al.*, *infra*). However, purification of the receptors after expression in *E. coli* and their insertion into lipid vesicles facilitates the use of these receptors in odorant ligand screening using a combination of photoaffinity labeling and Trp fluorescence (Kiefer *et al.*, *Biochemistry* 1996 10 35, 16077-16084). In addition, a functional human OR receptor protein has been expressed in HEK-293 cells and oocytes and found to interact with odorant ligands (Wetzel *et al.*, *J. Neurosci.* 1999 19, 7426-7433). There have also been, a number of successful efforts of expressing cDNA in insect Sf9 cells using *baculovirus* vectors (Mombaerts *Annu. Rev. Neuorsci.* 1999) as well as assays with neuronal tissue (Malnic *et al.*, *Cell* 1999 96, 713-723; 15 Zhao *et al.*, 1998; Firestein *et al.*, WO 98/50081). In addition, recent work accomplished the expression of chimeric mouse olfactory receptor sequences in HEK-293 cells and showed their reactivity towards a panel of odorant ligands, some at micromolar concentrations (Krautwurst *et al.*, *Cell* 1998 95 917-926). The drawback to expression in heterologous cell systems is the lack of working signal transduction pathways which can be used to detect responses to odorant 20 ligands; these drawbacks can be overcome with methods known in the art (e. g. U.S. Pat. No. 5,798, 275). There are also methods of expressing and assaying functional neuronal receptors in neuronal cells, including methods for detecting particular odorant ligand specificity (Malnic *et al.*, *supra*; Zhao, *supra*; Firestein *et al.*, *supra*).

25 Other publications of interest are: *Chemical Senses* 6: 343-349 (1981); *Proc. Natl. Acad. Sci. USA* 79: 670-674 (1982); *Proc. Natl. Acad. Sci. USA* 81(6): 1859-1863 (1984); *Nature* 316: 255-258 (1985); *Brain Research* 368: 329-338 (1986); *J. Biol. Chem.* 261: 1299-1305 (1986); *Proc. Natl. Acad. Sci. USA* 83(13): 4947-4951 (1986); *J. Neurosci.* 6: 2146-2154 (1986); *J. Neurochem.* 47: 1527-1533 (1986); *Chemical Senses* 13: 191-204 30 (1988); *Biochem. J.* 260:121-126 (1989); *J. Biol. Chem.* 264: 6780-6785 (1989); *Biochim. Biophys. Acta* 1013: 68-72 (1989); *J. Biol. Chem.* 264: 18803-18807 (1989); *Biochemistry* 29: 7433-7440 (1990); *FEBS lett.* 270: 24-29 (1990); *Chemical Senses* 15: 529-536 (1990); *Eur. J. Biochem.* 196: 51-58 (1991); *Nature* 349: 790-793 (1991); *Neurosci. Lett.* 141: 115-

118 (1992); Developmental Brain Res. 73: 7-16 (1993); Proc. Natl. Acad. Sci., USA 90: 3715-3719 (1993); Human Mol. Genetics 3: 229-235 (1994); Eur. J. Biochem. 225: 1157-1168 (1994); European Journal of Biochemistry 238: 28-37 (1996); Receptors and Channels 4: 141-147 (1996); Genomics 37(2): 147-160 (1996); Protein Science 8: 969-977 (1999); Genomics 53: 56-68 (1998); Genomics 61:24-36 (1999); Genomics 63: 227-245 (2000); Trends in Neurosci. 7:35-36 (1984); Ann. Rev. Neurosci. 9:329-355 (1986); Trends Biochem. Sci. 12:63-66 (1987); Nature 351: 275-276 (1991); Nature 353: 799-800 (1991); Current Biol. 3(10): 668-674 (1993); Nature 372:321-322 (1994); Essays in Biochemistry. 33: 93-104 (1998); and Nature, 398 (6725): 285-287 (1999).

10 However, despite the forgoing, there has been relatively little work with human olfactory receptors, in particular in determining the sequences of large numbers of receptors, and less progress in determining the correspondence between particular human olfactory receptors and the scent(s) to which they respond.

15 All publications cited herein are hereby incorporated by reference in their entirety.

DISCLOSURE OF THE INVENTION

20 An object of the invention is to determine the correspondence between ORs and the scent(s) to which they respond. Once this is accomplished, scents can be both analyzed and re-created for enhancing human experiences or eliciting particular responses. The present invention pertains to isolated polynucleotide sequences encoding polypeptides involved in olfactory sensation. The present invention also pertains to the proteins encoded by said nucleotide sequences. The present invention also encompasses vectors comprising the
25 nucleotide sequences of the invention and further, host cells transfected with said vectors. The present invention also allows for the determination of primary scents and the identification of the odor receptors which are encoded to detect these primary scents as well as the determination of receptor complex scent components and the identification of combinations of odor receptors which are encoded to detect such receptor complex scent
30 components scents.

The invention provides isolated polynucleotide sequences encoding polypeptides involved in olfactory sensation that are isolated from human olfactory epithelial tissue. The invention further provides expression vectors containing such nucleotide sequences. Also provided by the invention are purified polypeptides encoded by the nucleotide sequences. The invention further provides transformed cells which comprise a suitable host cell transfected with a suitable expression vector containing the nucleotide sequence encoding the receptor. The present invention also encompasses nucleotide sequences isolated from human olfactory epithelial tissue which encode receptors capable of binding odorant molecules. The invention further provides expression vectors containing such nucleotide sequences and homologues of both the polynucleotides and polypeptides. Further, the invention provides a means of using the nucleotide sequences of the invention in a method of screening odorant ligands to determine the specific binding of odorant molecules to a particular receptors, and further, determining the component odorant molecules of subjectively experienced smells, determining the combination odorant molecules and receptor stimulation or inhibition to re-create a particular scent. The binding of odorant molecules by the receptors encompassed in the present invention includes binding resulting in both the agonism (excitation/activation) and antagonism (inhibition/blocking) of receptor function(s) upon binding of the molecule.

Accordingly, the invention includes an isolated polynucleotide comprising a sequence encoding a polypeptide which is involved in olfactory sensation. The OR polypeptides encoded are found within the sequences depicted in polynucleotide sequences SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a nucleotide sequence at least 95% homologous to said sequences. The invention also encompasses the translation products of those sequences. The invention further comprises expression vectors comprising said sequences, host cells containing such expression vectors and/or expressing the polypeptide encoded therein, or phage displaying the polypeptide encoded by the sequences. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention. The invention further encompasses fragments of said polynucleotides which can be used as probes or primers to identify additional polynucleotide sequences through techniques known in the art, including those fragments depicted in SEQ ID NOs: 74-105.

The invention also includes additional isolated polynucleotide comprising a sequence encoding a polypeptide which is involved in olfactory sensation. The OR polypeptides

encoded are found within the sequences depicted in polynucleotide sequences SEQ ID NO:153 through SEQ ID NO: 1084, or a nucleotide sequence at least 95% homologous to said sequences. The invention also comprises the translation products of those sequences. The invention further comprises expression vectors comprising said sequences, host cells containing
5 such expression vectors and/or expressing the polypeptide encoded therein, or phage displaying the polypeptide encoded by the sequences. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention.

10 The invention also encompasses an isolated and purified olfactory receptor polypeptide comprising the sequence of SEQ ID NO: 1085 through SEQ ID NO: 2008, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of SEQ ID NO: 1085 through SEQ ID NO: 2008 and having olfactory receptor function. Host cells expressing such polypeptides and phages displaying such
15 polypeptides are also encompassed by the invention. The use of functional fragments of receptors is also encompassed by the invention. Preparations of receptors, further including biological or synthetic molecules which maintain the stability and functional structure of the receptors, are also included in the invention.

Scents can be captured, analyzed and recorded by a sensory device using various
20 methods. Scent capture can be initiated by the user or by an automatic sensing system. A scent can be analyzed in terms of its interaction with olfactory neurons of a mammalian, preferably human, olfactory system, or by the expression of individual receptors under appropriate conditions and appropriate assay conditions in multiwell plates or in terms of its perception by a panel of mammalian, preferably human, subjects. The interaction with olfactory neurons can
25 be determined experimentally, in vitro, by determining the interaction of an odorant with olfactory receptors of a given type. Alternatively, the interaction with olfactory receptor can be determined using a computer simulation which provides information regarding the interaction of an odorant with the olfactory receptors. A panel of subjects can be used to represent odors in terms of their perception. The data so generated can be used to represent a scent in a manner
30 which can be recorded in digital or other format, stored in media such as computer memory, disks, or printed format, and transmitted over a data network. The representation of the scent can be used to re-create the scent at a local or remote site using an emitter module. The

representation of the scent allows for scent editing, where desirable aspects of an odor are enhanced or added and undesirable aspects are attenuated or eliminated.

Accordingly, the invention also embraces libraries of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising the
5 expression products of at least two polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084, where the polynucleotides encode functional olfactory receptors; or functional fragments of the expression products. Libraries of at least 50, 100, 200, or 500 receptors are also encompassed by the invention.

10 Also encompassed by the invention are libraries of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising at least two polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008, where the polypeptides are functional olfactory receptors; or functional fragments of the polypeptides. Libraries of at least 50, 100, 200, or 500 receptors are also encompassed by the invention.

15 The invention also embraces methods for determining the binding pattern of a composition with olfactory receptors, involving exposing the composition to an olfactory receptor library, and determining whether the composition binds to each olfactory receptor, thereby determining the overall binding pattern of the composition. In additional embodiments, the method also involves determining the approximate binding constant with
20 which the composition, or the various chemicals within the composition, bind to the receptors; determining whether a receptor or functional fragment thereof is activated; and determining the absolute amount of activation, or amount of activation relative to another receptor or a control substance. The composition can consist essentially of one compound or chemical, or can comprise at least two compounds or chemicals.

25 The invention also embraces DNA arrays or DNA chips comprising the DNA segments derived from any combination of, or each of, SEQ ID NO: 153 through SEQ ID NO: 1084. The invention also embraces a method of determining differences among one or more individuals with respect to their olfactory faculties, comprising the steps of comparing the olfactory DNA of each individual against the array or chip.

30 The invention also embraces a method to determine single nucleotide polymorphisms in olfactory receptors, comprising the steps of uniquely amplifying olfactory receptor sequences from DNA obtained from one or more individuals, based on

primers designed according to the first 25 bases and the last 25 bases of any combination of, or each of, SEQ ID NO: 153 through SEQ ID NO: 1084, and determining the similarities and differences between said amplified DNA and the corresponding receptor from SEQ ID NO: 153 through SEQ ID NO: 1084.

5

Brief Description of the Drawings

Figure 1 depicts the isolated polynucleotide sequences, which encode polypeptides involved in olfactory sensation, corresponding to SEQ ID NOs: 1 - 73.

Figure 2 depicts the isolated polynucleotide sequences, which encode polypeptides involved in olfactory sensation, corresponding to SEQ ID NOs: 111 - 152.

Detailed Description of the Invention

15

The present invention provides isolated polynucleotides comprising sequences that encode polypeptides which are involved in olfactory sensation and which can be used to screen odorant ligands, e.g., odorant receptor agonists and antagonists.

Definitions

The term "olfactory receptor" (OR) refers to a polypeptide involved in olfactory sensation. An "olfactory receptor polynucleotide" or "OR polynucleotide" is a polynucleotide encoding a polypeptide involved in olfactory sensation.

The term "odorant ligand" as employed herein refers to a molecule that has the potential to bind to an olfactory receptor. Equivalent terms employed herein include "odorant", "odorant molecule" and "odorant compound". The term "binding" or "interaction" as used herein with respect to odorant ligands refers to the interaction of ligands with the receptor polypeptide where the ligands may serve as either agonists and/or antagonists of a given receptor or receptor function. An odorant ligand may thus directly cause a perception of odor (an agonist), or may block the perception of odor (an antagonist). An odorant ligand may include, but is not limited to, molecules which interact with polypeptides involved in olfactory

sensation. Odorant ligands and molecules which interact with olfactory receptors are generally small, approximately 1000 Daltons, more preferably approximately 750 Daltons, more preferably approximately 500 Daltons, or even more preferably approximately 300 Daltons, hydrophobic molecules with a variety of functional groups. Small changes in structure can induce profound changes in odorant ligand binding and hence in the odor perceived by an individual.

A more detailed description of these sequences, as well as how these sequences were obtained, is provided below.

10

As used herein, a "polynucleotide" is a polymeric form of nucleotides of any length, which contain deoxyribonucleotides, ribonucleotides, and/or their analogs. The terms "polynucleotide", "nucleotide" and "nucleic acid" as used herein are used interchangeably. Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The term "polynucleotide" includes double-, single-stranded, and triple-helical molecules. Unless otherwise specified or required, any embodiment of the invention described herein that is a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double stranded form. Not all linkages in a polynucleotide need be identical.

20

The following are non-limiting examples of polynucleotides: a gene or gene fragment, exons, introns, mRNA, tRNA, rRNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, primers, and adaptors. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. The use of uracil as a substitute for thymine in a deoxyribonucleic acid is also considered an analogous form of pyrimidine.

25

In the context of polynucleotides, a "linear sequence" or a "sequence" is an order of nucleotides in a polynucleotide in a 5' to 3' direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polynucleotide. A "partial sequence" is a linear sequence of part of a polynucleotide which is known to comprise additional residues in one or both directions.

30

If present, modification to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by

conjugation with a labeling component. Other types of modifications included in this definition are, for example, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoamidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), those containing pendant moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., α -anomeric nucleic acids, peptide nucleic acids, etc.), as well as unmodified forms of the polynucleotide(s).

Further, any of the hydroxyl groups ordinarily present in the sugars may be replaced by phosphonate groups, phosphate groups, protected by standard protecting groups, or activated to prepare additional linkages to additional nucleotides, or may be conjugated to solid supports. The 5' and 3' terminal OH groups can be phosphorylated or substituted with amines or organic capping group moieties of from 1 to 20 carbon atoms. Other hydroxyls may also be derivatized to standard protecting groups.

Polynucleotides can also contain analogous forms of ribose or deoxyribose sugars that are generally known in the art, including, but not limited to, 2'-O-methyl-, 2'-O-allyl, 2'-fluoro- or 2'-azido-ribose, carboxycyclic sugar analogs, α -anomeric sugars, epimeric sugars such as arabinose, xyloses or lyxoses, pyranose sugars, furanose sugars, sedoheptuloses, acyclic analogs and abasic nucleoside analogs such as methyl riboside.

Although conventional sugars and bases will be used in applying the method of the invention, substitution of analogous forms of sugars, purines and pyrimidines can be advantageous in designing a final product, as can alternative backbone structures like a polyamide backbone such as those used in peptide nucleic acids (PNAs).

A polynucleotide or polynucleotide region has a certain percentage (for example, 75%, 80%, 85%, 90%, 95% or 99%) of "sequence identity" to another sequence means that, when aligned, that percentage of bases are the same in comparing the two sequences.

Homology, as described herein, means that the polypeptide sequences that are encoded by the nucleic acids demonstrate a certain relatedness (i.e., there exists regions of conserved amino acids), but not the same amino acid identity. There is complete or 100% homology at a particular amino acid residue when the amino acids of sequences being compared are the same (there is identity) or represent a conservative amino acid substitution (there is homology). A

“conservative amino acid substitution” occurs when a particular amino acid is substituted by an alternate amino acid of similar charge density, hydrophobicity/hydrophilicity, size and/or configuration (e.g., Val for Ile). A “nonconservative amino acid substitution” occurs when a particular amino acid is substituted by an alternative amino acid of differing properties, that is, charge density, hydrophobicity/hydrophilicity, size and/or configuration (e.g., Val for Tyr). The nucleic acid sequences within the scope of the present invention include those nucleic acids which differ in exact sequence from those listed in SEQ ID NO:1 through SEQ ID NO:73 and SEQ ID NO:111 through SEQ ID NO:152 but which encode identical or homologous polypeptide amino acid sequences.

10 A “primer” is a short polynucleotide, generally with a free 3’ -OH group, that binds to a target potentially present in a sample of interest by hybridizing with the target, and thereafter promoting polymerization of a polynucleotide complementary to the target.

15 An “adaptor” is a short, partially-duplexed polynucleotide that has a blunt, double-stranded end and a protruding, single-stranded end. It can be ligated, through its double-stranded end, to the double-stranded end of another polynucleotide. This provides known sequences at the ends of thus modified polynucleotides. Often adaptors contain specific sequences for primer binding and/or restriction endonuclease digestion.

20 A “probe” when used in the context of polynucleotide manipulation refers to a polynucleotide which is provided as a reagent to detect a target potentially present in a sample of interest by hybridizing with the target. Usually, a probe will comprise a label or a means by which a label can be attached, either before or subsequent to the hybridization reaction. Suitable labels include, but are not limited to radioisotopes, fluorochromes, chemiluminescent compounds, dyes, and enzymes.

25 “Transformation” or “transfection” refers to the insertion of an exogenous polynucleotide into a host cell, irrespective of the method used for the insertion, for example, lipofection, transduction, infection or electroporation. The exogenous polynucleotide may be maintained as a non-integrated vector, for example, a plasmid, or alternatively, may be integrated into the host cell genome.

30 A polynucleotide is said to “encode” a polypeptide if, in its native state or when manipulated by methods well known to those skilled in the art, it can be transcribed and/or translated to produce the polypeptide, a homologous polypeptide or a fragment thereof. For purposes of this invention, and to avoid cumbersome referrals to complementary strands, the anti-sense (or complementary) strand of such a polynucleotide is also said to encode the

sequence; that is, a polynucleotide sequence that "encodes" a polypeptide includes both the conventional coding strand and the complementary sequence (or strand).

The terms "polypeptide", "oligopeptide", "peptide" and "protein" are used interchangeably herein to refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, it may be interrupted by non-amino acids, and it may be assembled into a complex of more than one polypeptide chain. The terms also encompass an amino acid polymer that has been modified naturally or by intervention; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation or modification, such as conjugation with a labeling component. Also included within the definition are, for example, polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids, etc.), as well as other modifications known in the art.

In the context of polypeptides, a "linear sequence" or a "sequence" is an order of amino acids in a polypeptide in an N-terminal to C-terminal direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polypeptide. A "partial sequence" is a linear sequence of part of a polypeptide which is known to comprise additional residues in one or both directions.

"Recombinant," as applied to a polynucleotide or gene, means that the polynucleotide is the product of various combinations of cloning, restriction and/or ligation steps, and other procedures that result in a construct that is distinct from a polynucleotide found in nature.

A "vector" is a self-replicating nucleic acid molecule that can be used to transfer an inserted nucleic acid molecule into and/or between host cells. The term includes vectors that function primarily for insertion of a nucleic acid molecule into a cell, vectors that function primarily for the amplification of nucleic acid, and expression vectors that function for transcription and/or translation of the DNA or RNA. Also included are vectors that provide more than one of the above functions.

"Expression vectors" are defined as polynucleotides which, when introduced into an appropriate host cell, can be transcribed into a mRNA capable of being translated into a polypeptide(s). An expression vector also comprises control elements operatively linked to the coding region to enable and/or facilitate expression of the polypeptide in the target cell. These can include transcriptional, translational, posttranscriptional, and posttranslational control elements, as are known in the art. An "expression system" usually connotes a suitable host cell comprised of an expression vector that can function to yield a desired expression product.

A "host cell" includes an individual cell or cell culture which can be or has been a recipient for vector(s) or for incorporation of nucleic acid molecules and/or proteins. Host cells include progeny of a single host cell, and the progeny may not necessarily be completely identical (in morphology or in genomic or total DNA complement) to the original parent cell
5 due to natural, accidental, or deliberate mutation. A host cell includes cells transfected in vivo with a polynucleotide(s) of this invention.

A "cell line" or "cell culture" denotes eukaryotic cells, derived from higher, multicellular organisms, grown or maintained in vitro. It is understood that the descendants of a cell may not be completely identical (either morphologically, genotypically, or phenotypically) to the parent cell.
10 Cells described as "uncultured" are obtained directly from a living organism, and are generally maintained for a limited amount of time away from the organism (i.e., not long enough or under conditions for the cells to undergo substantial replication).

As used herein, "expression" includes transcription and/or translation.

"Heterologous" means derived from (i.e., obtained from) a genotypically distinct entity
15 from the rest of the entity to which it is being compared. For example, a polynucleotide may be placed by genetic engineering techniques into a plasmid or vector derived from a different source, thus becoming a heterologous polynucleotide. A promoter which is linked to a coding sequence with which it is not naturally linked is a heterologous promoter.

An "isolated" or "purified" polynucleotide, polypeptide or cell is one that is
20 substantially free of the materials with which it is associated in nature. By substantially free is meant at least 50%, preferably at least 70%, more preferably at least 80%, even more preferably at least 90%, even more preferably at least 99%, and even more preferably at least 99.9% free of the materials with which it is associated in nature. As used herein, an "isolated" polynucleotide or polypeptide also refers to recombinant polynucleotides or polypeptides,
25 which, by virtue of origin or manipulation: (1) are not associated with all or a portion of a polynucleotide or polypeptide with which they are associated in nature, (2) are linked to a polynucleotide or polypeptide other than that to which they are linked in nature, or (3) do not occur in nature, or (4) in the case of polypeptides, arise from expression of recombinant polynucleotides. Thus, for example, an isolated substance may be prepared by using a
30 purification technique to enrich it from a source mixture. Enrichment can be measured on an absolute basis, such as weight per volume of solution, by specific activity or it can be measured in relation to a second, potentially interfering substance present in the source mixture. Increasing enrichments of the embodiments of this invention are increasingly more preferred.

Thus, for example, a 2-fold enrichment is preferred, 10-fold enrichment is more preferred, 100-fold enrichment is more preferred, 1000-fold enrichment is even more preferred. A substance can also be provided in an isolated state by processes such as chemical synthesis or recombinant expression.

5 A "reagent" polynucleotide, polypeptide, or antibody, is a substance provided for a reaction, the substance having some known and desirable function in the reaction. A reaction mixture may also contain a "target", such as a polynucleotide, antibody, polypeptide, or assembly of polypeptides that the reagent is capable of reacting with. For example, in some types of diagnostic tests, the presence and/or amount of the target in a sample is determined by
10 adding a reagent, allowing the reagent and target to react, and measuring the amount of reaction product (if any).

 "Hybridization" refers to a reaction in which one or more polynucleotides react to form a complex that is stabilized via hydrogen bonding between the bases of the nucleotide residues. The hydrogen bonding may occur by Watson-Crick base pairing, Hoogsteen binding, or in any
15 other sequence-specific manner. The complex may comprise two strands forming a duplex structure, three or more strands forming a multi-stranded complex, a single self-hybridizing strand, or any combination of these. A hybridization reaction may constitute a step in a more extensive process, such as the initiation of an amplification reaction such as PCR, or the enzymatic cleavage of a polynucleotide by a ribozyme.

20 When hybridization occurs in an antiparallel configuration between two single-stranded polynucleotides, those polynucleotides are described as "complementary". A double-stranded polynucleotide can be "complementary" to another polynucleotide if hybridization can occur between one of the strands of the first polynucleotide and the second. The degree to which one polynucleotide is complementary with another is quantifiable in terms of the proportion of bases in
25 opposing strands that are expected to form hydrogen bonds with each other, according to generally accepted base-pairing rules of A-T, A-U and G-C.

 A "stable duplex" of polynucleotides, or a "stable complex" formed between any two or more components in a biochemical reaction, refers to a duplex or complex that is sufficiently long-lasting to persist between formation of the duplex or complex and subsequent detection,
30 including any optional washing steps or other manipulation that may take place in the interim.

 A substance is said to be "selective" or "specific" if it reacts or associates more frequently, more rapidly, with greater duration and/or with greater affinity with a particular cell or substance than it does with alternative cells or substances. An odorant ligand "specifically

binds" to a target if it binds with greater affinity, avidity, more readily, and/or with greater duration than it binds to other substances.

As used herein, "naturally occurring," "native," or "wild type" refers to endogenous polynucleotides and the protein(s) expressed thereby. These terms include full-length and
5 processed polynucleotides and polypeptides. Processing can occur in one or more steps, and these terms encompass all stages of processing. For instance, polypeptides having or lacking a signal sequence are encompassed by the invention. "Non-naturally occurring", "non-native", or "non-wild type" refer to all other polynucleotides and polypeptides.

A "polymerase chain reaction" ("PCR") is a reaction in which replicate copies are made
10 of a target polynucleotide using one or more primers, and a catalyst of polymerization, such as a reverse transcriptase or a DNA polymerase, and particularly a thermally stable polymerase enzyme. Methods for PCR are taught in U.S. Patent Nos. 4,683,195 (Mullis) and 4,683,202 (Mullis et al.). All processes of producing replicate copies of the same polynucleotide, such as PCR or gene cloning, are collectively referred to herein as "amplification."

15 According to this invention, a "genomic DNA library" is a clone library which contains representative nucleotide sequences from the DNA of a given genome. It is constructed using various techniques that are well known in the art, for instance, by enzymatically or mechanically fragmenting the DNA from an organism, organ, or tissue of interest, linking the fragments to a suitable vector, and introducing the vector into appropriate cells so as to
20 establish the genomic library. A genomic library contains both transcribed DNA fragments as well as nontranscribed DNA fragments.

In comparison, a "cDNA library" is a clone library that differs from a genomic library in that it contains only transcribed DNA sequences and no nontranscribed DNA sequences. It is established using techniques that are well known in the art, i.e., selection of mRNA (e.g. by
25 polyA) making single stranded DNA from a population of cytoplasmic mRNA molecules using the enzyme RNA-dependent DNA polymerase (i.e., reverse transcriptase), converting the single-stranded DNA into double-stranded DNA, cloning the resultant molecules into a vector, and introducing the vector into appropriate cells so as to establish the cDNA library.

Alternately, a cDNA library need not be cloned into a vector and/or established in cells, but can
30 be screened using PCR with gene-specific primers, as is well known in the art.

An "individual" is a vertebrate, preferably a mammal, more preferably a human.

General Techniques

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology and biochemistry, which are within the skill of the art. Such techniques are explained fully in the literature, such as: "Molecular Cloning: A Laboratory Manual", second edition (Sambrook et al., 1989); "Oligonucleotide Synthesis" (M.J. Gait, ed., 1984); "Animal Cell Culture" (R.I. Freshney, ed., 1987); "Methods in Enzymology" (Academic Press, Inc.); "Gene Transfer Vectors for Mammalian Cells" (J.M. Miller & M.P. Calos, eds., 1987); "Current Protocols in Molecular Biology" (F.M. Ausubel et al., eds., 1987 and annual updates); "PCR: The Polymerase Chain Reaction", (Mullis et al., eds., 1994); "Current Protocols in Immunology" (J.E. Coligan et al., eds., 1991).

Basis for identification and description of the polynucleotides and polypeptides

The polynucleotide sequences were identified using oligonucleotide primers which were complementary to OR membrane-spanning regions. A number of different primers were used to elicit a variety of nucleotide sequences which encode polypeptides involved in olfactory sensation. The identification and isolation of nucleotide sequences which encode polypeptides involved in olfactory sensation and the polypeptides that they encode is vital for determining the response of receptors to odorant molecules, the elucidation of scent representations, profiles, or fingerprints, the reproduction of scent representations, profiles, or fingerprints and the editing of scent representations, profiles, or fingerprints.

Polynucleotides encoding polypeptides involved in olfactory sensation

The present invention provides isolated polynucleotides encoding polypeptides which are involved in olfactory sensation, vectors containing these polynucleotides, host cells containing these polynucleotides, and compositions comprising these polynucleotides. These polynucleotides are isolated and/or produced by chemical and/or recombinant methods, or a combination of these methods. The present invention includes polynucleotides isolated from the human olfactory epithelium which encode polypeptides which are involved in olfactory sensation, vectors containing these polynucleotides, host cells containing these polynucleotides, and compositions comprising these polynucleotides. Unless specifically stated otherwise,

“polynucleotides” shall include all embodiments of the polynucleotides of this invention. These polynucleotides are useful as probes, primers, in expression systems, and, in a preferred embodiment, in screening methods as described herein. In one embodiment the polynucleotides of the present invention can be isolated by creating a cDNA library using
5 template RNA from human olfactory epithelium tissue. A detailed example is related in Example 1, below.

The advantage of constructing a cDNA library for isolation of the desired nucleotide sequences is that the likelihood of obtaining pseudogenes is greatly reduced compared to using a genomic DNA library for the same purpose. cDNA libraries contain only mRNA expressed
10 in the tissue used for the construction of the library, in this case, the human olfactory epithelium. The preferred olfactory epithelium tissue should express only those nucleotide sequences which are relevant for olfactory function, thereby excluding nonfunctioning pseudogenes and also GPCRs which may be similar in primary structure (amino acid sequence) but are not encoded in OSNs. As the number of GPCRs utilized in human signal transduction
15 pathways is extremely wide and varied, cDNA libraries constructed using olfactory tissue are preferable for isolating nucleotide sequences that encode polypeptides which are involved in olfactory sensation, inasmuch as genomic libraries can contain abundant nucleotide sequences which encode for a variety of GPCRs performing numerous functions, and are likely to contain pseudogenes.

20 The isolation of polynucleotide sequences which encode polypeptides involved in olfactory sensation is described in Example 1. Accordingly, this invention provides isolated polynucleotides that contain sequences encoding polypeptides or portions thereof which are involved in olfactory sensation, wherein the polypeptide is at least 10 amino acids in length, and wherein the polynucleotide sequences are depicted in SEQ ID NOs:1-73 and SEQ ID
25 NOs:111-152.

The invention includes modifications to said polynucleotides described above such as deletions, substitutions, additions, or changes in the nature of any nucleic acid moieties. A “modification” is any difference in nucleotide sequence as compared to a polynucleotide shown herein to encode a polypeptide involved in olfactory sensation, and/or any difference in
30 the nucleic acid moieties of the polynucleotide(s), wherein such a modified polynucleotide encodes a polypeptide involved in olfactory sensation or a variant of said polypeptide that is useful in the practice of the invention. Such changes can be useful to facilitate cloning and modify expression of polynucleotides encoding polypeptides which are involved in olfactory

sensation. Such changes also can be useful for conferring desirable properties to the polynucleotide(s), such as stability. The definition of polynucleotide provided herein gives examples of these modifications. Hence, the invention also includes variants of the nucleic acid sequences disclosed herein, which include nucleic acid substitutions, additions, and/or deletions.

The invention also encompasses polynucleotides encoding polypeptides involved in olfactory sensation, including polynucleotides that are full-length, processed, coding, non-coding (including flanking region) or portions thereof, provided that these polynucleotides contain a region encoding at least a portion of a polypeptide involved in olfactory sensation. (That is, the region encodes a functional fragment of an olfactory receptor or other polypeptide involved in olfactory sensation.) Also embodied are the mRNA, cDNA and genomic DNA sequences and fragments thereof that include a polynucleotide sequence comprising a coding sequence for a portion of a polypeptide involved in olfactory sensation.

Genes encoding human olfactory receptors, and optionally including related genomic sequences such as regulatory sequences, can be obtained using olfactory receptor cDNAs as hybridization probes. Under high stringency hybridization conditions, an OR cDNA will hybridize to its cognate OR gene. Use of lower stringency hybridization conditions allows the isolation of OR genes that are related to, but not identical with, the gene corresponding to a particular OR cDNA.

Conditions for hybridization are well-known to those of skill in the art and can be varied within relatively wide limits. Hybridization stringency refers to the degree to which hybridization conditions disfavor the formation of hybrids containing mismatched nucleotides, thereby promoting the formation of perfectly matched hybrids or hybrids containing fewer mismatches; with higher stringency correlated with a lower tolerance for mismatched hybrids. Factors that affect the stringency of hybridization include, but are not limited to, temperature, pH, ionic strength, and concentration of organic solvents such as formamide and dimethylsulfoxide. As is well known to those of skill in the art, hybridization stringency is increased by higher temperatures and/or lower ionic strengths. See, for example, Ausubel et al., supra; Sambrook et al., supra; M.A. Innis et al. (eds.) PCR Protocols, Academic Press, San Diego, 1990; B.D. Hames et al. (eds.) Nucleic Acid Hybridisation: A Practical Approach, IRL Press, Oxford, 1985; and van Ness et al., (1991) Nucleic Acids Res. 19:5143-5151. The degree of stringency can be adjusted not only during a hybridization reaction, but also in post-hybridization washes, as is known to those of skill in the art.

The invention also encompasses polynucleotides encoding polypeptides involved in olfactory sensation, functionally equivalent variants and derivatives of full-length polypeptides involved in olfactory sensation and functionally equivalent fragments. For instance, changes in a DNA sequence that do not change the encoded amino acid sequence, as well as those that result in conservative substitutions of amino acid residues, non-deleterious non-conservative substitutions, one or a few amino acid deletions or additions, and substitution of amino acid residues by amino acid analogs, will not significantly affect properties of the encoded polypeptide. Polypeptides homologous to the polypeptides encoded by the polynucleotides described herein can also be identified using algorithms and methods well-known to those of skill in the art, such as those described in Ausubel, "Current Protocols in Molecular Biology," Chapter 19; see also Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272; Madden, T.L., Tatusov, R.L. & Zhang, J. (1996) "Applications of network BLAST server" Meth. Enzymol. 266:131-141; Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25:3389-3402; and Zhang, J. & Madden, T.L. (1997) "PowerBLAST: A new network BLAST application for interactive or automated sequence analysis and annotation." Genome Res. 7:649-656. A preferred method of determining homology is the BLAST set of similarity search programs (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410. Polypeptides which are 40% homologous, 50% homologous, 60% homologous, 70% homologous, 80% homologous, 90% homologous, 95% homologous, or 99% homologous to the polypeptides encoded by the polynucleotides described herein are encompassed by the invention.

Nucleotide substitutions that do not alter the amino acid residues encoded can be useful for optimizing gene expression in different systems. Suitable substitutions are known to those of skill in the art and are made, for instance, to reflect preferred codon usage in the particular expression systems. In another example, alternatively spliced polynucleotides can give rise to different functionally equivalent fragments or variants of an polypeptide involved in olfactory sensation. Alternatively processed polynucleotide sequence variants are defined as polynucleotide sequences corresponding to mRNAs that differ in sequence from one another but are derived from the same genomic region, for example, mRNAs that result from: 1) the

use of alternative promoters; 2) the use of alternative polyadenylation sites; and/or 3) the use of alternative splice sites.

Preparation of polynucleotides involved in olfactory sensation

5 The polynucleotides of this invention can be obtained using chemical synthesis, recombinant methods, or PCR.

Methods of chemical polynucleotide synthesis are well known in the art and need not be described in detail herein. One of skill in the art can use the sequences provided herein and a commercial DNA synthesizer to produce a desired DNA sequence.

10 For preparing polynucleotides which encode polypeptides involved in olfactory sensation using recombinant methods, a polynucleotide comprising a desired sequence can be inserted into a suitable vector, and the vector in turn can be introduced into a suitable host cell for replication and amplification. Polynucleotides may be inserted into host cells by any means known in the art. Cells are transformed by introducing an exogenous polynucleotide by direct
15 uptake, endocytosis, transfection, F-mating, particle bombardment, liposome mediation, or electroporation. Once introduced, an exogenous polynucleotide can be maintained within the cell as a non-integrated vector (such as a plasmid) or integrated into the host cell genome. The polynucleotide encoding a polypeptide involved in olfactory sensation can be isolated from the host cell by methods well known within the art. See, e.g., Sambrook et al. (1989).

20 Alternatively, PCR allows amplification of DNA sequences. PCR technology is well known in the art and is described in U.S. Pat. Nos. 4,683,195, 4,800,159, 4,754,065 and 4,683,202, as well as *PCR: The Polymerase Chain Reaction*, Mullis et al. eds., Birkhausw Press, Boston (1994).

25 RNA can be obtained in a number of ways in an appropriate vector and the vector is transformed into a suitable host cell. When the inserted DNA is transcribed into RNA, the RNA can then be isolated using methods well known to those of skill in the art, as set forth in Sambrook et al., (1989), for example. RNA can also be obtained through in vitro reactions. For example, the polynucleotide, which encodes a polypeptide involved in olfactory sensation, can be inserted into a vector that contains appropriate transcription promoter sequences.

30 Commercially available RNA polymerases will specifically initiate transcription at their promoter sites and continue the transcription process through the adjoining DNA polynucleotides. Placing the polynucleotide sequences which encode polypeptides involved in

olfactory sensation between two such promoters allows the generation of sense or antisense strands of desired RNA.

5 ***Cloning and expression vectors comprising polynucleotide sequences encoding polypeptides involved in olfactory sensation***

The present invention further includes a variety of vectors containing polynucleotides encoding polypeptides involved in olfactory sensation. These vectors can be used for expression of recombinant polypeptides as well as a source of polynucleotides which encode polypeptides involved in olfactory sensation. Cloning vectors can be used to obtain replicate
10 copies of the polynucleotides, which encode polypeptides involved in olfactory sensation, they contain, or as a means of storing the polynucleotides in a depository for future recovery. Expression vectors (and host cells containing these expression vectors) can be used to obtain polypeptides produced from the polynucleotides they contain. Suitable cloning and expression vectors include any known in the art, e.g., those for use in in vitro, bacterial, mammalian, yeast
15 and insect expression systems. Specific vectors and suitable host cells are known in the art and need not be described in detail herein. For example, see Gacesa and Ramji, *Vectors*, John Wiley & Sons (1994).

Cloning and expression vectors typically contain a selectable marker (for example, a gene encoding a protein necessary for the survival or growth of a host cell transformed with the
20 vector), although such a marker gene can be carried on another polynucleotide sequence co-introduced into the host cell. Only those host cells into which a selectable marker has been introduced will survive and/or grow under selective conditions. Typical selectable markers encode protein(s) that (a) confer resistance to antibiotics or other toxins substances, e.g., ampicillin, neomycin, methotrexate, etc.; (b) complement auxotrophic deficiencies; or (c)
25 supply critical nutrients not available from complex media. The choice of the proper marker gene will depend on the host cell, and appropriate genes for different hosts are known in the art. Cloning and expression vectors also typically contain a replication system recognized by the host.

Suitable cloning vectors may be constructed according to standard techniques, or may
30 be selected from a large number of cloning vectors available in the art. While the cloning vector selected may vary according to the host cell intended to be used, useful cloning vectors will generally have the ability to self-replicate in an appropriate host, may possess a single target for one or more particular restriction endonucleases, and/or may carry genes for a marker

that can be used in selecting clones containing the vector. Suitable examples include plasmids and bacterial viruses, e.g., pUC18, pUC19, m13mp18, m13mp19, pBR322, pMB9, ColE1, pCR1, RP4, phage DNAs, and shuttle vectors such as pSA3 and pAT28. These and many other cloning vectors are available from commercial vendors such as BioRad, Stratagene, and
5 Invitrogen.

Expression vectors generally are replicatable polynucleotide constructs that contain a polynucleotide encoding a polypeptide involved in olfactory sensation of interest. The polynucleotide, which encodes a polypeptide involved in olfactory sensation, encoding the polypeptide is operatively linked to suitable transcriptional controlling elements, such as
10 promoters, enhancers and terminators. For expression (i.e., translation), one or more translational controlling elements are also usually required, such as ribosome binding sites, translation initiation sites, and stop codons. These controlling elements (transcriptional and translational) may be derived from the gene encoding polypeptides involved in olfactory sensation, or they may be heterologous (i.e., derived from other genes and/or other organisms).
15 A polynucleotide sequence encoding a signal peptide can also be included to allow a polypeptide involved in olfactory sensation to cross and/or lodge in cell membranes or be secreted from the cell. A number of expression vectors suitable for expression in eukaryotic cells including yeast, insect, avian, plant and mammalian cells are known in the art. Common vectors, such as YEp13 and the Sikorski series pRS303-306, 313-316, 423-426 can also be
20 used. Vectors pDBV52 and pDBV53 are suitable for expression. Another example of an expression vector/host cell system is the baculovirus (e.g., nuclear polyhedrosis virus)/insect cell (e.g., sf9 cells) system.

Human olfactory receptor polypeptides are expressed from olfactory receptor cDNA by methods well-known to those of skill in the art. A cDNA or portion thereof is inserted in an
25 expression vector using standard molecular cloning techniques. Coupled in vitro transcription and translation of such a vector results in expression of the OR protein encoded by the cDNA. In vivo expression of a OR polypeptide is accomplished by inserting an OR cDNA into a eucaryotic or procaryotic expression vector, of which many are known in the art, to generate an OR expression construct. The OR expression construct is introduced into an appropriate
30 host cell in which the OR sequences are expressed (by transcription and translation) and optionally secreted, and the expressed OR polypeptide is obtained from the cell growth medium and/or from cell lysates.

A number of expression vectors are known in the art. Prokaryotic expression vectors include, but are not limited to, T7 RNA polymerase/T7 promoter-based vectors, bacteriophage λ -based vectors and various types of fusion vectors. Fusion vectors include, but are not limited to, lacZ and trpE fusion vectors, maltose binding protein fusion vectors, glutathione-S-transferase fusion vectors, and thioredoxin fusion vectors. Baculovirus-based vectors are used for expression in insect cell systems. Expression in mammalian cells (such as HEK, COS and CHO cells) utilizes vectors containing a mammalian origin of replication (such as, for example, a SV40 origin), an efficient promoter (optionally including one or more enhancer sequences), mRNA processing signals (e.g., splice sites and polyadenylation sites), one or more selectable markers, and optionally a prokaryotic replicon to allow propagation and manipulation of the construct in prokaryotic cells. Alternatively, expression in mammalian cells is achieved through the use of any of a number of mammalian viral vectors including, but not limited to, retroviruses, lentiviruses, Semliki Forest viruses, vaccinia viruses, adenoviruses and adeno-associated viruses.

Vectors containing the polynucleotides of interest can be introduced into the host cell by any of a number of appropriate means, including electroporation, direct injection, transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; and infection (where the vector is an infectious agent, such as a virus). The choice of means of introducing vectors or polynucleotides encoding polypeptides involved in olfactory sensation will often depend on the host cell, as will be well known to those of skill in the art.

Host cells transformed with polynucleotides encoding polypeptides involved in olfactory sensation

Another embodiment of this invention are host cells transformed with (i.e., comprising) polynucleotides encoding polypeptides involved in olfactory sensation, and/or vectors having polynucleotide(s) sequences encoding polypeptides involved in olfactory sensation, as described above. Both prokaryotic and eukaryotic host cells may be used. Prokaryotic hosts include bacterial cells, for example *E. coli*, *B. subtilis*, and mycobacteria. Among eukaryotic hosts are yeast, insect, avian, plant and mammalian cells. Host systems are known in the art and need not be described in detail herein.

The host cells of this invention can be used, *inter alia*, as repositories of polynucleotides encoding polypeptides involved in olfactory sensation, and/or vehicles for

production of polynucleotides encoding polypeptides involved in olfactory sensation, and/or polypeptides involved in olfactory sensation . They may also be used as vehicles for *in vivo* delivery of polypeptides involved in olfactory sensation .

5 ***Uses for and methods using polynucleotides encoding polypeptides involved in olfactory sensation***

To determine whether a vector containing polynucleotides is capable of expressing in eukaryotic cells, cells such as, for example, COS-7 (primate origin), CHO (rodent origin), HEK-293 (human origin), or HeLa (human origin) cells can be transfected with the vector.

- 10 Expression of a polypeptide(s) encoded by the vector is then determined by, for example, RIA, ELISA, immunofluorescence of fixed cells, or western blotting of cell lysate using an antibody as a probe. Antibodies can be obtained using, as immunogen, peptide sequences synthesized from the protein sequences encoded by the known polynucleotide sequence. Polypeptides can be purified by, for example, phase partitioning, affinity methods, gel filtration and ion
- 15 exchange, as well as additional methods known by those skilled in the art. Further characterization of the expressed polypeptide can be achieved by purification of the polypeptide using techniques known in the art.

Polypeptides involved in olfactory sensation

- 20 The present invention encompasses polypeptides involved in olfactory sensation. Expression of said polypeptides is localized in the olfactory neurons located in the olfactory epithelium, as described earlier. The polypeptides may comprise any novel sequence encoded by a nucleotide sequence as depicted in SEQ ID NO:1 through SEQ ID NO:73 and SEQ ID NO:111 through SEQ ID NO:152.

- 25 The invention includes modifications to polypeptides involved in olfactory sensation including functionally equivalent fragments of the polypeptides involved in olfactory sensation which do not significantly affect their properties and variants which may have enhanced or decreased activity. Collectively, these modifications may be termed "analogs" of or a fragment of polypeptides involved in olfactory sensation. Modification of polypeptides is routine practice in
- 30 the art and need not be described in detail herein. Examples of modified polypeptides include polypeptides with conservative substitutions of amino acid residues, one or more deletions or additions of amino acids which do not significantly deleteriously change the functional activity, or use of chemical analogs. Amino acid residues which can be conservatively substituted for

one another include but are not limited to: glycine/alanine; valine/isoleucine/leucine; asparagine/glutamine; aspartic acid/glutamic acid; serine/threonine; lysine/arginine; and phenylalanine/tyrosine. Such conservative substitutions are known in the art, and preferably, the amino acid substitutions would be such that the substituted amino acid would possess
5 similar chemical properties as that of the original amino acid. These polypeptides also include glycosylated and non-glycosylated polypeptides, as well as polypeptides with other post-translational modifications, such as, for example, glycosylation with different sugars, acetylation, and phosphorylation. Amino acid modifications can range from changing or modifying one or more amino acids to complete redesign of a region. Other methods of
10 modification include using coupling techniques known in the art, including, but not limited to, enzymatic means, oxidative substitution and chelation. Modified polypeptides involved in olfactory sensation are made using established procedures in the art.

The invention also encompasses fusion proteins comprising one or more polypeptides involved in olfactory sensation. For purposes of this invention, an fusion protein contains one
15 or more polypeptides involved in olfactory sensation and another amino acid sequence to which it is not attached in the native molecule, for example, a heterologous sequence or a homologous sequence from another region. Useful heterologous sequences include, but are not limited to, sequences that provide for secretion from a host cell, intracellular trafficking, and stability/degradation. Other useful heterologous sequences are ones which facilitate
20 purification. Examples of such sequences are known in the art and include those encoding epitopes such as Myc, HA (derived from influenza virus hemagglutinin), His-6, or FLAG. Other heterologous sequences that facilitate purification are derived from proteins such as glutathione S-transferase (GST), maltose-binding protein (MBP), or the Fc portion of immunoglobulin.

25

Preparation of polypeptides involved in olfactory sensation

The polypeptides of this invention can be made by procedures known in the art. The polypeptides can be produced by recombinant methods (i.e., single or fusion polypeptides) or by chemical synthesis. Polypeptides, especially shorter polypeptides up to about 50 amino
30 acids, are conveniently made by chemical synthesis. Methods of chemical synthesis are known in the art and are commercially available. For example, a polypeptide can be produced by an automated polypeptide synthesizer employing the solid phase method. Polypeptides can also be made by chemical synthesis using techniques known in the art.

Polypeptides can also be made by expression systems, using recombinant methods. The availability of polynucleotides encoding polypeptides permits the construction of expression vectors encoding intact (i.e., native) polypeptide, functional equivalents and functional fragments thereof, modified forms or recombinant forms. A polynucleotide
5 encoding the desired polypeptide, or a fusion protein, can be ligated into an expression vector suitable for any convenient host. Both eukaryotic and prokaryotic host systems can be used. The polypeptide is then isolated from lysed cells or from the culture medium and purified to the extent needed for its intended use. Purification or isolation of the polypeptides expressed in host systems can be accomplished by any method known in the art (e.g. partitioning exclusion,
10 ion exchange chromatograph, gel filtration, etc.). Other controlling transcription or translation segments, such as signal sequences that direct the polypeptide to a specific cell compartment (i.e., for secretion), can also be used. Examples of prokaryotic host cells are known in the art and include, for example, *E. coli* and *B. subtilis*. Examples of eukaryotic host cells are known in the art and include yeast, avian, insect, plant, and animal cells such as COS7, HeLa, CHO,
15 HEK-293 and other mammalian cells.

Alternatively, in vitro expression systems may also be used to produce polypeptides involved in olfactory sensation. A plasmid containing a polynucleotide encoding polypeptides involved in olfactory sensation, under the control of an appropriate promoter, can be transcribed and the resultant RNA translated in vitro through the use of commercially
20 available reagents. Such methods can be used to produce relatively pure samples of the polypeptide and are known in the art.

Preferably, the polypeptides are at least partially purified from other cellular constituents. In one embodiment, the polypeptides are at least 70%, more preferably at least 80%, even more preferably at least 90% or most preferably at least 95% pure. In this context,
25 purity can be calculated as a weight percent of the total protein content of the preparation. More highly purified polypeptides may also be obtained and are encompassed by the present invention. Methods of protein purification are known in the art and are not described in detail herein. For membrane-bound proteins, the lipid content of the preparation, which is required to maintain the structure and function of the protein, is excluded from the purity calculation. That
30 is, if a preparation weighing 10 mg has 5 mg lipid, 4 mg of desired protein, and 1 mg of undesired proteins, the purity is calculated as 80% (desired protein content divided by total protein content). Preparations of biological or synthetic molecules suitable for maintaining structure and function of membrane proteins are described in Etemadi AH (1985) *Adv Lipid*

Res 1985;21:281-428; Villalobo A (1990) *Biochimica Et Biophysica Acta*, 1017(1):1-48; Montal M (1987) *Journal Of Membrane Biology* 98(2): 101-115; Scotto AW et al. (1987) *Biochemistry* 26(3): 833-839; Jain MK and Zakim D (1987) *Biochimica Et Biophysica Acta* 906(1): 33-68; Czerski L and Sanders CR (2000) *Anal Biochem* 284(2):327-33 (lipid-detergent mixtures or "bicelles"); Hrafnisdottir S and Menon AK (2000) *J Bacteriol* 182(15):4198-206 (proteoliposomes); Puu G et al. (2000) *Biosens Bioelectron* 15(1-2):31-41 (protein-lipid preparations on solid surfaces); Schafmeister CE et al. (1993) *Science* 262(5134):734-8 ("peptitergents").

10 *Uses of polypeptides involved in olfactory sensation*

The polypeptides of this invention have a variety of uses. They can be used, for example, to screen odorant ligands in order to determine the scent representations, scent profiles or scent fingerprints of particular odorant molecules and further to characterize the effect of functional groups and chemical characteristics on perceived smell. Methods for screening odorant compounds using odorant receptors in neuronal cells are known in the art (Firestein et al., WO 98/50081; Duchamp-Viret *et al.*, *Science* 1999, 284 2171-2174; Sato *et al.*, *J. Neurophys.* 1994 72 2980-2989; Malnic *et al.*, *Cell* 1999 96 713-723; Zhao *et al.*, *Science* 1998 279, 237-242). There are also methods which can be employed to screen odorant compounds which do not require neuronal cells and are known in the art (Kauvar et al., U. S. Pat. No. 5,798,275; Kiefer *et al.*, *Biochemistry* 1996 35 16077-16084; Krautwurst *et al.*, *Cell* 1998 95 917-926).

Analysis of the scent can be performed in a number of ways. Various embodiments of the scent analysis system are presented. Examples of how these embodiments might operate are also presented, although it should be emphasized that the invention is not limited by any particular theory of olfactory perception or scent analysis.

Olfactory Space

The sensory subsystem comprises a series of olfactory receptors, which selectively bind with the chemical component(s) making up the scent. The scent can be characterized in terms of which of the approximately 1,000 olfactory receptors the scent component(s) bind to, and the strength of the interaction of the component(s) with those receptors. Each olfactory receptor can be considered an orthogonal basis vector; the entire set of olfactory receptors can be considered a set of basis vectors spanning "olfactory space." This is analogous to vectors

pointing along the x, y, and z directions in three-dimensional space, where any point in space can be represented by a combination of the x, y, and z basis vectors (with each of the x, y, and z vectors multiplied by the appropriate scalar quantity). The intensity of interaction of a scent with an olfactory receptor determines the magnitude of the vector along that particular "axis" in olfactory space. Thus, every scent can be uniquely described by a vector representation in olfactory space.

A representation of a scent in such a manner that the scent can later be re-created is defined as scent profiling. The aforementioned vector representation is one example of a scent profile.

Primary Scents

For the purposes of this invention, a receptor primary scent component is defined as a chemical that interacts with one and only one scent receptor. A receptor complex scent component is defined as a chemical that interacts with more than one scent receptor; the receptor complex scent component can interact with each of the scent receptors to different degrees, to equal degrees, or can interact with some receptors to the same degree and others to different degrees.

Olfactory receptors are proteins which fall in the class of seven transmembrane domain G protein-coupled receptors, and are found in olfactory neurons *in vivo*. Binding of an odorant to an olfactory receptor causes second messenger systems to become activated or inhibited in the cell, leading to increased cellular production of second messenger molecules such as cyclic AMP. These second messenger systems in turn lead to the depolarization of the olfactory neuron, or other changes in the state of the neuron, which provides the signal to the nervous system that the odorant has been detected.

With a complete set of receptor primary scent components, any scent can be re-created with the knowledge to the degree to which it interacts with each olfactory receptor. The instant invention encompasses such complete sets of receptor primary scent components. Other embodiments of the invention encompass sets of receptor primary scent component chemicals which provide the ability to re-create a particularly desired subset of scents, but not necessarily all possible scents. Still more embodiments encompass sets of receptor primary scent component chemicals which provide the ability to approximate particular scents, while not necessarily exactly re-creating the interaction profile of the particular scents.

In some cases, a receptor complex scent will be an acceptable approximation to a receptor primary scent. That is, if a given receptor complex scent interacts with a first scent receptor strongly, but interacts with other scent receptors less strongly, it can be considered an approximation to a receptor primary scent component for the first receptor. Such a receptor complex scent component is described by the term receptor quasi-primary scent component. One embodiment of the invention encompasses sets of receptor quasi-primary scent component chemicals suitable for re-creating all scents. Another embodiment of the invention encompasses sets of receptor quasi-primary scent component chemicals suitable for re-creating a particularly desired subset of scents, but not necessarily all possible scents. Yet another embodiment encompasses sets of receptor quasi-primary scent component chemicals which provide the ability to approximate particular scents, while not necessarily exactly re-creating the interaction profile of the particular scents.

The identification of receptor primary or quasi-primary scent component chemicals provides the most conceptually straightforward method of re-creating scents. However, another embodiment of the invention encompasses the use of receptor complex scent components for re-creating scents. An example of such an embodiment would be re-creation of a scent that activates olfactory receptors designated OR1, OR2, OR3, OR4, OR5 and OR6 (for the sake of illustration, it is assumed that the olfactory receptors are stimulated to an equal extent). If one is in possession of two receptor complex scent component chemicals (RCSC's) where RCSC1 activates OR1 and OR5, and RCSC2 activates OR2, OR3, OR4, and OR6, then one can reproduce the original scent by mixing RCSC1 and RCSC2 to re-create the original olfactory receptor activation profile. In practice, the profiles of various receptor complex scent components will be much more complicated than the forgoing example, and components which inhibit olfactory activation as well as stimulate activation can be included in the sets. However, once receptor activation profiles of sufficient receptor complex scent components are known, computer algorithms can be utilized to create the appropriate combination of receptor complex scent components. Using vector representations of the olfactory receptor activation profiles for a set of receptor complex scent components, one can create linear combinations of such receptor complex scent components in order to represent a particular scent. For the example given above, such a vector representation would look like (1, 0, 0, 0, 1, 0) for the first receptor complex scent component and (0, 1, 1, 1, 0, 1) for the second receptor

complex scent component, while the vector representation of the scent to be re-created is (1, 1, 1, 1, 1, 1). If x_1 and x_2 are the relative proportions of the first receptor complex scent component and the second receptor complex scent component, respectively, to be combined to re-create the scent, then the problem can be represented as a series of linear equations:

$$1x_1 + 0x_2 = 1$$

$$0x_1 + 1x_2 = 1$$

$$0x_1 + 1x_2 = 1$$

$$0x_1 + 1x_2 = 1$$

$$1x_1 + 0x_2 = 1$$

$$0x_1 + 1x_2 = 1$$

and the solutions for x_1 and x_2 are $x_1 = 1$, $x_2 = 1$. Solutions to systems of linear equations have been thoroughly studied and many algorithms are available for implementation on computers, including algorithms which evaluate the accuracy of an approximate solution when an exact solution cannot be determined. (See, e.g., Dettman, J.W., *Introduction to Linear Algebra and Differential Equations*, Dover Pubs., 1986; Press W.H. et al., *Numerical Recipes in C: The Art of Scientific Computing*, 2nd ed., Cambridge University Press, 1993; Vetterling (ed.) *Numerical Recipes in C: The Art of Scientific Computing/Disk V 2.02*, Cambridge University Press, 1997.) These methods can also be used to determine whether a set of receptor complex scent components is suitable for re-creating a given scent. For example, if the scent to be recreated is represented by the vector (1, 1, 1, 1, 1, 2), there will be no solution to the resulting system of linear equations using the two receptor complex scent components in the illustration above. In this instance, one or more additional receptor scent components will need to be identified in order to be able to re-create the scent in terms of the receptor primary scent components. Alternatively, the scent represented by (1, 1, 1, 1, 1, 1) may be an acceptable approximation to the scent represented by (1, 1, 1, 1, 1, 2). Integers are used in this example for clarity, but the vectors can contain any real number representing a measured intensity; for example, (1.1, 0.997, 1.08, 1.2, 0.88888..., 2.00001) may be an acceptable approximation to the scent represented by (1, 1, 1, 1, 1, 2).

It will be readily appreciated that the choice of a complete set of receptor primary, quasi-primary, or complex scent component chemicals (capable of generating all scents) versus a partial set of receptor primary, quasi-primary, or complex scent component chemicals (capable of generating, exactly or approximately, a subset of scents) depends on the application for which scent re-creation is desired.

A special category of receptor scent components are chemicals which bind to a receptor without activating it. If these non-activating chemicals prevent chemicals which do activate the receptors from binding, the non-activating chemicals act to "turn off" those receptors. These non-activating chemicals, or receptor binding antagonists, are particularly useful in editing scents, as they can be added to a scent to attenuate or eliminate particular aspects of the scent. In the vector example above, if a particular receptor antagonist blocks OR2, OR3, and OR4, but not OR1, OR5 or OR6, then it can be represented in vector format as (0, -1, -1, -1, 0, 0). In the reproduction of (1, 1, 1, 1, 1, 2) from the vectors (1, 0, 0, 0, 1, 0) and (0, 1, 1, 1, 0, 1), the following combination can be used:

$1 \times (1, 0, 0, 0, 1, 0) + 2 \times (0, 1, 1, 1, 0, 1) + 1 \times (0, -1, -1, -1, 0, 0)$ to yield the vector (1, 1, 1, 1, 1, 2). In some instances, enough of a particular receptor binding antagonist is used to eliminate any possibility of activation by a receptor scent component, in which case the vector entry for the receptor(s) which are blocked by that antagonist contains 0 in the vector position corresponding to that receptor(s).

Perceptive primary scents are defined as scents that give a single scent perception, for example, the scent "lemon" as perceived by a human. A perceptive primary scent can be composed of one or more receptor primary scent components, one or more receptor complex scent components, or a mixture of one or more receptor primary scent components and one or more receptor complex scent components. Since perceptive primary scents are to some extent subjective, identification of perceptive primary scents can be performed by using a panel of subjects who evaluate and describe scents. A perceptive complex scent is made up of more than one perceptive primary scent. The boundaries between a perceptive primary scent and a perceptive complex scent are also to some extent subjective; for example, one person may describe a scent as "pizza," while another person may describe the same scent as "sausage, cheese and tomato sauce." That is, one person may perceive a scent as a perceptive primary scent for "pizza," while another person may perceive the same scent as a perceptive complex scent made up of several individual perceptive primary scents. In order to standardize perceptive scents, a panel of five or more, preferably ten or more, more preferably fifty or

more, still more preferably one hundred or more, people can be surveyed to label various perceptive scents. When a plurality, preferably a majority, more preferably 66 2/3 % or greater, still more preferably 95 % or greater, even more preferably 99% or greater, of the panel identifies a scent as the same scent (e.g., of a panel of 100 people, 95 describe a scent as
5 "pizza," while the other 5 describe the scent otherwise), the scent can be labeled as a perceptive scent (the perceptive scent can be primary or complex, depending on whether the panel identifies it as a single scent or a mixture of scents).

In fields where existing classification schemes already exist, the perceptive primary and complex scents can be indexed according to those schemes. For example, the SFP (Société
10 Française des Parfumeurs) has drawn up a classification system based on 5 main groups, subdivided into classes. Such a classification can be used for selecting perceptive primary scents and used as guides for combining the scents.

Selecting Chemicals for Scent Re-creation

15 A scent which has been represented as a set of basis vectors in olfactory space can in principle be re-created simply by mixing the receptor primary scent components, receptor quasi-primary scent components, or receptor complex scent components needed to interact the olfactory receptors in the same pattern as the original scent. Such an approach requires 1) a method to generate a representation of the original scent in olfactory space, and 2) suitable
20 receptor primary scent component chemicals which can be mixed in the appropriate manner.

Identification of receptor scent components can be performed by various methods. One such method assays the interaction of candidate components with each olfactory receptor. The receptors can be expressed *in vitro* and assays can be set up to monitor the interaction of various candidate components with each individual receptor. Chemicals which interact with
25 one and only one olfactory receptor are receptor primary scent components, while chemicals which interact with more than one olfactory receptor are receptor complex scent components (and can possibly be receptor quasi-primary scent components, depending on the interaction profile it displays with the olfactory receptors). Such an approach can use methods known in the art, for example those of Breer *et al.*, Ann. N. Y. Acad. Sci. (1998) 855:175-81 or Malnic *et al.*, *Cell* (1999) 96(5):713-23. Breer *et al.* expressed olfactory receptors in Sf9 cells and
30 evaluated the second-messenger response to various odorants. Malnic *et al.* isolated olfactory neurons from mice and utilized calcium imaging to study the response of the neurons to different odorants, while using RT-PCR to determine which olfactory receptor was expressed

in the neuron under study. U.S. Patent No. 5,798,275 describes a method for evaluating interaction of compounds with members of a reference panel of proteins. WO 98/50081 discloses methods for detecting particular odorant ligand specificity for particular odorant receptors in nasal epithelium tissue of mammals such as rats and mice.

5

Selection of Receptor Primary Scents by in silico Methods

An alternative method utilizes *in silico* screening techniques--that is, computer simulation methods--for selecting candidate components. Protein-ligand screening can be used to select compounds which bind to particular receptors in order to identify receptor primary
10 scent components. Examples of such programs are DOCK, AutoDock, GOLD, FlexX, LUDI, GROWMOL, and HOOK. (See Wang, J., Kollman, P.A., Kuntz I.D., "Flexible ligand docking: a multistep strategy approach," *Proteins* 36(1):1-19 (1999) and references therein.) These programs function by taking a protein structure and either matching compounds of known structure to the protein structure to determine the protein-ligand interaction, or by
15 "growing" a molecule in the active site or binding site of a protein to determine what molecule will best interact with the protein.

Olfactory receptor proteins are membrane proteins, and experimental determination of the three-dimensional structures of membrane proteins has lagged the corresponding structural determination of water-soluble proteins for various reasons. However, alternative methods for
20 constructing the three-dimensional structures of proteins are available. The primary (amino acid) sequences of many olfactory receptors are known. This information can be used to model a three-dimensional structure of a receptor protein using various algorithms and computer programs known in the art. The resulting model structure can then be used as the basis for evaluating interaction of candidate components with the receptor.

25 Alternatively, given known chemical structures which give rise to a particular odor, analysis of the structures can indicate the particular portion of the chemical structure which is responsible for the odor. This is analogous to "pharmacore analysis" used in medicinal chemistry to determine the important portion of drugs.

Methods for developing compounds which bind to receptors and other proteins of
30 known structure, and determining interactions between ligands and receptors, are described in various references. The DOCK program evaluates the fit of a ligand into a protein molecule of known structure (see Gschwend, D.A., Good, A.C. and Kuntz, I.D., "Molecular Docking Towards Drug Discovery", *J. Mol. Recognition* 9, 175-86 (1996); Kuntz, I.D., Meng, E.C., and

B.K. Shoichet, "Structure-Based Strategies For Drug Design and Discovery", *Acc. Chem. Res.* 27, 117-123 (1994); and Kuntz, I.D., "Structure-based strategies for drug design and discovery", *Science* 257, 1078-1082 (1992); see also

<http://www.cmp Pharm.ucsf.edu/kuntz/dock.html>). Using a known (or modeled) structure of an

5 olfactory receptor, DOCK can be used to screen for compounds which bind to the receptor.

The program AMBER (see Cornell, WD, Cieplak P, Bayly CI, Gould IR, Merz KM Jr, Ferguson DM, Spellmeyer DC, Fox T, Caldwell JW and Kollman PA. "A second generation force field for the simulation of proteins and nucleic acids," *Journal of the American Chemical Society* 117, 5179-5197 (1995); Computer Simulation of Biomolecular Systems, A. Wilkinson,

10 P. Weiner, W. Van Gunsteren, eds. Volume 3, p. 83-96, P. Kollman, R. Dixon, W. Cornell, T. Fox, C. Chipot and A. Pohorille; Bayly CI, Cieplak P, Cornell WD and Kollman PA. "A well-behaved electrostatic potential based method using charge restraints for deriving atomic charges - the RESP model," *Journal of Physical Chemistry* 97(40), 10269-10280 (1993);

Cornell WD, Cieplak P, Bayly CI and Kollman PA. "Application of RESP charges to calculate conformational energies, hydrogen bond energies, and free energies of solvation," *Journal of the American Chemical Society* 115(21), 9620-9631 (1993); see also

<http://www.amber.ucsf.edu/amber/amber.html>) can be used to calculate more precise

interaction energies between candidate ligands. Other examples of such methods are described in, for example, U.S. Patent No. 5,866,343, directed to determining the energetically favorable

20 binding site between two molecules; U.S. Patent No. 5,854,992, a system and method for structure-based drug design which takes into account binding free energy as it "grows" candidate molecules into a receptor binding site; and U.S. Patent No. 5,495,423, which describes a method for ligand design (principally applicable to peptidic ligands).

The foregoing methods typically depend on a known three-dimensional structure for the
25 receptor. When such a structure cannot or has not been determined experimentally, a structure can be modeled using computer algorithms. Blundell TL, Sibanda BL, Sternberg MJ, Thornton JM, "Knowledge-based prediction of protein structures and the design of novel molecules," *Nature* 326(6111):347-52 (1987); Shortle D, "Structure prediction: The state of the art," *Curr Biol* 9(6):R205-9 (1999), Morea V, Leplae R, Tramontano A, "Protein structure prediction and design," *Biotechnol Annu Rev* 4:177-214 (1998) and Onuchic JN, Luthey-Schulten Z, Wolynes PG, "Theory of protein folding: the energy landscape perspective," *Annu Rev Phys Chem* 30 48:545-600 (1997) address various methods of predicting protein structure from sequence data.

Various implementations for predicting protein structure from amino acid sequences are discussed in U.S. Patent Nos. 5,878,373 and 5,884,230.

If the structure, or even the identity, of the targeted receptor cannot be determined, alternative computational techniques can be used to generate information regarding possible
5 ligands which will interact with the receptor. Quantitative structure-activity relationships (QSAR; see Green, S.M. and Marshall, G.R., "3-D QSAR: A current perspective," *Trends Pharmacol Sci* 16:285 (1995); and 3D QSAR in Drug Design: Theory, Methods and Applications, Kubinyi, H. Ed.; Escom, Leiden.), including QSAR refinements such as comparative molecular field analysis (ComFA) (Cramer, R. D. et al. "Comparative Molecular
10 Field Analysis ComFA 1. Effect Of Shape On Binding Of Steroids To Carrier Proteins," *J. Am. Chem. Soc.* 110: 5959 (1988)); and pharmacophore mapping (Martin YC, Bures, MG, Danaher EA, DeLazzer J, Lico I, Pavlik PA, "A fast new approach to pharmacophore mapping and its application to dopaminergic and benzodiazepine agonists," *J Comput Aided Mol Des* 7(1):83-102 (1993)) have been used to design pharmacophores that can interact with the receptor. U.S.
15 Patent No. 5,699,268 provides a method for producing computer-simulated receptors which functionally mimic biological receptors; the simulated receptors are essentially abstractions of structurally useful information from compounds which are known to interact with a receptor. U.S. Patent No. 5,901,069 describes a method of automatically refining a set of chemicals using structure/activity data. U.S. Patent No. 5,862,514 describes a method of simulating
20 synthesis of compounds of desired biological activity and evaluating their activity via further simulations.

Application of structure-function relationships to classification of odors has been described by Chastrette M., Rallet E. "Structure-minty odour relationships: Suggestion of an interaction pattern," *Flavour and Fragrance Journal*, 13(1):5-18 (1998); Chastrette M., De
25 Saint Laumer J.Y., Peyraud J.F., "Adapting the structure of a neural network to extract chemical information. Application to structure-odour relationships," *SAR QSAR Environ Res* 1 (2-3):221-231 (1993), Chastrette M., "Trends in structure-odor relationships," *SAR QSAR Environ Res* 6(3-4):215-254 (1997) and Jain et al., "A shape-based machine learning tool for drug design," *J Comput Aided Mol Des* 8(6):635-652 (1994). These methods can be useful in
30 determining the "chemical distance" between odors. For example, isoamyl acetate is typically experienced as a banana-like odor, while octyl acetate is typically experienced as an orange-like odor, which gives a measure of how the chain length of the alkoxy portion of the ester influences perception.

Olfactory Receptors and Libraries of Olfactory Receptors

The olfactory receptors of the invention can be used to analyze and describe the interaction of scent odorant molecules with each receptor. This can be done individually, receptor-by-receptor and odorant molecule by odorant molecule. However, a combinatorial approach provides a much more powerful method of analyzing and describing the interaction of scent odorant molecules with olfactory receptors.

In one embodiment, the invention comprises libraries of olfactory receptors. These libraries are used to screen compositions for interaction with receptors. A composition can be a single compound (essentially a pure chemical), or a mixture of two or more compounds or chemicals. The compositions can be presented to the library in vapor form, or in solutions, typically aqueous solutions.

The method for determining the binding pattern of a composition with olfactory receptors comprises the steps of: exposing the composition to an olfactory receptor library; and determining whether the composition binds to each olfactory receptor of the library, thereby determining the overall binding pattern of the composition. While it is desirable to determine whether the composition binds to each of the olfactory receptors, in certain cases, determining the binding pattern to a subset of the receptors is suitable. Such a situation can arise if the complete pattern is not needed, or if the experiment cannot determine binding to a receptor for a particular reason. (Determining the binding to a subset is equivalent to reducing the olfactory receptor library to that subset of receptors.)

Typically, the libraries are prepared as arrays, where the position of each olfactory receptor is known on the array. The arrays can take the form of multiwell plates, solid substrates such as chips or wafers, or any other form allowing identification of the receptor location. The arrays can be prepared in order to simply assess binding, or can be prepared in order to assess degree of activation as described above, using, for example, the technique of Malnic *et al.*, *Cell* 1999 96, 713-723. Alternatively, an *in silico* array of structures can be prepared, using the known primary structure of the receptors and the modeling techniques described above.

The libraries contain at least two olfactory receptors. In increasing order of preference, the libraries contain at least 5, 10, 20, 30, 40, 50, 75, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1500, 1600, 1800, or 2000 olfactory receptors. The

receptors are presented as ordered arrays. For example, a 96-well plate can contain 96 receptor preparations. Upon exposure to a composition, the plate can be scanned, and the response of each receptor in each well can be evaluated. This leads to a 96-element vector description of the composition in terms of those 96 olfactory receptors.

5 In one embodiment, binding to the olfactory receptors is assessed. In another embodiment, the approximate binding constant of the composition to the olfactory receptors is determined. In yet another embodiment, the degree of activation of the olfactory receptor by the composition is determined. For receptor antagonists, binding will occur, but no activation will occur; the invention embraces the identification of such
10 antagonists.

 The compositions for use are varied. A set of all volatile compounds can be used. A standard set of perfumes or odorants can be used. A set of commercially used scents can be used. Sets of compounds particularly useful in the invention are disclosed in co-pending United States Patent Application Serial No. 09/620,753. However, it must be emphasized
15 that the invention is not limited to any one set or classification of compounds.

 Preferred subsets of olfactory receptor polynucleotide sequences include:

SEQ ID NOS: 163, 331, 414, 425, 672, 762, 919, and 1027;

SEQ ID NOS: 809 and 1067;

SEQ ID NO: 744;

20 SEQ ID NOS: 207, 336, 441, and 615;

SEQ ID NOS: 157, 168, 197, 221, 250, 334, 340, 412, 413, 459, 491, 618, 690,
694, 759, 760, 761, 767, 819, 860, 872, 873, 917, 936, 939, 940, 947, 952, 958, 959, 1023,
1034, 1038, 1043, and 1044;

SEQ ID NOS: 783, 785, 882, 888, 922, and 925;

25 SEQ ID NOS: 707, 748, 752, 755, 756, 790, and 997;

SEQ ID NOS: 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075,
1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, and 1084;

SEQ ID NOS: 163, 239, 331, 335, 368, 381, 385, 414, 425, 514, 572, 596, 603,
628, 638, 642, 672, 674, 689, 744, 762, 809, 835, 885, 896, 919, 920, 938, 948, 972, 999,
30 1007, 1014, and 1027;

SEQ ID NOS: 164, 173, 176, 180, 182, 184, 185, 188, 190, 194, 207, 210, 213, 214,
215, 217, 219, 220, 223, 226, 227, 229, 230, 234, 235, 240, 249, 255, 265, 270, 273, 274,

276, 277, 279, 281, 289, 291, 293, 294, 298, 302, 307, 311, 318, 319, 321, 330, 336, 339,
341, 342, 343, 348, 351, 356, 359, 361, 365, 366, 367, 368, 370, 372, 373, 374, 375, 376,
378, 379, 380, 382, 383, 384, 385, 388, 391, 392, 393, 398, 400, 401, 403, 408, 420, 423,
427, 428, 431, 434, 435, 438, 439, 440, 441, 447, 448, 450, 455, 458, 464, 465, 468, 471,
5 473, 474, 475, 478, 479, 481, 482, 484, 485, 492, 494, 499, 502, 508, 511, 512, 513, 515,
526, 532, 534, 541, 543, 545, 546, 550, 552, 553, 557, 558, 560, 563, 564, 568, 572, 576,
582, 583, 584, 585, 586, 588, 599, 600, 605, 606, 607, 608, 609, 610, 615, 620, 621, 631,
632, 636, 638, 640, 642, 645, 648, 650, 651, 652, 654, 656, 657, 661, 662, 664, 668, 679,
680, 686, 687, 689, 691, 696, 699, 700, 702, 706, 713, 720, 721, 723, 729, 734, 738, 745,
10 768, 772, 773, 775, 791, 798, 799, 823, 857, 898, 900, 901, 903, 914, 931, 933, 937, 941,
945, 948, 956, 965, 969, 983, 992, 993, 994, 999, 1003, 1005, 1009, 1010, 1011, 1019,
1028, 1035, 1037, 1052, 1061, 1062, and 1063

SEQ ID NOS: 157, 161, 163, 168, 197, 200, 205, 218, 221, 242, 250, 331, 334,
340, 412, 413, 414, 419, 425, 452, 453, 454, 456, 459, 462, 491, 591, 618, 622, 663, 665,
15 667, 670, 672, 690, 694, 695, 709, 759, 760, 761, 762, 767, 819, 820, 822, 826, 832, 846,
847, 860, 872, 873, 877, 881, 887, 908, 911, 913, 917, 919, 921, 936, 939, 940, 942, 944,
947, 951, 952, 955, 958, 959, 960, 964, 975, 977, 979, 986, 1023, 1027, 1034, 1038, 1043,
1044, 1049, and 1051;

SEQ ID NOS: 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 164, 165, 166,
20 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184,
185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202,
203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220,
221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238,
240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257,
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15 668, 669, 670, 671, 673, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687,
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707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724,
725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742,
743, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761,
20 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780,
781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798,
799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 810, 811, 812, 813, 814, 815, 816, 817,
818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 836,
837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854,
25 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872,
873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 886, 887, 888, 889, 890, 891,
892, 893, 894, 895, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910,
911, 912, 913, 914, 915, 916, 917, 918, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930,
931, 932, 933, 934, 935, 936, 937, 939, 940, 941, 942, 943, 944, 945, 946, 947, 949, 950,
30 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968,
969, 970, 971, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987,
988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 1000, 1001, 1002, 1003, 1004, 1005,

1006, 1008, 1009, 1010, 1011, 1012, 1013, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, and 1064;

5 and any and all combinations of the foregoing sets.

The polypeptide translation products of those polynucleotide sequences form sets of preferred olfactory receptor polypeptides, as well as any and all combinations of those polypeptide sets. The preferred sets of polypeptide translation products, and any and all combinations thereof, are also preferred sets for use as libraries of olfactory receptors for
10 scent analysis.

Scent Fingerprinting

It will be appreciated that in many instances, analysis of a scent (whether in terms of
15 receptor primary scent components, receptor quasi-primary scent components, receptor complex scent components, or other scent representations) is of great utility in and of itself, in addition to the utility of that analysis in scent re-creation. Thus, another embodiment of the invention encompasses "scent fingerprinting," which comprises analysis of a scent profile when re-creation of that scent may not be necessary or desirable. The distinction between scent
20 profiling, as defined above, and scent fingerprinting, as defined here, is that scent profiling is a representation of a scent relative to a mammalian olfactory system in such a manner as to provide useful information about the interaction of the scent with that olfactory system, such as sufficient information to enable re-creation of the scent from receptor primary scent components. In contrast, scent fingerprinting can, but does not necessarily, provide such
25 information.

Various applications and examples of scent fingerprinting can include, but are not limited to, the following illustrative situations. Natural gas is widely used as a heating and fuel supply, but is in itself odorless. Utility companies routinely add small amounts of odorants such as mercaptans to allow detection of natural gas leaks in households. Should a leak occur
30 at an unattended site, however, potentially dangerous quantities of natural gas can accumulate. In such areas, a device which can recognize odorants would be useful.

Another use of scent fingerprinting is quality control of a manufacturing process. Many food items, such as freshly-baked bread and pastries, sauces, and cheeses, have distinct

odors. A manufacturer can record a scent fingerprint for a given food item, e.g. spaghetti sauce for packaging in jars. The quality of the product can then be monitored at various stages in manufacture and storage, and deviations from the established scent fingerprint can be used to alert the manufacturer to problems in manufacture or storage. Quality control scent fingerprints
5 are not limited to food items, but can be used in any circumstance where a volatile component of an item of manufacture can be used as a quality control indicator, e.g., perfume, deodorants, solvent mixtures, etc.

While scent fingerprints need not be meaningful in terms of a mammalian olfactory system, it will be readily appreciated that a scent profile, which does represent a scent in a
10 manner relevant to an olfactory system, is a special type of scent fingerprint. Additionally, the response of a device which yields a scent fingerprint of an odor (such as the "artificial nose" described in U.S. Pat. Nos. 5,571,401, 5,698,089, 5,788,833, 5,891,398 and 5,911,872) can be calibrated against the response of a mammalian olfactory system in order to transform the scent fingerprint generated by the device into a true scent profile which can be utilized to re-create an
15 odor using receptor primary scent components, receptor quasi-primary scent components, or receptor complex scent components. The invention encompasses such data transformations.

Scent Editing

Representation of a scent as a scent profile provides the capability of editing the scent.
20 A scent profile which represents a scent in terms of perceptive primary scent components is the most straightforward representation to edit. An example is the perceptive complex primary scent of "burned pizza" comprised of perceptive primary scent components of sausage, cheese, tomato sauce, and burned dough. In order to edit the scent to provide a more pleasant re-creation, the perceptive primary scent component of burned dough would simply be eliminated.

25 Other scent profiles can be edited using a knowledge of the perception of a particular components. Using our six-receptor example, suppose that the (1, 0, 0, 0, 1, 0) receptor complex scent component is known to provide an unpleasant aspect of the scent, while the (0, 1, 1, 1, 0, 1) component is known to provide the pleasant aspect of the scent. The first complex scent component can be omitted from the edited scent profile, leaving (0, 1, 1, 1, 0, 1)
30 as the edited scent profile. (This would also alter the index values for scent re-creation, from 1 and 1, to 0 and 1.) More complex editing situations can be manipulated using computer algorithms as discussed above.

Individual scent components can be omitted, added, weakened, or intensified, and different scent components can be adjusted in different manners or degrees, depending on the desired result. The editing can be done interactively, with each edited scent emitted by the emitter module for evaluation by the user, or can be done automatically, with
 5 removal/weakening or addition/intensifying of particular components specified in advance, on either an absolute scale or relative to other components.

The following examples are presented to illustrate, but not to limit, the invention.

EXAMPLES

10 **Example 1: Isolation of human olfactory receptor cDNAs**

Total RNA was extracted from human olfactory epithelium and polyA⁺ RNA was obtained by oligo-dT selection. This RNA served as template for cDNA synthesis using reagents from the SMART cDNA Library construction kit (Clontech K1051-1; Palo Alto, CA). The Superscript IITM reverse transcriptase (Life Technologies, Gaithersburg, MD)
 15 was used for first-strand synthesis.

Double-stranded cDNA was passed through a Chroma-Spin⁺ STE-100 column (Clontech) to remove unreacted primers and cDNA fragments shorter than 100 nucleotides. The olfactory epithelial cDNA population was then subjected to amplification using primers homologous to conserved regions in GPCRs. The first primer set was homologous
 20 to transmembrane segment 2 (TM2) and the second set was homologous to TM 7.5. The TM2 primer set contained 32 oligonucleotides, representing all possible nucleotide sequences capable of encoding the TM2 amino acid sequence motif P-M-Y-F/L-F/Y-F/L, and designed to be non-degenerate at their 3' ends. Sequences of the TM2 primers are as follows:

25

	CCN ATG TAY TTN CTC CTA	SEQ ID NO: 74
	CCN ATG TAY TTN CTC CTC	SEQ ID NO: 75
	CCN ATG TAY TTN CTC CTG	SEQ ID NO: 76
	CCN ATG TAY TTN CTC CTT	SEQ ID NO: 77
30	CCN ATG TAY TTN CTC TTA	SEQ ID NO: 78
	CCN ATG TAY TTN CTC TTC	SEQ ID NO: 79
	CCN ATG TAY TTN CTC TTG	SEQ ID NO: 80
	CCN ATG TAY TTN CTC TTT	SEQ ID NO: 81
	CCN ATG TAY TTN CTT CTA	SEQ ID NO: 82
35	CCN ATG TAY TTN CTT CTC	SEQ ID NO: 83
	CCN ATG TAY TTN CTT CTG	SEQ ID NO: 84

	CCN ATG TAY TTN CTT CTT	SEQ ID NO: 85
	CCN ATG TAY TTN CTT TTA	SEQ ID NO: 86
	CCN ATG TAY TTN CTT TTC	SEQ ID NO: 87
	CCN ATG TAY TTN CTT TTG	SEQ ID NO: 88
5	CCN ATG TAY TTN CTT TTT	SEQ ID NO: 89
	CCN ATG TAY TTN TTC CTA	SEQ ID NO: 90
	CCN ATG TAY TTN TTC CTC	SEQ ID NO: 91
	CCN ATG TAY TTN TTC CTG	SEQ ID NO: 92
	CCN ATG TAY TTN TTC CTT	SEQ ID NO: 93
10	CCN ATG TAY TTN TTC TTA	SEQ ID NO: 94
	CCN ATG TAY TTN TTC TTC	SEQ ID NO: 95
	CCN ATG TAY TTN TTC TTG	SEQ ID NO: 96
	CCN ATG TAY TTN TTC TTT	SEQ ID NO: 97
	CCN ATG TAY TTN TTT CTA	SEQ ID NO: 98
15	CCN ATG TAY TTN TTT CTC	SEQ ID NO: 99
	CCN ATG TAY TTN TTT CTG	SEQ ID NO: 100
	CCN ATG TAY TTN TTT CTT	SEQ ID NO: 101
	CCN ATG TAY TTN TTT TTA	SEQ ID NO: 102
	CCN ATG TAY TTN TTT TTC	SEQ ID NO: 103
20	CCN ATG TAY TTN TTT TTG	SEQ ID NO: 104
	CCN ATG TAY TTN TTT TTT	SEQ ID NO: 105

The TM7.5 primer set was designed to contain the reverse complement of all sequences capable of encoding the TM7.5 amino acid sequence motif P-F/L/I/V-I/V-F/Y-

25 S/T-L. The sequences of the TM7.5 primers are as follows:

	YYTNGTNYTNRYNCYGATANATNATNGGRTT	SEQ ID NO: 106
	YTRTTNCKNAGNWRTANATRAANGGRTT	SEQ ID NO: 107
	TCYTTRTTNCKNAGNGWRTANAYNASNGGRTT	SEQ ID NO: 108
30	TCNTSRTTNCKNARNsARTANATNATNGGRTT	SEQ ID NO: 109
	RTTNCKNARNsWRTANATRAANGGRTT	SEQ ID NO: 110

Reagents and enzymes for amplification were from the Advantage cDNA amplification kit (Clontech). A primary amplification reaction was constructed as follows:

35	5 µl olfactory epithelial cDNA (10-20 µg/ml)
	5 µl 10X PCR reaction buffer (Clontech)
	1 µl TM2 primer set (10 µM)
	1 µl TM7.5 primer set (10 µM)
	1 µl dNTP mix (10 mM each dATP, dCTP, dGTP, dTTP)
40	36 µl PCR-grade H ₂ O
	1 µl Advantage polymerase mix (Clontech)

Amplification was conducted in a PE 480 thermal cycler, using 28 cycles of 95°C for 15 sec, 45°C for 45 sec and 72°C for 2 min. After cycling, the amplification mixture was treated for 1 hour at 37°C with 10 Units of BspEI and 10 Units of PstI restriction enzymes, to degrade non-specific amplification products.

5 The primary amplification products were size-fractionated by agarose gel electrophoresis, and amplification products having a length between 600 and 800 base pairs were selected for secondary amplification.

10 The secondary amplification reaction was conducted identically to the primary amplification reaction, except that the size-selected primary amplification product was used as template. Secondary amplification reactions containing products which generated a specific gel band of between 600 and 800 base pairs were extracted once with phenol/chloroform and once with chloroform, and nucleic acids were precipitated from the reactions by addition of 0.1 volume of 3M NaOAc (pH 4.8), 20 µg glycogen, and 1.5 volumes of cold 95% ethanol. The precipitate was collected by centrifugation, dried and
15 resuspended in 15 µl distilled water. After the precipitate dissolved, 3 µl loading dye was added, and the sample was subjected to electrophoresis on a 1.0% low-melting agarose gel containing ethidium bromide. Electrophoresis was conducted at 60V for approximately 40 min, with a 1 kb marker in adjoining lanes.

20 Following electrophoresis, the gel was illuminated with long-wavelength ultraviolet light, and the band was excised from the gel. The gel slice was placed in a 0.5 ml tube, and the tube was heated at 68°C for 15 min. The temperature of the tube was then equilibrated at 45°C. (This is conveniently accomplished in a thermal cycler.) AgarACE™ (Promega) was then added to the tubes, according to the manufacturer's instructions, and incubation at 45°C was continued for 15 min. As a general rule, 2 µl of enzyme per 50 µl of gel slice is
25 adequate. Following AgarACE™ digestion, the digestion mixture was extracted with phenol/chloroform according to the manufacturer's instructions, and nucleic acids were precipitated by addition of 0.1 volume of 3M NaOAc (pH 4.8), 20 µg glycogen, and 1.5 volumes of cold 95% ethanol. The precipitate was collected by centrifugation, dried and resuspended in 5 µl distilled water.

30 Gel-purified amplification products were cloned using the TOPO XL PCR Cloning Kit (Invitrogen) according to the manufacturer's instructions. After cloning, individual

colonies were selected at random for nucleotide sequence analysis of the inserts, using procedures for sequence determination that are well-known to those of skill in the art.

Example 2: Use of olfactory receptor polypeptides for screening

5 Components of a scent are identified by determining the interaction between one or more potential odorant molecules and one or more OR polypeptides. For example, if a known original scent involves binding to a particular set of ORs, any subsequent set of molecules which bind to that same set of ORs and stimulate or inhibit the response of the ORs to the same extent as the original scent is capable of re-creating that original scent. If
10 each of the subsequent set of molecules interacts with one and only one OR, then the set of molecules is composed of receptor primary scent components. In similar fashion, scents which involve binding of multiple ORs can be recreated by identifying a molecule, or combination of molecules, which binds to that particular set of ORs.

 Binding of molecules to ORs is determined by a number of methods that are well-
15 known in the art including, but not limited to, in vitro and in silico methods as described herein. Binding of molecules to ORs can also be determined or approximated by using quantitative structure-activity relationships as described herein.

Example 3: Identification of agonists and antagonists of olfactory receptors

20 Interaction of an odorant with a particular OR embedded in the membrane of an olfactory neuron will activate a signaling cascade within the neuron, ultimately resulting in the perception of a particular smell. A molecule, produced for example by combinatorial chemistry, which activates a similar or identical signaling cascade, will induce the perception of the same smell. Such a molecule would be considered a OR agonist. An OR
25 agonist, once identified, can be used as a probe to identify additional agonists, as well as antagonists, of that particular OR.

 Assays for the activation and the end product(s) of signaling cascades are known in the art. For example, direct Ca^{++} imaging can be employed, using either dye -labeled Ca^{++} or dyes that are sensitive to Ca^{++} concentration. Such dyes, and techniques for their use,
30 are available from, for example, Molecular Dynamics (Sunnyvale, CA) and Molecular Probes (Eugene, OR).

Because ORs are transmembrane proteins, identification of agonists and/or antagonists for a particular OR require that the OR is present either in a living cell or in a membrane preparation.

In one embodiment of a method for the determination of OR agonists or
5 antagonists, a known OR agonist is labeled *in situ*, or is resynthesized with an attached label, and is bound to an OR. The effect of various test molecules on the binding of the labeled OR agonist is then determined. Labeling of an OR agonist is accomplished by any of a number of methods that are known to those of skill in the art including, but not limited to, various fluorescent labels (for example, chemical fluorochromes or green fluorescent
10 protein). Binding of the OR agonist is measured by any of a number of competitive binding assays, as are known in the art. A test molecule that displaces the agonist from the OR (*i.e.*, reduces the binding of the agonist) is identified as a candidate agonist or antagonist of the particular OR. In a subsequent experiment, the candidate molecule is bound to the OR, and the effect on the signaling cascade induced by the original agonist is
15 determined. A similar of higher level of activation is indicative of an agonist; while a reduced level of activation of the signaling cascade reflects the action of an antagonist.

In additional embodiments of the displacement assay, an unlabeled agonist is used, and its degree of binding is determined by mass spectrometry. *See*, for example, U.S. Patent No. 5,894,063; U.S. Patent No. 5,719,060; and Wei *et al.* (1999) *Nature* 399:243-
20 246.

In another embodiment, fluorescent microparticles ("beads"), which can be separated by flow cytometry, are used to identify OR agonists and antagonists. Such beads are available, for example, from Luminex (Austin, TX). Multiple different ORs are attached to the beads, wherein each distinct color of bead is associated with a particular
25 OR. The collection of beads, containing different ORs, is exposed to a test molecule or a collection of test molecules, such as can be synthesized by combinatorial chemistry, and binding of the test molecule(s) is determined, for example, by use of a labeled ligand of the test molecule(s). The beads are sorted according to their color by flow cytometry. Correlation of test molecule binding with bead color allows the determination of test
30 molecules capable of binding to the OR. Agonist or antagonist function of an OR binding molecule is determined by methods described *supra*.

Example 4: Summary of search parameters for homology searches

Step 1: (masking) rempolyatmask raw sequence on -NONE- [?] with remAT_moderate (15) . Continue to step 2.

5 Step 2: (masking) mask masked sequence from step 1 on RepBase [N] with mask_moderate (85) . Continue to step 3.

Step 3: (masking) mask masked sequence from step 2 on VecBase [N] with mask_moderate (85) . Continue to step 4.

Step 4: blastn masked sequence from step 3 on NR-Nuc [N] with blastn_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 5. Otherwise, stop.

10 Step 5: blastx masked sequence from step 3 on NR-Pro [P] with blastx_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 6. Otherwise, stop.

Step 6: blastn masked sequence from step 3 on GB_CurAwareness-Nuc [N] with blastn_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 7. Otherwise, stop.

15 Step 7: blastx masked sequence from step 3 on GB_CurAwareness-Pro [P] with blastx_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 8. Otherwise, stop.

Step 8: tblastx masked sequence from step 3 on NR-Nuc [N] with tblastx_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 9. Otherwise, stop.

20 Step 9: blastn masked sequence from step 3 on EST [N] with blastn_10_hits (V=10 B=10) . If the P/Z score is $> 1.0E-50$, or no hits are found go to step 10. Otherwise, stop.

Step 10: blastn masked sequence from step 3 on STS [N] with blastn_10_hits (V=10 B=10) . Stop.

Example 5: Summary of search results

Step	Program	Databases	Score	Sequences By Best Hit's				No Hits	Run	Not Finished	Not Run	
				Score								
1	rempolyat mask	NONE-[P]	P/Z/ E	0	> 1.0 >=	0	>= 1.0 >	0	74	74	0	0
2	mask	RepBase[N]	P/Z/ E	0	> 1.0 >=	0	>= 1.0 >	0	74	74	0	0
3	mask	VecBase[N]	P/Z/ E	0	> 1.0 >=	0	>= 1.0 >	0	74	74	0	0
4	blastn	NR-Nuc[N]	P/Z/ E	46	< 1.0E-20 <=	28		0	74	0		0
5	blastx	NR-Pro[P]	P/Z/ E	16	< 1.0E-20 <=	34		0	50	0		24
6	blastn	GB_CurAwareness-Nuc[N]	P/Z/ E	17	< 1.0E-20 <=	31		0	48	0		26
7	blastx	GB_CurAwareness-Pro[P]	P/Z/ E	13	< 1.0E-20 <=	28		2	43	0		31
8	tblastx	NR-Nuc[N]	P/Z/ E	14	< 1.0E-20 <=	29		0	43	0		31
9	blastn	EST[N]	P/Z/ E	10	< 1.0E-20 <=	33		0	43	0		31
10	blastn	STS[N]	P/Z/ E	5	< 1.0E-20 <=	33		0	38			

5

Example 6. Datamining and analysis from GenBank

Datamining. A datamining pipeline was built to detect all available OR-like sequences in the public databases and to update the results as new database versions are released. tblastn (Altschul et al., 1997) was used to compare amino acid query sequences to the non-redundant version of GenBank (partitions nt, htg and est_human, all updated to August 6th, 2000), with a non-stringent expectation value cutoff of 1e-4. The queries used included 96 curated OR sequences representing all known families (SEQ ID NO:2651 through SEQ ID NO:2747) and 249 additional HORDE entries (SEQ ID NO:2402 through SEQ ID NO:2650). In a second round 105 newly mined mouse genes (SEQ ID NO:2296 through SEQ ID NO:2401) and 344 newly mined human genes (SEQ ID NO:2009 through SEQ ID NO:2295) were used as additional queries (all datasets are available

electronically). All resulting database entries were catalogued by species and subdivided into four types: mRNA, EST, DNA and genomic, the latter including entries annotated with keyword HTGS_PHASE1-3, or with length at least 10 kb. Low-pass genomic sampling sequences were ignored (keyword HTGS_PHASE0). In addition, a set of 132 olfactory sequence tag (OST) sequences was used. All sequences used were split into contigs according to annotation or, where unavailable, according to runs of at least 50 Ns. All resulting contigs were analyzed for interspersed repeats using RepeatMasker (Smit and Green, 1997). Subcontigs were defined as segments between interspersed repeats, ignoring simple repeats and low-complexity regions.

10 *Localization of genomic clones.* The University of Santa Cruz (UCSC) Working Draft Sequence ("golden path", <http://genome.ucsc.edu>) presents a first tentative assembly of the finished and draft human genomic sequence based on the WUSTL clone map (<http://genome.wustl.edu/gsc>). The "golden path" data was used to assign a coordinate to each finished or unfinished genomic clone, in Mb from the p telomere. In parallel, the
15 Unified DataBase (UDB) was used to assign similar Mb coordinates to the clones, based on their marker contents (Chalifa-Caspi et al., 1998). The two maps are largely colinear, and were integrated based on the coordinates of clones that could be localized in both. Clones for which no coordinate could be obtained by either method were assigned a chromosome according to UDB, by sequence similarity to another mapped clone, by annotation, or by e-
20 PCR (Schuler, 1997).

Detection of OR sequences. Each subcontig was compared using FASTY (Pearson et al., 1997) to a curated set of OR protein sequences from several species, yielding a conceptual translation product. The possibility of a pseudogene being disrupted by the insertion of interspersed repeats was taken into account, with the two or more resulting
25 parts being therefore located in different subcontigs. Such compatible candidate sequences were automatically joined into a combined reconstructed pseudogene. Whenever possible, all resulting sequences were trimmed or extended to use a suitable ATG codon for initiation and to end at a stop codon, but avoiding those stop codons that yield products shorter than 275 amino acids. The sequences were finally split into OR or non-OR by comparing them
30 to previously recognized OR sequences and to a non-redundant database of non-OR GPCRs which we extracted from Swiss-Prot. To be automatically classified as an OR, a

new sequence has to be at least 40% identical over at least 100 amino acids to another OR. A more stringent cutoff (50%) was required for shorter sequences.

Definition of OR genes. A given gene could be represented in more than one overlapping genomic clone. Such redundancy was removed by considering two sequences
 5 as representing the same gene, if they are in the same chromosome, located in clones less than 300 kb apart and at least 99% identical at the nucleotide level. An exception to this rule is when two genes coappear in the same clone, in which case they were considered to be distinct genes. Sequences localized to a chromosome but without a coordinate were only compared to other sequences within that chromosome, and finally those sequences
 10 lacking a chromosomal assignment were compared to the rest, applying only the criterion of sequence similarity. For each resulting gene with more than one constituent sequence, a consensus nucleotide sequence was created after multiple alignment by ClustalW (Higgins et al., 1996) using the fast comparison parameter. This was followed by conceptual translation and end trimming to suitable start and stop codons, as above. Genes with length
 15 at least 275 amino acids without frame disruptions (frameshifts, in-frame stop codons or disrupting interspersed repeats) were considered to be full-length and apparently intact. For partial sequences without frame disruptions no statement could be made on their apparent functionality, except when the partial sequences were observed in the genome as such, in which case they were considered to be pseudogenes. Finally, each OR gene was
 20 assigned a family and subfamily by amino acid sequence similarity to previously classified OR genes.

The references cited in this example are: Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhang, J., Zhang, Z., Miller, W. and Lipman, D. J. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* 25:
 25 3389-402; Chalifa-Caspi, V., Prilusky, J. and Lancet, D. (1998) The Unified Database. Weizmann Institute of Science, Bioinformatics Unit and Genome Center (Rehovot, Israel). World Wide Web URL: bioinformatics.weizmann.ac.il/udb; Higgins, D. G., Thompson, J. D. and Gibson, T. J. (1996) Using CLUSTAL for multiple sequence alignments. *Methods Enzymol* 266: 383-402; Pearson, W. R., Wood, T., Zhang, Z. and Miller, W. (1997)
 30 Comparison of DNA sequences with protein sequences. *Genomics* 46: 24-36; Schuler, G. D. (1997) Sequence mapping by electronic PCR. *Genome Res* 7: 541-50; and Smit, A. F.

A. and Green, P. (1997) RepeatMasker at URL: repeatmasker.genome.washington.edu/cgi-bin/RM2_req.pl.

5 Tables 1 and 2 contain additional information regarding SEQ ID NO. 153 to SEQ ID NO. 1085. The explanation of the entries in Tables 1 and 2 is as follows:

Symbol: The Human Genome Organization gene symbol, as allotted by a procedure to be published soon. OR = Olfactory Receptor, numeral to the immediate right - family designation, capital letters - subfamily designation, rightmost numeral - individual gene within subfamily, n appearing when such number is not assigned yet; P = Pseudogene.

10 All ORs within a family share at least 40% protein sequence identity.

All ORs within a subfamily share at least 60% protein sequence identity.

HORDE: The H serial number within the Human Olfactory Receptor Data Exploratorium (URL bioinfo.weizmann.ac.il/HORDE). The numeral 38 represents the HORDE build (version), gxxx is the individual gene number.

15 Digi: Appearance of a DSnn serial number here means that the sequence has been PCR-amplified from human olfactory epithelial cDNA using degenerate primers at the transmembrane helix 2 and transmembrane helix 7. See separate page for explanations on the analysis of the DS entries.

20 OST: OSTnnn is the serial number of the sequence in the Olfactory Sequence Tag collection in the Lancet laboratory (URL bioinfo.weizmann.ac.il/HORDE). Appearance here means that the sequence has been PCR-amplified from human genomic DNA using degenerate primers at the transmembrane helix 2 and transmembrane helix 7. There are a total of 112 OST sequences.

25 Trivial name: One or more aliases given to the same gene by different laboratories. Many of the trivial names are of the form ORnn-xx, whereby nn is a chromosome number and xx is an arbitrary numerical identifier.

Tran: (transcribed) Plus appears if the entry was sequenced from cDNA, or was found in the Expressed Sequence Tags (EST) databases. Plus also appears if in the public databases the gene was annotated as mRNA.

30 Int.: (intact) "Yes" indicates that the gene may be intact, as there are no obvious sequence frame disruptions. "Put" (putative) indicates the same, except that the known sequence is short, hence there may be disruptions in the unsequenced segments. "Pol"

indicates a polymorphism between intact and pseudogenic alleles. When no word appears, this indicates a pseudogene.

E: (Extent) FL indicates that the Full Length sequence is known (typically 310 ± 30 amino acids).

5 D: The number of sequence disruptions in the known sequence of a pseudogene.

C: The human chromosomal location of the OR gene, assigned as described under Mb coord.

Mb coord: The location of the OR gene within a human chromosome, in megabase units, beginning at the p-telomere and ending at the q-telomere, computed based on
10 integrating information from Unified Database (URL is bioinfo.weizmann.ac.il/udb) and the University of California Santa Cruz (URL is genome.ucsc.edu).

CDR: The 17 amino acids suggested to line the odorant ligand binding pocket, delineated by the extracellular 2/3 of transmembrane helices 3,4 and 5. The assignment is based on an algorithm at URL

15 bioinformatics.weizman.ac.il/HORDE/humanGenes/CDR.html.

%: (% id) The percent protein identity between the human sequence in the current line and the known rodent (rat or mouse) OR sequence to which it bears the highest similarity.

S: (Species) Rat (R) or mouse (M).

20 Acc: The Genbank accession number of the clone that contains the rodent sequence.

Range: The positions x ... y of the first and last bases within the rodent which constitute the OR coding region. If $x > y$ then the OR is on the reverse strand.

Table 1

25

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
153	OR10D3	H38g001			HSHTPCR09			
154	OR7EnP	H38g002						FL
155	OR1D5	H38g003		OST901	OR17-31	+	pol	FL
156	OR10NnP	H38g00						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
157	OR2F1	H38g00 5		OST902	OLF3;OR7-139;OR7-140	+	yes	FL
158	OR7EnP	H38g00 6						FL
159	OR8FnP	H38g00 7						FL
160	OR2Q1P	H38g00 8			DJ0669B10;OR7-2			FL
161	OR2W1	H38g00 9			AL035402- B;dJ88J8.1;hs6M1-15		yes	FL
162	OR7EnP	H38g01 0				+		FL
163	OR6B1	H38g01 1	DS119		OR7- 3;WUGSC:H_DJ0669B10. 3	+	yes	FL
164	OR10Kn	H38g01 2					yes	FL
165	ORnP	H38g01 3				+		FL
166	OR4F2P	H38g01 4			HS191N21;dJ191N21.4; hs6M1-11			FL
167	OR7EnP	H38g01 5						FL
168	OR1F2P	H38g01 6			OLFMP2	+	yes	FL
169	OR2P1P	H38g01 7			AL035402- A;dJ88J8.2;hs6M1-26			
170	OR7E43P	H38g01 8		OST903	OR4-116			FL
171	OR4F1	H38g01 9			HSDJ0609N19			FL
172	OR7E55P	H38g02 0		OST904	OR2DG;OR3.2			FL
173	OR13Dn	H38g02 1					yes	FL
174	OR4CnP	H38g02 2						FL
175	OR10D1P	H38g02 3		OST074	HSHTPCRX03	+		FL
176	OR4Cn	H38g02					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
177	OR8GnP	H38g02 5						
178	OR13CnP	H38g02 6						FL
179	OR4CnP	H38g02 7						FL
180	OR13Cn	H38g02 8					yes	FL
181	OR4CnP	H38g02 9						
182	OR51Bn	H38g03 0					yes	FL
183	OR7E5P	H38g03 1		OST905	OR11-12			FL
184	OR13Cn	H38g03 2					yes	FL
185	OR4Sn	H38g03 3					yes	FL
186	OR51BnP	H38g03 4						FL
187	OR6JnP	H38g03 5						FL
188	OR51Bn	H38g03 6					yes	FL
189	OR7EnP	H38g03 7						FL
190	OR2An	H38g03 8					yes	FL
191	OR7E22P	H38g03 9			OR3.6;OR6DG			FL
192	OR7E4P	H38g04 0			OR11-11a			FL
193	OR7E66P	H38g04 1		OST906	OR3.3;OR3DG;hg630			FL
194	OR6Mn	H38g04 2					yes	FL
195	OR2ALnP	H38g04 3						
196	OR6MnP	H38g04 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
197	OR4D1	H38g04 5			AC005962-A;HSTPCR16	+	yes	FL
198	OR5D2P	H38g04 6		OST907	OR11-7a;OR912-91			FL
199	OR7E38P	H38g04 7		OST127	AC004967	+		FL
200	OR4D2	H38g04 8			AC005962-B		yes	FL
201	OR7E7P	H38g04 9			AC004967-A			FL
202	OR5AHnP	H38g05 0						
203	OR2U2P	H38g05 1			AL050339- B;dJ974I11.2;hs6M1- 23			FL
204	OR2U1P	H38g05 2			974I11;AL050339- C;dJ974I11.3;hs6M1- 24			FL
205	OR2H2	H38g05 3			AC006137- A;dJ271M21.2;hs6M1- 12		yes	FL
206	OR2H5P	H38g05 4		OST616	HS271M21;hs6M1-13			FL
207	OR2In	H38g05 5				+	yes	FL
208	OR11HnP	H38g05 6						FL
209	OR7EnP	H38g05 7				+		
210	OR9In	H38g05 8					yes	FL
211	OR2AFnP	H38g05 9						FL
212	OR13KnP	H38g06 1						FL
213	OR13Cn	H38g06 2					yes	FL
214	OR13Fn	H38g06 3					yes	FL
215	OR9Qn	H38g06 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
216	OR2TnP	H38g06 5						FL
217	OR4Kn	H38g06 6					yes	FL
218	OR2B8P	H38g06 7			dJ313I6.4;hs6M1-29P		yes	FL
219	OR2Tn	H38g06 8					yes	FL
220	OR4Kn	H38g06 9					yes	FL
221	OR2A4	H38g07 0			WUGSC:H_DJ0988G15.2	+	yes	FL
222	OR7EnP	H38g07 1						FL
223	OR4Kn	H38g07 2					yes	FL
224	OR13InP	H38g07 3						FL
225	OR7EnP	H38g07 4						FL
226	OR6Jn	H38g07 5					yes	FL
227	OR4Mn	H38g07 6					yes	FL
228	OR4VnP	H38g07 7						FL
229	OR6Xn	H38g07 8					yes	FL
230	OR51Gn	H38g07 9					yes	FL
231	OR6EnP	H38g08 0						FL
232	OR4NnP	H38g08 1						FL
233	OR6MnP	H38g08 2						FL
234	OR4Nn	H38g08 3					yes	FL
235	OR4Cn	H38g08 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
236	OR4KnP	H38g08 5						FL
237	ORnP	H38g08 6						
238	OR5D3	H38g08 7		OST908	OR11-8b;OR11-8c			
239	OR2G1P	H38g08 8	DS13;D S16	OST619	dJ974I11.4;hs6M1-25	+		FL
240	OR4Kn	H38g08 9					yes	FL
241	OR8BnP	H38g09 0						FL
242	OR2B2	H38g09 1			OR6-1;dJ193B12.4		yes	FL
243	OR7EnP	H38g09 2						FL
244	OR4KnP	H38g09 3						FL
245	OR2AD1P	H38g09 4			dJ25J6.1;hs6M1-8P			FL
246	OR1AAnP	H38g09 5						FL
247	OR1E3P	H38g09 6			OR17-210			FL
248	OR8BnP	H38g09 7						FL
249	OR5Hn	H38g09 8					yes	FL
250	OR1G1	H38g09 9		OST909	OR17-130;OR17-209	+	yes	FL
251	OR5HnP	H38g10 0						FL
252	ORnP	H38g10 1						
253	ORnP	H38g10 2						
254	OR4PnP	H38g10 3						FL
255	OR13Hn	H38g10 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
256	OR7D1P	H38g10 5		OST910	CIT-B-440L2;OR19-131;OR19-A			FL
257	OR4KnP	H38g10 6						FL
258	OR7E24	H38g10 7		OST911	CIT-B-440L2;OR19-8	+		FL
259	OR51NnP	H38g10 8						FL
260	OR7E18P	H38g10 9		OST912	OR19-14;TPCR26	+		FL
261	OR7E19P	H38g11 0		OST913	HSCIT-B-440L2;OR19-7;TPCR110	+		FL
262	OR7E41P	H38g11 1		OST914	OR11-20;hg84			FL
263	OR2R1	H38g11 2		OST058				FL
264	OR10ACnP	H38g11 3						FL
265	OR51Ln	H38g11 4					yes	FL
266	OR52JnP	H38g11 5						FL
267	OR9LnP	H38g11 6						
268	OR51PnP	H38g11 7						FL
269	OR5HnP	H38g11 8						FL
270	OR51An	H38g11 9					yes	FL
271	OR5HnP	H38g12 0						FL
272	ORnP	H38g12 1						
273	OR52En	H38g12 2					yes	FL
274	OR5Hn	H38g12 3					yes	FL
275	OR4CnP	H38g12 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
276	OR52En	H38g12 5					yes	FL
277	OR10Dn	H38g12 6					yes	FL
278	OR5HnP	H38g12 7						FL
279	OR13An	H38g12 8					yes	FL
280	OR5HnP	H38g12 9						FL
281	OR5Kn	H38g13 0					yes	FL
282	OR7EnP	H38g13 1						FL
283	OR4DnP	H38g13 2						FL
284	OR2ARnP	H38g13 3						
285	OR7E29P	H38g13 4		OST032				FL
286	OR4CnP	H38g13 5						FL
287	OR5PnP	H38g13 6						FL
288	OR7EnP	H38g13 7						FL
289	OR56An	H38g13 8					yes	FL
290	OR56AnP	H38g13 9						
291	OR5Pn	H38g14 0					yes	FL
292	OR7E53P	H38g14 1		OST915	OR3-142;OR3-143			FL
293	OR5Pn	H38g14 2					yes	FL
294	OR52Ln	H38g14 3					yes	FL
295	OR5E1	H38g14 4			HSTPCR24	+		FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
296	OR56AnP	H38g14 5						
297	OR4KnP	H38g14 6						
298	OR52Ln	H38g14 7					yes	FL
299	OR7EnP	H38g14 8						
300	OR52XnP	H38g14 9						FL
301	ORnP	H38g15 0						
302	OR56An	H38g15 1					yes	FL
303	OR56AnP	H38g15 2						
304	OR1R1P	H38g15 3			OR17-1			FL
305	OR52EnP	H38g15 4						FL
306	OR51AnP	H38g15 5						FL
307	OR51An	H38g15 6					yes	FL
308	OR4CnP	H38g15 7						FL
309	OR52JnP	H38g15 8						FL
310	OR4RnP	H38g15 9						
311	OR52Jn	H38g16 0					yes	FL
312	OR4CnP	H38g16 1						FL
313	OR51AnP	H38g16 2						FL
314	OR7EnP	H38g16 3						FL
315	OR5MnP	H38g16 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
316	OR10ABn P	H38g16 5						FL
317	OR52SnP	H38g16 6						FL
318	OR5Mn	H38g16 7					yes	FL
319	OR10Sn	H38g16 8					yes	FL
320	OR5MnP	H38g16 9						FL
321	OR10Gn	H38g17 0					yes	FL
322	ORnP	H38g17 1						FL
323	OR5MnP	H38g17 2						FL
324	OR10GnP	H38g17 3						
325	OR10TnP	H38g17 4						FL
326	ORnP	H38g17 5						
327	OR10RnP	H38g17 6						FL
328	OR5MnP	H38g17 7						FL
329	OR7EnP	H38g17 8						FL
330	OR10Tn	H38g17 9					yes	FL
331	OR1E1	H38g18 0	DS37;D S43;DS 46	OST916	HGMP07I;OR17-2;OR17- 32	+	yes	FL
332	OR5BKnP	H38g18 1						
333	OR5MnP	H38g18 2						FL
334	OR3A3	H38g18 3		OST917	OR17-137;OR17- 16;OR17-201	+	yes	FL
335	OR10ADn P	H38g18 4	DS10			+		FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
336	OR10Rn	H38g18 5				+	yes	FL
337	OR5TnP	H38g18 6						FL
338	OR4GnP	H38g18 7						FL
339	OR6Yn	H38g18 8					yes	FL
340	OR1E2	H38g18 9		OST918	OR17-135;OR17-93	+	yes	FL
341	OR8Hn	H38g19 0					yes	FL
342	OR4Fn	H38g19 1					yes	FL
343	OR10Kn	H38g19 2					yes	FL
344	OR7LnP	H38g19 3						
345	OR8InP	H38g19 4						FL
346	OR10RnP	H38g19 5						
347	OR2AFnP	H38g19 6						FL
348	OR8Kn	H38g19 7					yes	FL
349	ORnP	H38g19 8						
350	OR8KnP	H38g19 9						FL
351	OR51Hn	H38g20 0					yes	FL
352	OR7EnP	H38g20 1						FL
353	ORnP	H38g20 2						
354	OR5BMnP	H38g20 3						FL
355	OR10GnP	H38g20 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
356	OR2Yn	H38g20 5					yes	FL
357	OR10DnP	H38g20 6						FL
358	OR3BnP	H38g20 7						FL
359	OR8Dn	H38g20 8					yes	FL
360	OR5RnP	H38g20 9						
361	OR10Gn	H38g21 0					yes	FL
362	OR5BDnP	H38g21 1						FL
363	OR5ALnP	H38g21 2						FL
364	OR52HnP	H38g21 3						
365	OR10Gn	H38g21 4					yes	FL
366	OR5Mn	H38g21 5					yes	FL
367	OR51Mn	H38g21 6					yes	FL
368	OR6Tn	H38g21 7	DS15;D S146;D S147			+	yes	FL
369	OR6DnP	H38g21 8						FL
370	OR4B1	H38g21 9		OST208			yes	FL
371	OR5ALnP	H38g22 0						FL
372	OR51Qn	H38g22 1					yes	FL
373	OR4Dn	H38g22 2					yes	FL
374	OR52Nn	H38g22 3					yes	FL
375	OR4Xn	H38g22 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
376	OR8Jn	H38g22 5					yes	FL
377	OR51JnP	H38g22 6						FL
378	OR10Gn	H38g22 7					yes	FL
379	OR52En	H38g22 8					yes	FL
380	OR4Xn	H38g22 9					yes	FL
381	OR10A2	H38g23 0	DS5;DS 53;DS5 6	OST363		+		FL
382	OR5Mn	H38g23 1					yes	FL
383	OR52En	H38g23 2					yes	FL
384	OR8Kn	H38g23 3					yes	FL
385	OR10An	H38g23 4	DS55			+	yes	FL
386	OR8LnP	H38g23 5						FL
387	OR5BPnP	H38g23 6						
388	OR52Nn	H38g23 7					yes	FL
389	ORnP	H38g23 8						
390	OR8JnP	H38g23 9						FL
391	OR5Mn	H38g24 0					yes	FL
392	OR52En	H38g24 1					yes	FL
393	OR5Tn	H38g24 2					yes	FL
394	OR52NnP	H38g24 3						FL
395	OR4B2P	H38g24 4		OST919	hg449			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
396	OR51KnP	H38g24 5						FL
397	OR52QnP	H38g24 6						FL
398	OR4Fn	H38g24 7					yes	FL
399	OR11MnP	H38g24 8						
400	OR52Nn	H38g24 9					yes	FL
401	OR56An	H38g25 0					yes	FL
402	OR5AWnP	H38g25 1						FL
403	OR52Nn	H38g25 2					yes	FL
404	ORnP	H38g25 3						
405	OR52EnP	H38g25 4						FL
406	OR5BHnP	H38g25 5						FL
407	OR4QnP	H38g25 6						FL
408	OR51En	H38g25 7					yes	FL
409	OR11KnP	H38g25 8						FL
410	OR12D1P	H38g25 9			AC004174- B;dJ994E9.7;hs6M1-19			FL
411	OR4NnP	H38g26 0				+		FL
412	OR11A1	H38g26 1			AC004174- A;dJ994E9.6;hs6M1-18	+	yes	FL
413	OR10C1	H38g26 2			AC004174;dJ994E9.5;h s6M1-17	+	yes	FL
414	OR2H1	H38g26 3	DS114		OLFR42A-9004-14;OR6- 2;dJ994E9.4;hs6M1-16	+	yes	FL
415	OR9RnP	H38g26 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
416	OR4FnP	H38g26 5						
417	OR7D4	H38g26 6		OST920	OR19-B;hg105			FL
418	OR7E25P	H38g26 7		OST921	CIT-B-440L2;OR19-C			FL
419	OR2D2	H38g26 8			OR11-610		yes	FL
420	OR10An	H38g26 9					yes	FL
421	OR2WnP	H38g27 0				+		
422	OR7E16P	H38g27 1		OST922	CIT-B-440L2;OR19- 133;OR19-9			FL
423	OR52Pn	H38g27 2					yes	FL
424	OR6AnP	H38g27 3						FL
425	OR7D2	H38g27 4	DS70;D S73	OST923	HTPCRHO3;OR19-4	+	yes	FL
426	OR52UnP	H38g27 5						FL
427	OR2AGn	H38g27 6					yes	FL
428	OR7G3	H38g27 7		OST085			yes	FL
429	OR56BnP	H38g27 8						FL
430	OR2AGnP	H38g27 9						FL
431	OR56Bn	H38g28 0					yes	FL
432	OR6AnP	H38g28 1						FL
433	OR4FnP	H38g28 2						FL
434	OR6Wn	H38g28 3					yes	FL
435	OR4Mn	H38g28 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
436	OR52YnP	H38g28 5						
437	OR11HnP	H38g28 6						FL
438	OR9An	H38g28 7					yes	FL
439	OR5Mn	H38g28 8					yes	FL
440	OR6Vn	H38g28 9					yes	FL
441	OR4Nn	H38g29 0				+	yes	FL
442	OR51AnP	H38g29 1						FL
443	OR9PnP	H38g29 2						
444	OR4H6P	H38g29 3			OR15-71;OR15-82			FL
445	OR51FnP	H38g29 4						FL
446	OR7E1P	H38g29 5			AC004923			FL
447	OR51Tn	H38g29 6					yes	FL
448	OR2Vn	H38g29 7					yes	FL
449	OR51HnP	H38g29 8						FL
450	OR51An	H38g29 9					yes	FL
451	OR2AInP	H38g30 0						FL
452	OR2F2	H38g30 1			OR7- 1;WUGSC:H_DJ0669B10. 1		yes	FL
453	OR1F12	H38g30 2			dJ313I6.5;hs6M1-35P		yes	FL
454	OR7G1P	H38g30 3			OR19-15		yes	FL
455	OR7G2	H38g30 4		OST260			yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
456	OR1M1	H38g30 5		OST924	OR19-6		yes	FL
457	OR51UnP	H38g30 6						
458	OR52Hn	H38g30 7					yes	FL
459	OR1F1	H38g30 8		OST925	OLFMF;OR16-36;OR16- 37;OR16-88;OR16- 89;OR16-90	+	yes	FL
460	OR10PnP	H38g30 9						
461	OR4FnP	H38g31 0						FL
462	OR2T1	H38g31 1			OR1-25		yes	FL
463	OR7EnP	H38g31 2						FL
464	OR51Gn	H38g31 3					yes	FL
465	OR2Tn	H38g31 4					yes	FL
466	OR5BGnP	H38g31 5						
467	OR5WnP	H38g31 6						FL
468	OR51Sn	H38g31 7					yes	FL
469	OR5WnP	H38g31 8						
470	OR51AnP	H38g31 9						FL
471	OR5Dn	H38g32 0					yes	FL
472	OR7EnP	H38g32 1						FL
473	OR51Fn	H38g32 2					yes	FL
474	OR5Dn	H38g32 3					yes	FL
475	OR52Rn	H38g32 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
476	ORnP	H38g32 5						FL
477	OR7EnP	H38g32 6						FL
478	OR6Qn	H38g32 7					yes	FL
479	OR4Fn	H38g32 8					yes	FL
480	OR7EnP	H38g32 9						
481	OR7En	H38g33 0					yes	FL
482	OR4Nn	H38g33 1					yes	FL
483	OR2ASnP	H38g33 2						
484	OR11Hn	H38g33 3					yes	FL
485	OR2Tn	H38g33 4					yes	FL
486	OR2TnP	H38g33 5						
487	OR2AKnP	H38g33 6						FL
488	ORnP	H38g33 7						
489	OR5DnP	H38g33 8						FL
490	OR7EnP	H38g33 9						
491	OR5L2	H38g34 0			HSHTPCR16	+	yes	FL
492	OR5Dn	H38g34 1					yes	FL
493	ORnP	H38g34 2						
494	OR10Qn	H38g34 3					yes	FL
495	OR9MnP	H38g34 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
496	OR7E62P	H38g34 5		OST926	OR2-4;OR2-52;OR2- 53;OR2-75			FL
497	OR9LnP	H38g34 6						FL
498	OR7E46P	H38g34 7		OST379				FL
499	OR1S1	H38g34 8		OST034			yes	FL
500	OR5DnP	H38g34 9						
501	OR9InP	H38g35 0						FL
502	OR5Dn	H38g35 1					yes	FL
503	OR9QnP	H38g35 2						FL
504	OR51CnP	H38g35 3						
505	OR5WnP	H38g35 4						
506	OR9InP	H38g35 5						FL
507	OR51AnP	H38g35 6						FL
508	OR5L1	H38g35 7		OST262			yes	FL
509	OR7EnP	H38g35 8				+		
510	OR5BLnP	H38g35 9						
511	OR51En	H38g36 0					yes	FL
512	OR51Dn	H38g36 1					yes	FL
513	OR52In	H38g36 2					yes	FL
514	OR4KnP	H38g36 3	DS67			+		FL
515	OR52In	H38g36 4					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
516	OR4KnP	H38g36 5						FL
517	OR52MnP	H38g36 6						FL
518	ORnP	H38g36 7						
519	ORnP	H38g36 8						
520	ORnP	H38g36 9						FL
521	ORnP	H38g37 0						
522	ORnP	H38g37 1						
523	ORnP	H38g37 2						
524	ORnP	H38g37 3						
525	ORnP	H38g37 4						
526	OR6Pn	H38g37 5					yes	FL
527	OR7EnP	H38g37 6						FL
528	ORnP	H38g37 7						
529	OR7EnP	H38g37 8						FL
530	ORnP	H38g37 9						
531	OR10XnP	H38g38 0						FL
532	OR10Zn	H38g38 1					yes	FL
533	OR6KnP	H38g38 2						FL
534	OR6Kn	H38g38 3					yes	FL
535	OR1FnP	H38g38 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
536	OR1ABnP	H38g38 5						
537	OR52MnP	H38g38 6						FL
538	OR1XnP	H38g38 7						FL
539	OR4FnP	H38g38 8						
540	OR52MnP	H38g38 9						FL
541	OR2Vn	H38g39 0					yes	FL
542	OR2V1P	H38g39 1		OST265				FL
543	OR2Zn	H38g39 2					yes	FL
544	OR52KnP	H38g39 3				+		
545	OR10Hn	H38g39 4					yes	FL
546	OR2Dn	H38g39 5					yes	FL
547	OR7EnP	H38g39 6						
548	OR11GnP	H38g39 7						FL
549	ORnP	H38g39 8						
550	OR11Gn	H38g39 9					yes	FL
551	OR11HnP	H38g40 0						FL
552	OR6Kn	H38g40 1					yes	FL
553	OR11Hn	H38g40 2					yes	FL
554	OR6KnP	H38g40 3						
555	OR11HnP	H38g40 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
556	OR6KnP	H38g40 5						FL
557	OR6Kn	H38g40 6					yes	FL
558	OR2Ln	H38g40 7					yes	FL
559	OR4GnP	H38g40 8						
560	OR6Nn	H38g40 9					yes	FL
561	OR2LnP	H38g41 0						
562	OR9A1	H38g41 1			HSHTPCR06			
563	OR6Nn	H38g41 2					yes	FL
564	OR10Hn	H38g41 3					yes	FL
565	OR7EnP	H38g41 4						FL
566	OR2AQnP	H38g41 5						
567	OR2LnP	H38g41 6						FL
568	OR5ARn	H38g41 7					yes	FL
569	OR7EnP	H38g41 8						FL
570	OR10AAn P	H38g41 9						FL
571	OR10JnP	H38g42 0						FL
572	OR5A1P	H38g42 1	DS69;D S71;DS 128;DS 129	OST181		+	yes	FL
573	OR2AHnP	H38g42 2						FL
574	OR10JnP	H38g42 3						FL
575	OR56BnP	H38g42						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		4						
576	OR5M1	H38g42 5		OST050			yes	FL
577	OR52WnP	H38g42 6						
578	OR5AMnP	H38g42 7						FL
579	OR52BnP	H38g42 8						FL
580	OR5MnP	H38g42 9						FL
581	OR5APnP	H38g43 0						FL
582	OR56Bn	H38g43 1					yes	FL
583	OR5APn	H38g43 2					yes	FL
584	OR52Bn	H38g43 3					yes	FL
585	OR9Gn	H38g43 4					yes	FL
586	OR52Kn	H38g43 5					yes	FL
587	OR5MnP	H38g43 6						FL
588	OR52Kn	H38g43 7					yes	FL
589	OR52KnP	H38g43 8				+		FL
590	OR52BnP	H38g43 9						FL
591	OR2B6P	H38g44 0			OR6-31		yes	FL
592	OR2WnP	H38g44 1						FL
593	OR2AnP	H38g44 2						FL
594	ORnP	H38g44 3						
595	OR2LnP	H38g44 4						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
596	OR2W2P	H38g44 5	DS148		dJ313I6.2;hs6M1-30P	+		FL
597	OR2LnP	H38g44 6						
598	OR2B7P	H38g44 7			dJ313I6.3;hs6M1-31P			FL
599	OR2Ln	H38g44 8					yes	FL
600	OR5BFn	H38g44 9					yes	FL
601	OR2LnP	H38g45 0						FL
602	OR7EnP	H38g45 1						
603	OR1H1	H38g45 2	DS122	OST26		+		FL
604	ORnP	H38g45 3						
605	OR4Dn	H38g45 4					yes	FL
606	OR1Ln	H38g45 5					yes	FL
607	OR5AXn	H38g45 6					yes	FL
608	OR5An	H38g45 7					yes	FL
609	OR5AYn	H38g45 8					yes	FL
610	OR13Gn	H38g45 9					yes	FL
611	OR5BBnP	H38g46 0						
612	OR9GnP	H38g46 1						FL
613	OR2TnP	H38g46 2						FL
614	ORnP	H38g46 3						FL
615	OR1Jn	H38g46 4				+	yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
616	OR2CnP	H38g46 5						FL
617	OR9GnP	H38g46 6						FL
618	OR2C1	H38g46 7			OLFmf3	+	yes	FL
619	OR51AnP	H38g46 8						
620	OR9Gn	H38g46 9					yes	FL
621	OR52Bn	H38g47 0					yes	FL
622	OR1K1	H38g47 1			hg99		yes	FL
623	OR51RnP	H38g47 2						FL
624	OR7EnP	H38g47 3						FL
625	OR52PnP	H38g47 4						FL
626	OR7EnP	H38g47 5						FL
627	OR7EnP	H38g47 6						
628	OR4KnP	H38g47 7	DS66		OR21-1	+		FL
629	OR4KnP	H38g47 8			OR21-2			FL
630	OR7EnP	H38g47 9						
631	OR51In	H38g48 0					yes	FL
632	OR51In	H38g48 1					yes	FL
633	OR2AnP	H38g48 2						
634	OR2A2	H38g48 3		OST008				FL
635	OR2AnP	H38g48 4						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
636	OR2Gn	H38g48 5					yes	FL
637	OR2AnP	H38g48 6						
638	OR6Fn	H38g48 7	DS20;D S21;DS 23;DS2 7;DS28 ;DS39; DS40;D S113;D S126;D S135;D S137;D S138;D S139;D S140;D S141;D S145			+	yes	FL
639	OR2AnP	H38g48 8						
640	OR2Gn	H38g48 9					yes	FL
641	OR7E37P	H38g49 0			hg533	+		FL
642	OR5AVn	H38g49 1	DS4;DS 6;DS11			+	yes	FL
643	OR2AJnP	H38g49 2						FL
644	OR13EnP	H38g49 3						FL
645	OR2Cn	H38g49 4					yes	FL
646	OR2TnP	H38g49 5						
647	OR2WnP	H38g49 6						
648	OR13Jn	H38g49 7					yes	FL
649	OR6RnP	H38g49 8						FL
650	OR5ATn	H38g49 9					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
651	OR2Zn	H38g50 0					yes	FL
652	OR4Ln	H38g50 1					yes	FL
653	OR4UnP	H38g50 2						FL
654	OR4Fn	H38g50 3					yes	FL
655	OR4FnP	H38g50 4						FL
656	OR4Fn	H38g50 5					yes	FL
657	OR4Fn	H38g50 6					yes	FL
658	OR4AnP	H38g50 7						FL
659	OR4LnP	H38g50 8						FL
660	OR7E33P	H38g50 9		OST927	hg688			FL
661	OR2Cn	H38g51 0					yes	FL
662	OR4Kn	H38g51 1					yes	FL
663	OR5U1	H38g51 2			ba150A6.4;hs6M1-28		yes	FL
664	OR4Kn	H38g51 3					yes	FL
665	OR5V1	H38g51 4			ba150A6.2;hs6M1-21		yes	FL
666	OR4QnP	H38g51 5						FL
667	OR12D3	H38g51 6			ba150A6.1;hs6M1-27		yes	FL
668	OR4Kn	H38g51 7					yes	FL
669	OR51CnP	H38g51 8						
670	OR1J2	H38g51 9		OST044	hg152		yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
671	OR5BJnP	H38g52 0						
672	OR1J1	H38g52 1	DS130	OST928	hg32	+	yes	FL
673	OR13En	H38g52 2					put	
674	OR4KnP	H38g52 3	DS1			+		FL
675	OR1LnP	H38g52 4						
676	OR2CnP	H38g52 5						
677	OR4TnP	H38g52 6						FL
678	OR5BnP	H38g52 7						
679	OR4Kn	H38g52 8					yes	FL
680	OR11Ln	H38g52 9					yes	FL
681	OR7E68P	H38g53 0		OST929	OR912-108;OR912- 109;OR912-110;OR912- 46;hg523;hg674			FL
682	OR7EnP	H38g53 1						FL
683	OR7E31P	H38g53 2		OST016;O ST205				FL
684	OR7EnP	H38g53 3						FL
685	OR5AKnP	H38g53 4						FL
686	OR5AKn	H38g53 5					yes	FL
687	OR5AKn	H38g53 6					yes	FL
688	OR5BQnP	H38g53 7						
689	OR1Nn	H38g53 8	DS136; DS142			+	yes	FL
690	OR1J4	H38g53 9		OST930	HSHTPCR01	+	yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
691	OR1Nn	H38g54 0					yes	FL
692	OR2AnP	H38g54 1						FL
693	OR2ANnP	H38g54 2						
694	OR5K1	H38g54 3			HSHTPCR10	+	yes	FL
695	OR2K2	H38g54 4			HSHTPCR06		yes	FL
696	OR8Hn	H38g54 5					yes	FL
697	ORnP	H38g54 6						
698	OR4AnP	H38g54 7						
699	OR4An	H38g54 8					yes	FL
700	OR6Sn	H38g54 9					yes	FL
701	OR4RnP	H38g55 0						
702	OR13Cn	H38g55 1					yes	FL
703	OR13DnP	H38g55 2						FL
704	OR7EnP	H38g55 3						FL
705	OR10PnP	H38g55 4						FL
706	OR8In	H38g55 5					yes	FL
707	OR8G1	H38g55 6			HSTPCR25	+	put	
708	ORnP	H38g55 7						
709	OR5F1	H38g55 8			OR11-10		yes	FL
710	OR5FnP	H38g55 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
711	OR6BnP	H38g56 0						FL
712	OR2D1	H38g56 1			hg27		put	
713	OR5ASn	H38g56 2					yes	FL
714	OR5SnP	H38g56 3						FL
715	OR5AQnP	H38g56 4						
716	OR6BnP	H38g56 5						FL
717	OR5JnP	H38g56 6						FL
718	OR9AnP	H38g56 7						FL
719	OR5BEnP	H38g56 8						FL
720	OR9An	H38g56 9					yes	FL
721	OR8Hn	H38g57 0					yes	FL
722	OR5BNnP	H38g57 1						
723	OR8Jn	H38g57 2					yes	FL
724	OR9NnP	H38g57 3						
725	OR7EnP	H38g57 4						FL
726	OR7E9P	H38g57 5		OST289				FL
727	OR8KnP	H38g57 6						
728	OR2AnP	H38g57 7						
729	OR8Kn	H38g57 8					yes	FL
730	OR7E39P	H38g57 9		OST931	hg611			

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
731	OR7E27P	H38g58 0		OST932	hg616			
732	OR2Hn	H38g58 1					put	
733	OR13CnP	H38g58 2						FL
734	OR13Cn	H38g58 3					yes	FL
735	OR2S1P	H38g58 4		OST611				FL
736	OR2AMnP	H38g58 5						
737	OR1N1	H38g58 6		OST933	OR1-26		put	
738	OR2S2	H38g58 7		OST715			yes	FL
739	OR7E26P	H38g58 8			OR1-51; OR1-72; OR1-73; OR912-95			
740	OR1F11	H38g58 9			hg91		put	
741	OR5ACnP	H38g59 0						FL
742	OR5B10P	H38g59 1			OR13-34; OR13-64; OR13-67			
743	OR2AnP	H38g59 2						FL
744	OR1E5	H38g59 3	DS117; DS143		OR13-66	+	put	
745	OR4Fn	H38g59 4					yes	FL
746	OR5CnP	H38g59 5						
747	OR2WnP	H38g59 6						
748	OR2L2	H38g59 7			HSHTPCRHO7	+	put	
749	OR4H8P	H38g59 8			OR14-58			
750	OR5D10P	H38g59 9			OR912-94			

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
751	OR7A12P	H38g60 0			OR14-11;OR14-59			
752	OR2L1	H38g60 1			HSHTPCR02	+	put	
753	OR2F3P	H38g60 2			OR14-60		put	
754	OR4H10P	H38g60 3		OST934	OR15-69;OR15-80;OR15-81			
755	OR5H1	H38g60 4			HSHTPCR14	+	put	
756	OR2K1	H38g60 5			HSHTPCR17	+	put	
757	OR7E11P	H38g60 6			OR11-2			
758	OR7A3P	H38g60 7		OST935	OR11-7b			
759	OR6A1	H38g60 8			OR11-55	+	yes	FL
760	OR5I1	H38g60 9			OLF1	+	yes	FL
761	OR2H3	H38g61 0			HUMORLMHC	+	yes	FL
762	OR10J1	H38g61 1	DS3;DS 14		HSHGMP07J	+	yes	FL
763	OR7E3P	H38g61 2			OR11-9			
764	OR1D6P	H38g61 3			OR11-13;OR11-22			
765	OR5D10P	H38g61 4			OR18-17;OR18-42;OR18-43;OR18-44			
766	OR5D5P	H38g61 5			OR18-79;OR912-47			
767	OR52A1	H38g61 6			HPFH1OR	+	yes	FL
768	OR2AEn	H38g61 7					yes	FL
769	OR6LnP	H38g61 8						FL
770	OR6LnP	H38g61 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
771	OR7MnP	H38g62 0						
772	OR13Cn	H38g62 1					yes	FL
773	OR13Cn	H38g62 2					yes	FL
774	OR2InP	H38g62 3				+		
775	OR4An	H38g62 4					yes	FL
776	OR2InP	H38g62 5				+		
777	OR4AnP	H38g62 6						FL
778	OR4AnP	H38g62 7						FL
779	OR8C1P	H38g62 8			OR11-175			
780	OR4AnP	H38g62 9						FL
781	OR7E15P	H38g63 0			OR11-392			
782	OR10A1	H38g63 2			OR11-403		put	
783	OR2An	H38g63 3				+	put	
784	OR7EnP	H38g63 4				+		FL
785	OR7En	H38g63 5				+	put	
786	OR51A1P	H38g63 6			HPFH6OR	+		FL
787	OR7E47P	H38g63 7			HSORBPL41;bpl41-16	+		FL
788	OR5B5P	H38g63 8			OR3-144;OR912-92			
789	OR1F10	H38g63 9			OR3-145		put	
790	OR8G2	H38g64 0			HSTPCR120	+	put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
791	OR1Sn	H38g64 1					yes	FL
792	OR4AnP	H38g64 2						FL
793	OR4AnP	H38g64 3						FL
794	OR4AnP	H38g64 4						FL
795	OR4AnP	H38g64 5						FL
796	OR4AnP	H38g64 6						FL
797	OR4AnP	H38g64 7						FL
798	OR4An	H38g64 8					yes	FL
799	OR4An	H38g64 9					yes	FL
800	OR7E42P	H38g65 0		OST001				
801	OR2M3P	H38g65 1		OST003				
802	OR4H11P	H38g65 2			OR4-114;OR4-115;OR4- 119			
803	OR7E57P	H38g65 3		OST007				
804	OR2B1P	H38g65 4			OR5-40;OR5-41		put	
805	OR7E34P	H38g65 5		OST011				
806	OR7E56P	H38g65 6		OST013				
807	OR3AnP	H38g65 7						
808	OR4H5P	H38g65 8			OR5-39;OR5-84			
809	OR1En	H38g65 9	DS47;D S115;D S120;D S121;D S123;D			+	put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
			S125					
810	OR51CnP	H38g66 0						
811	OR2WnP	H38g66 1						FL
812	OR51B1P	H38g66 2			AF149710			FL
813	OR7E81P	H38g66 3		OST021				
814	OR7E44P	H38g66 4		OST022				
815	OR5B7P	H38g66 5			OR6-55;OR6-57			
816	OR7E36P	H38g66 6		OST024				
817	OR2A5	H38g66 7			OR7-138;OR7-141		put	
818	OR5B1P	H38g66 8		OST936	OR8-122;OR8-123			
819	OR8B8	H38g66 9			HSTPCR85	+	yes	FL
820	OR8B4P	H38g67 0			AC002556-D		yes	FL
821	ORnP	H38g67 1						FL
822	OR8B3	H38g67 2			AC002556-B		yes	FL
823	OR2Bn	H38g67 3					yes	FL
824	OR8B6P	H38g67 4			AC002556-G			FL
825	OR8B5P	H38g67 5			AC002556-A			FL
826	OR4E2	H38g67 6			AE000658-A		yes	FL
827	OR8B7P	H38g67 7			AC002556-F			FL
828	OR11JnP	H38g67 8						FL
829	OR4E1P	H38g67 9			AE000658			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
830	OR10DnP	H38g68 0						
831	ORnP	H38g68 1						
832	OR8D2	H38g68 2			AC002556-E		yes	FL
833	OR11InP	H38g68 3						FL
834	OR11JnP	H38g68 4						FL
835	OR10AnP	H38g68 5	DS12;D S65			+		FL
836	OR8C3P	H38g68 6			OR912-106;OR912- 45;pDJ9j14			FL
837	OR2DnP	H38g68 7						FL
838	OR4PnP	H38g68 8						
839	OR7E21P	H38g68 9		OST035	OR4DG			
840	OR2M1	H38g69 0		OST037			put	
841	OR7AnP	H38g69 1						
842	OR5D11P	H38g69 2			OR8-125;OR8-127			
843	OR7E50P	H38g69 3			OR8-126			
844	OR7E45P	H38g69 4		OST049				
845	OR7E77P	H38g69 5		OST060				
846	OR8B2	H38g69 6			AC002556-C		yes	FL
847	OR8D1	H38g69 7		OST004	pDJ9j14		yes	FL
848	OR8B1P	H38g69 8		OST937	OR11-561			FL
849	OR7A1P	H38g69 9		OST938	OLF4p;OR19-3;hg513			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
850	OR7E8P	H38g70 0			OR11-11a;pDJ392a17			FL
851	OR4DnP	H38g70 1						FL
852	OR7E80P	H38g70 2		OST939	pDJ392a17			FL
853	OR4DnP	H38g70 3						FL
854	OR7E10P	H38g70 4			AC000385-A			FL
855	OR10B1P	H38g70 5			AC003956-A;OR19-19			FL
856	OR2InP	H38g70 6				+		
857	OR4Dn	H38g70 7					yes	FL
858	OR5ACn	H38g70 8					put	
859	OR2I1	H38g70 9			AC004179- A;dJ271M21.7;hs6M1- 14	+		
860	OR10H1	H38g71 0			AC004510	+	yes	FL
861	OR7E59P	H38g71 1		OST119				
862	OR7E28P	H38g71 2		OST128				
863	OR5B3	H38g71 3		OST129			put	
864	OR2A6	H38g71 4		OST182			put	
865	OR6Cn	H38g71 5					put	
866	OR7E54P	H38g71 6		OST185				
867	OR7E48P	H38g71 7		OST193				
868	OR67AnP	H38g71 8						FL
869	OR4DnP	H38g71 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
870	OR4CnP	H38g720						FL
871	OR4DnP	H38g721						FL
872	OR10H2	H38g722			AC004597-A	+	yes	FL
873	OR10H3	H38g723			AC004597-B	+	yes	FL
874	OR55CnP	H38g724						
875	OR55BnP	H38g725						
876	OR52VnP	H38g726						FL
877	OR2B3	H38g727			OR6-4;dJ80I19.1;hs6M1-1		yes	FL
878	OR52TnP	H38g728						FL
879	OR2J1P	H38g729			OR6-5;dJ80I19.2;hs6M1-4			FL
880	OR52HnP	H38g730						FL
881	OR2J3	H38g731			OR6-6;dJ80I19.7;hs6M1-3		yes	FL
882	OR52An	H38g732				+	put	
883	OR4Qn	H38g733					put	
884	OR52BnP	H38g734						FL
885	OR2N1P	H38g735	DS9		OR6-7;dJ80I19.3;hs6M1-2	+		FL
886	OR51EnP	H38g736				+		
887	OR2J2	H38g737			OR6-8;dJ80I19.4;hs6M1-6		yes	FL
888	OR2In	H38g738				+	put	
889	OR2J4P	H38g739			OR6-9;dJ80I19.5;hs6M1-5			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
890	OR7E40P	H38g74 0		OST215				
891	OR2H4P	H38g74 1			OR6- 3;dJ80I19.6;hs6M1-7			FL
892	OR7E52P	H38g74 2		OST245				
893	OR2InP	H38g74 3				+		
894	OR6C1	H38g74 4		OST267			put	
895	OR7E30P	H38g74 5		OST339				
896	OR5BAnP	H38g74 6	DS132			+		
897	OR7H1P	H38g74 7		OST940	CIT-B-440L2			FL
898	OR5B2	H38g74 8		OST073			yes	FL
899	OR5AZnP	H38g74 9						FL
900	OR5Bn	H38g75 0					yes	FL
901	OR52Bn	H38g75 1					yes	FL
902	OR5BnP	H38g75 2						FL
903	OR52Dn	H38g75 3					yes	FL
904	OR7A11	H38g75 4		OST527	CIT-HSP-87m17			FL
905	OR5BnP	H38g75 5						FL
906	OR51AnP	H38g75 6						FL
907	OR7A15P	H38g75 7		OST941	CIT-HSP-87m17;OR19- 1;OR19-134;OR19-146			FL
908	OR7C2	H38g75 8			CIT-HSP-87m17;OR19- 18		yes	FL
909	OR7E23P	H38g75 9		OST942	OR21-3			FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
910	OR2E1	H38g76 0			HS29K1;HSNH0569I24;hs6M1-9			
911	OR1I1	H38g76 1			F20569;OR19-20		yes	FL
912	OR1RnP	H38g76 2						FL
913	OR4F3	H38g76 3			AC004908		yes	FL
914	OR2AEn	H38g76 4					yes	FL
915	OR2InP	H38g76 5				+		
916	OR52AnP	H38g76 6				+		
917	OR7C1	H38g76 7		OST943	CIT-HSP-146e8;OR19-5;TPCR86	+	yes	FL
918	OR2A3P	H38g76 8			AC004889-B			FL
919	OR7A5	H38g76 9	DS8;DS19;DS61;DS68;DS112	OST944	HTPCR2	+	yes	FL
920	OR2InP	H38g77 0	DS72			+		
921	OR7A10	H38g77 1		OST027	CIT-HSP-146e8		yes	FL
922	OR2An	H38g77 2				+	put	
923	OR2M2	H38g77 3		OST423			put	
924	OR7A8P	H38g77 4		OST042	OR19-11;hg83			FL
925	OR2An	H38g77 5				+	put	
926	OR7E20P	H38g77 6		OST516				
927	OR2AnP	H38g77 7				+		
928	OR5BHnP	H38g77 8				+		
929	OR1En	H38g77					put	

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
930	OR1EnP	H38g78 0						
931	OR5Bn	H38g78 1					yes	FL
932	OR8RnP	H38g78 2						
933	OR5ANn	H38g78 3					yes	FL
934	OR5ANnP	H38g78 4						FL
935	OR5BRnP	H38g78 5						FL
936	OR2A1	H38g78 6			AC004889-A	+	yes	FL
937	OR10An	H38g78 7					yes	FL
938	OR2A9	H38g78 8	DS149		HSDJ0798C17	+		FL
939	OR2A7	H38g78 9			HSDJ0798C17	+	yes	FL
940	OR10A3	H38g79 0			HSHTPCR12	+	yes	FL
941	OR10Cn	H38g79 1					yes	FL
942	OR7A2P	H38g79 2			OLF4p;OR19-18;hg1003		yes	FL
943	OR10WnP	H38g79 3						FL
944	OR7A17	H38g79 4			HSHTPCR19		yes	FL
945	OR5Bn	H38g79 5					yes	FL
946	OR5BnP	H38g79 6						FL
947	OR1Q1	H38g79 7		OST226	HSTPCR106;OR9-A;hRPK-465_F_21	+	yes	FL
948	OR2Hn	H38g79 8	DS133; DS144; DS150			+	yes	FL
949	OR7EnP	H38g79						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
950	OR7A14	H38g80 0		OST945	OR19-12			
951	OR1B1	H38g80 1			OR9-B;hrPK-465_F_21		yes	FL
952	OR12D2	H38g80 2			AC004171;dJ994E9.8;h s6M1-20	+	yes	FL
953	OR7EnP	H38g80 3						FL
954	OR8BnP	H38g80 4						FL
955	OR1L1	H38g80 5			OR9-C;hrPK- 465_F_21;hg23		yes	FL
956	OR11An	H38g80 6					yes	FL
957	OR7AnP	H38g80 7						
958	OR1C1	H38g80 8			HSTPCR27	+	yes	FL
959	OR1D2	H38g80 9		OST946	OR17-4	+	yes	FL
960	OR1L3	H38g81 0			OR9-D;hrPK-465_F_21		yes	FL
961	OR12DnP	H38g81 1						FL
962	OR4G1P	H38g81 2			OLB			FL
963	OR2B4P	H38g81 3			AL050339- A;dJ974I11.1;hs6M1- 22			
964	OR11H1	H38g81 4			OR22-1		yes	FL
965	OR4Fn	H38g81 5					yes	FL
966	OR56AnP	H38g81 6						FL
967	OR8NnP	H38g81 7						FL
968	OR7EnP	H38g81 8						
969	OR4Pn	H38g81					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
		9						
970	OR6Cn	H38g82 0					put	
971	OR5BCnP	H38g82 1						
972	OR10QnP	H38g82 2	DS64			+		FL
973	OR5BnP	H38g82 3						FL
974	OR10PnP	H38g82 4						FL
975	OR1L4	H38g82 5		OST046	OR9-E;hRPK-465_F_21		yes	FL
976	OR2APnP	H38g82 6						
977	OR1L6	H38g82 7		OST947	HShRPK-465_F_21;hg16		yes	FL
978	OR6UnP	H38g82 8						FL
979	OR5C1	H38g82 9			OR9-F;hRPK-465_F_21		yes	FL
980	OR11InP	H38g83 0						FL
981	OR4AnP	H38g83 1						FL
982	OR4GnP	H38g83 2						FL
983	OR10Vn	H38g83 3					yes	FL
984	OR4G2P	H38g83 4			HS14a-1-B			FL
985	OR10VnP	H38g83 5				+		
986	OR4F4	H38g83 6			HS14a-1-A		yes	FL
987	OR4G3P	H38g83 7			OLC-7501			FL
988	OR5AKnP	H38g83 8						FL
989	OR10YnP	H38g83 9						FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
990	OR4GnP	H38g84 0						FL
991	ORnP	H38g84 1						
992	OR4Fn	H38g84 2					yes	FL
993	OR8A1	H38g84 3		OST025			yes	FL
994	OR8Bn	H38g84 4					yes	FL
995	OR6DnP	H38g84 5						
996	OR7E14P	H38g84 6		OST948	OR11-5	+		FL
997	OR2M4	H38g84 7		OST710	HSHTPCR18	+	put	
998	OR4WnP	H38g84 8						
999	OR4Fn	H38g84 9	DS36			+	yes	FL
1000	OR7EnP	H38g85 0						
1001	OR4GnP	H38g85 1						FL
1002	OR10JnP	H38g85 2						
1003	OR52En	H38g85 3					yes	FL
1004	OR4RnP	H38g85 4						FL
1005	OR4Cn	H38g85 5					yes	FL
1006	OR4AnP	H38g85 6						
1007	OR4AnP	H38g85 7	DS54			+		
1008	OR4AnP	H38g85 8						FL
1009	OR9Gn	H38g85 9					yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1010	OR10An	H38g86 0					yes	FL
1011	OR4Cn	H38g86 1					yes	FL
1012	OR10VnP	H38g86 2						
1013	OR10UnP	H38g86 3						FL
1014	OR7E2P	H38g86 4	DS127		OR11-6;hg94	+		FL
1015	OR7E35P	H38g86 5		OST018				FL
1016	OR9KnP	H38g86 6						
1017	OR7E13P	H38g86 7		OST949	OR11-4			FL
1018	OR7EnP	H38g86 8						FL
1019	OR9Kn	H38g86 9					yes	FL
1020	ORnP	H38g87 0						FL
1021	OR7EnP	H38g87 1		OST950	OR11-1;hg500	+		FL
1022	OR7EnP	H38g87 2						FL
1023	OR3A4P	H38g87 3		OST951	OR17-24;OR17-25	+	yes	FL
1024	OR8QnP	H38g87 4						
1025	OR7EnP	H38g87 5						FL
1026	OR7EnP	H38g87 6						FL
1027	OR3A1	H38g87 7	DS2		OLFRA03;OR17- 40;hg138	+	yes	FL
1028	OR5Gn	H38g87 8					yes	FL
1029	OR5MnP	H38g87 9						

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1030	OR7EnP	H38g88 0						FL
1031	OR5G1P	H38g88 1		OST952	OR11- 104;OR93;OR93Hum			FL
1032	OR5PnP	H38g88 2						FL
1033	OR10AEn P	H38g88 3						
1034	OR3A2	H38g88 4		OST953	OR17-228	+	yes	FL
1035	OR10Jn	H38g88 5					yes	FL
1036	OR1D3P	H38g88 6		OST954	OR17-23			FL
1037	OR10Jn	H38g88 7					yes	FL
1038	OR1D4	H38g88 8			OR17-30	+	yes	FL
1039	OR5GnP	H38g88 9						FL
1040	OR4SnP	H38g89 0						FL
1041	OR5GnP	H38g89 1						FL
1042	OR9HnP	H38g89 2						FL
1043	OR1A1	H38g89 3			OR17-7	+	yes	FL
1044	OR1A2	H38g89 4			OR17-6	+	yes	FL
1045	OR8AnP	H38g89 5						FL
1046	OR1P1P	H38g89 6			OR17-208	+		FL
1047	OR7E12P	H38g89 7		OST955	AC000378-A;OR11- 3;hg1058	+		FL
1048	OR4A1P	H38g89 8			OR11-30			FL
1049	OR10G3	H38g89 9			AE000658-D		yes	FL

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1050	OR10G1P	H38g90 0			AE000658-C			FL
1051	OR10G2	H38g90 1			AE000658-B		yes	FL
1052	OR5Tn	H38g90 2					yes	FL
1053	OR7EnP	H38g90 3						FL
1054	OR7EnP	H38g90 4						FL
1055	OR4AnP	H38g90 5						FL
1056	OR4C1	H38g90 6			HSHTPCR11	+		FL
1057	OR1EnP	H38g90 7						
1058	OR7KnP	H38g90 8						FL
1059	OR4CnP	H38g90 9						FL
1060	OR1RnP	H38g91 0						FL
1061	OR5AUn	H38g91 1					yes	FL
1062	OR4Cn	H38g91 2					yes	FL
1063	OR4Cn	H38g91 3					yes	FL
1064	OR13DnP	H38g91 4						FL
1065	OR5n	H38g91 5	DSU116			+		
1066	OR2Hn	H38g91 6	DSU150			+		
1067	ORn	H38g91 7	DSU151			+	put	
1068	ORn	H38g91 8	DSU17			+		
1069	ORn	H38g91 9	DSU18			+		

SEQ ID #	Symbol	HORDE	Digi	OST	Trivial	Tran	Int.	E
1070	ORn	H38g92 0	DSU35			+		
1071	OR6Fn	H38g92 1	DSU41			+		
1072	ORn	H38g92 2	DSU49			+		
1073	ORn	H38g92 3	DSU50			+		
1074	OR10An	H38g92 4	DSU57			+		
1075	ORn	H38g92 5	DSU58			+		
1076	OR2Ln	H38g92 6	DSU59			+		
1077	OR10Jn	H38g92 7	DSU60			+		
1078	OR1Kn	H38g92 8	DSU63			+		
1079	OR10Dn	H38g92 9	DSU7			+		
1080	ORn	H38g93 0	DSU32			+		
1081	OR2Ln	H38g93 1	DSU38			+		
1082	ORn	H38g93 2	DSU62			+		
1083	ORn	H38g93 3	DSU48			+		
1084	OR2n	H38g93 4	DSU111			+		

Table 2

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SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
153	OR10D3	0	11	137.96SDVISV	69	M	AC074177.4	12106 ... 13038
154	OR7EnP	4	4	11.58	MVACGVLDLHIIDSFAL	53	R	AF091580.1	7 ... 663
155	OR1D5	0	17	3.75	LVVTNLLYLLLLTGIFT	49	M	AF073967.1	2 ... 649

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
156	OR10Nn P	4	11	138.02	LQSGGVVHILFGNVLAT	82	M	AC074177.4	159287 ... 158526
157	OR2F1	0	7	148.62	LLGGFTSSVQIISSLLT	56	M	AF073974.1	41 ... 649
158	OR7EnP	7	4	11.58	MAGGELLDLHILPALGL	54	M	AF073989.1	547 ... 1515
159	OR8FnP	6	11	137.96	LLVICEMGAHCVCNIF	75	M	AC069561.1 0	51687 ... 50743
160	OR2Q1P	2	7	148.62	LLCGFSANMEIVSGVIL	49	M	AC020865.3	190954 ... 189954
161	OR2W1	0	6	33.74	LMGSCMINVLLVLGIVT	88	M	AF102516.1	52 ... 669
162	OR7EnP	7	4	11.58	MVACGVLDLHITHSFGL	53	R	AF091580.1	7 ... 663
163	OR6B1	0	7	148.62	LIMCCGIIAKFDLAIFF	61	M	NM_010983. 1	178 ... 975
164	OR10Kn	0	1	154.34	MLGSSACVVTILGALI	79	M	AC073778.1	168744 ... 167803
165	ORnP	13	11	138.02	VPYCIGGHLICLSLSS	33	M	AC074177.4	12106 ... 13038
166	OR4F2P	4	6	186.49	IHGGMVLHFQFVNSICG	50	M	AB030896.1	1 ... 906
167	OR7EnP	3	4	11.58	MVACGVLDLHIIDSFGL	54	M	AF102536.1	22 ... 669
168	OR1F2P	0	16	6.15	MSADNGVNLHLIEAVTT	72	R	M64377.1	1 ... 939
169	OR2P1P	7	6	33.74	FGGSCMSNQSALVRXSV	48	M	NM_008762. 1	1 ... 936
170	OR7E43 P	5	4	5.57	MAGGELFDLHIMPAFGL	54	M	AF102536.1	22 ... 669
171	OR4F1	4	6	0.23	IHGGMVLHFQFVNSICG	50	M	AB030896.1	1 ... 906
172	OR7E55 P	5	3	89.94	MAGDEFDLHILPAFGL	53	M	AF073989.1	547 ... 1515
173	OR13Dn	0	9	86.89	MLGSCWITLQLMTNSLI	61	M	AC023789.5	371264 ... 372220
174	OR4CnP	3	16		AHGAIVGHIQFVNSICL	74	M	AF102522.1	40 ... 660
175	OR10D1 P	1	11	137.96	LHGCCGFQFLGSMPS	83	M	AC074177.4	128803 ... 129726
176	OR4Cn	0	16		LHGGIVGHVQLVNSICL	86	M	AB030895.1	1 ... 924

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
177	OR8GnP	0	11	137.96	LSAICGLGIHFVLSNIM	73	M	AC074177.4	106297 ... 105361
178	OR13CnP	2	9	86.85	MFGACGGNLQLMASFLG	82	M	AJ251154.1	2703 ... 1747
179	OR4CnP	5	16		LHEAIVLHIQFINSCL	61	M	AF102522.1	40 ... 660
180	OR13Cn	0	9	86.81	MLGTCGINVQFMATFIT	69	M	AJ133425.1	61 ... 1014
181	OR4CnP	0	16		LHGGIMGHIQLVNSMCL	63	M	AB030895.1	1 ... 924
182	OR51Bn	0	11		AHSVSGRSPVRPLITIL	76	M	AF071080.2	15931 ... 16851
183	OR7E5P	2	11	51.76	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
184	OR13Cn	0	9	86.77	MFGSCVSNVQLMSNFL	71	M	AJ251154.1	2703 ... 1747
185	OR4Sn	0	16		LHGGIAAHLQLVNSISA	56	M	AB030895.1	1 ... 924
186	OR51BnP	4	11		VHYPEWRSPPPPLVIFL	72	M	AF071080.2	15931 ... 16851
187	OR6JnP	1	14	2.72	CFGTFFGSFPLDLSVIC	50	R	M64378.1	1 ... 933
188	OR51Bn	0	11		SHAISGRSPISPQTTVL	76	M	AF071080.2	26330 ... 27262
189	OR7EnP	2	11	71.8	MFACGVLDLHIIDSFGL	55	M	AF102536.1	22 ... 669
190	OR2An	0	6	144.32	TSAVCTTLIHLVGAGLG	81	M	L14566.1	62 ... 667
191	OR7E22P	3	3	89.94	MVACDVLDLHIIDSFGL	56	M	AF073989.1	547 ... 1515
192	OR7E4P	2	11	71.8	IVACDVLDLHIMHSFGL	55	M	AF102536.1	22 ... 669
193	OR7E66P	9	3	89.94	MAGGELLFLHIMPAFGL	55	M	AF073989.1	547 ... 1515
194	OR6Mn	0	11	138.18	TFGTFGGSFVNLSVIS	50	M	NM_010991.1	1 ... 939
195	OR2ALnP	11	11	112.69	ILGTCASNFDFFNHLLL	32	M	AL359352.1	85325 ... 86251
196	OR6MnP	2	11	138.18	TGGTFGGSCPVNLSILT	50	M	NM_010991.1	1 ... 939
197	OR4D1	0	17	60.7	IHGGVAGHVQLMNSLVI	90	M	AC019272.4	62255 ... 61317
198	OR5D2P	3	11	51.09	LCVVTWCTLFTSANES	48	M	AC073947.3	29192 ... 30115

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
199	OR7E38P	7	7	95.91	MAGGELFHLHIMPAFGL	55	R	AF091580.1	7 ... 663
200	OR4D2	0	17	60.7	IHGGVAGHVQLKNSLDV	89	M	AC019272.4	183633 ... 182701
201	OR7E7P	4	7	95.91	MIACGVLDLHIIDSFGL	56	R	AF091580.1	7 ... 663
202	OR5AHnP	0	19	68.97RSGIMC	77	M	AC020957.2	48184 ... 49107
203	OR2U2P	5	6	33.53	LVYSCIVNIPYTMCIIV	49	M	AC044846.2	105668 ... 104736
204	OR2U1P	2	6	33.53	LVCTCMINILCCVVIFA	54	M	AF102516.1	52 ... 669
205	OR2H2	0	6	33.19	ILGTCVIEVQSVASILV	89	M	AL078630.1	41097 ... 40165
206	OR2H5P	7	6	33.19	FLGTCVIEVQSMASILV	84	M	AL078630.1	41097 ... 40165
207	OR2In	0	6	33.19	LLGSCASNAQLMARILL	74	M	AL078630.1	151152 ... 150391
208	OR11HnP	5	13		IFNTCLCWIPLCLSVIG	60	M	AF121972.1	171 ... 1109
209	OR7EnP	6			AAACDVIDLHITHSFGL	56	M	AF073964.1	41 ... 649
210	OR9In	0	11	54.06	FTAGCGCGLRCIFGVIA	50	R	AF091579.1	7 ... 663
211	OR2AFnP	11	X	140.17	MLGTCGHVTLAGISTLL	43	R	L34074.1	73 ... 1011
212	OR13KnP	5	X	140.17	MFGMCVIIHIGIGTLL	43	R	L34074.1	73 ... 1011
213	OR13Cn	0	9	86.77	MFGSCVSNVQLLSNFL	68	M	AJ251154.1	2703 ... 1747
214	OR13Fn	0	9	86.77	MLGSCGTTVESMISLLM	55	M	AJ133428.1	61 ... 1017
215	OR9Qn	0	11	54.08	FTGSCGASVRSIFAVIA	47	M	AF146372.1	509 ... 1456
216	OR2TnP	1	1	254.77	ILIGFGDMLVMCCMLI	71	M	AF102527.1	22 ... 669
217	OR4Kn	0	14	0.08	IHVGMIVHSHFTNSISS	56	M	AF259072.1	104176 ... 105099
218	OR2B8P	0	6	31.6	LLGSCTINLQLLVSILV	62	R	L34074.1	73 ... 1011

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
219	OR2Tn	0	1	254.77	MLAGVALDLLITCCMLT	57	M	AF102527.1	22 ... 669
220	OR4Kn	0	14	0.08	IHTGIAMHSQFMTSIAS	53	M	AF259072.1	104176 ... 105099
221	OR2A4	0	6	144.76	TSAVCTTLIHLVGAGLG	81	M	L14566.1	62 ... 667
222	OR7EnP	6	2	161.53	MVACDVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
223	OR4Kn	0	14	0.08	MHGGILVHSQFMTSIAV	57	M	AF259072.1	104176 ... 105099
224	OR13InP	6	9	86.85	MYGSCVLNNVVIGKTLL	41	M	AJ251155.1	15491 ... 16423
225	OR7EnP	8	2	161.53	MVACDVLDLHIFFDFGL	54	M	AF073989.1	547 ... 1515
226	OR6Jn	0	14	2.72	CFGTFGGSFPLDLVIC	50	R	M64378.1	1 ... 933
227	OR4Mn	0	14	0.08	LHGAMLGHIQLMSSISV	54	M	AC019272.4	183633 ... 182701
228	OR4VnP	10	11	51.09	IHGIIVLHFQMVNSFAV	50	M	AB030896.1	1 ... 906
229	OR6Xn	0	11	138.36	AFGTFSVICQLGATVIG	46	M	AF106007.1	178 ... 975
230	OR51Gn	0	11	3.7	LHSSSSRLPLLGVVTVV	55	M	NM_013617.1	1 ... 921
231	OR6EnP	3	14	2.72	SFGTFCTLIPLGIASLG	82	M	NM_010991.1	1 ... 939
232	OR4NnP	2	14	0.08	LHGGGAGHIQLMNSMTL	54	M	AC019272.4	62255 ... 61317
233	OR6MnP	7	11	138.18	IFGTFGGARLVXSMTV	37	R	M64378.1	1 ... 933
234	OR4Nn	0	14	0.08	LHGGGAGHIQLMNSMTL	57	M	AC019272.4	62255 ... 61317
235	OR4Cn	0	11	51.09	LHGGIGGHIQFVNSMCA	65	M	AF102522.1	40 ... 660
236	OR4KnP	4	14	0.08	IHAGMGTHSQFMDSMGT	51	M	AF259072.1	104176 ... 105099
237	ORnP	8	11	137.59	AIAITVVVAHAAAGVVA	35	M	AC069559.8	73704 ... 74636
238	OR5D3	0	11	51.15	FCVVTAWCTYFISANES	46	R	U50948.1	34 ... 978
239	OR2G1P	6	6	33.53	LLGSCVSNIQVLASLLL	84	M	AL359352.1	85325 ... 86251

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
240	OR4Kn	0	14	0.08	IHTGMIVHSQFINSLS	51	M	AF259072.1	104176 ... 105099
241	OR8BnP	2	11	137.59	LCVFSGMGAHNIVVGIV	68	M	AC069559.8	120212 ... 119283
242	OR2B2	0	6	31.47	LLGSCASNQWLISFLI	89	R	L34074.1	73 ... 1011
243	OR7EnP	3	2	73.87	MVACDVLRLRIIDSFGL	54	M	AF073989.1	547 ... 1515
244	OR4KnP	3	14	0.08	IHTGIVVHSQFMTSIAI	57	M	AB030896.1	1 ... 906
245	OR2AD1P	6	6	33.87	FLGACTSSIVLVFGFLV	51	M	AL136158.1 4	162423 ... 161461
246	OR1AAnP	8	X	140.17	MIVDNTIVLHLIIGVII	48	M	AC068902.1 1	144125 ... 143193
247	OR1E3P	1	17	2.99	MLGVSLHLHLMMGILI	74	R	M64392.1	1 ... 942
248	OR8BnP	3	11	137.59	FCVFSGMGAHNIVVGIV	63	M	AC069561.1 0	96653 ... 95690
249	OR5Hn	0	3	104.18	FAGTCFGHIHLVLSIQF	55	R	AF091575.1	52 ... 663
250	OR1G1	0	17	2.99	LMVMAAMHLHLITGTGI	56	R	M64392.1	1 ... 942
251	OR5HnP	2	3	104.18	FAVTCGGHIHFVFSIQF	46	M	AC068904.1 5	165039 ... 165965
252	ORnP	5	X	140.17	MLVTCSHHFLSFTGIWS	36	R	U50948.1	34 ... 978
253	ORnP	11	X	140.17	LIVTFAKITTTQDHHHH	29	M	AC069561.1 0	127636 ... 126698
254	OR4PnP	2	11	51.09	LHGDIAHSQLVNSISL	51	M	AB030895.1	1 ... 924
255	OR13Hn	0	X	140.17	TLATCTTVAMLITSTLL	47	M	AJ251154.1	35662 ... 36615
256	OR7D1P	5	19	11.38	VMAGTAIFVHLLATLGF	64	R	AF091580.1	7 ... 663
257	OR4KnP	2	18	47.77	IHNGIVVHSQFMTSIAI	55	M	AB030896.1	1 ... 906
258	OR7E24	1	19	11.38	MVACDLIDLHIIMGFGL	60	R	AF091580.1	7 ... 663
259	OR51NnP	2	11	3.6	LHGFSARSPSLGVLTV	49	R	AF079864.1	632 ... 1576
260	OR7E18P	6	19	11.38	VAGCOLLDLHIMLAFL	59	M	AF102536.1	22 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
261	OR7E19 P	2	19	11.38	MYVCDVLNLHIMDSFGL	58	M	AF073989.1	547 ... 1515
262	OR7E41 P	7	11	14.36	IVVCDMLDLHIHSTFGL	55	M	AF073989.1	547 ... 1515
263	OR2R1	3	7	148.69	LLGGFVVNMELISSVLV	77	M	AF073974.1	41 ... 649
264	OR10AC nP	7	7	148.69	MVGCGGRVGLLLACLLL	46	M	AC073778.1	168744 ... 167803
265	OR51Ln	0	11	3.79	LHTFSARVPTLGVVTLV	54	R	AF079864.1	632 ... 1576
266	OR52Jn P	3	11	3.79	MHTGSSRLPILGVALDA	57	M	AF121979.1	53 ... 1106
267	OR9LnP	9	8	45.22	TVVNNFFFFFFFIDLIA	37	M	AC069561.1 0	147203 ... 146274
268	OR51Pn P	4	11	3.79	MHSISARLPALGVVSML	48	M	AF071080.2	2641 ... 1697
269	OR5HnP	4	3	104.18	FAVTCLGHIHFFFSIQL	50	R	AF091575.1	52 ... 663
270	OR51An	0	11	3.79	EHSVSVKLPFTYFGCLV	48	R	AF079864.1	632 ... 1576
271	OR5HnP	6	3	104.18	FAVTCLGHIHFVFSIQF	46	M	AC068904.1 5	165039 ... 165965
272	ORnP	11	17	17.43	LLPCILSIALLYYYYYY	27	M	AL359352.1	9138 ... 8177
273	OR52En	0	11	3.79	MHTGSARFPFFYCAILF	57	M	AF121979.1	53 ... 1106
274	OR5Hn	0	3	104.18	FVVTCLGHIHFVFAVQF	53	R	AF091575.1	52 ... 663
275	OR4CnP	3	11	50.21	VHRGVVGHIQFVNSICL	73	M	AF102522.1	40 ... 660
276	OR52En	0	11	3.79	MHTLSGRFPSLYCANLF	60	M	AF121979.1	53 ... 1106
277	OR10Dn	0	11	138	LHGCGGIHILLGNVLSI	86	M	AC074177.4	12106 ... 13038
278	OR5HnP	2	3	104.18	FVVTCLGHIHFVFAIQF	54	R	AF091575.1	52 ... 663
279	OR13An	0	10	47.91	LTASLALNIHLIADYGV	67	M	AF102520.1	16 ... 669
280	OR5HnP	2	3	104.18	FGGTCLGHIHILLSIQF	57	R	AF091575.1	52 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
281	OR5Kn	0	3	104.47	FCETCGAHIHLFSVQF	45	M	AC069559.8	36251 ... 35322
282	OR7EnP	9	21	17.99	MAGGELFHLQIMPAFGL	57	M	AF073989.1	547 ... 1515
283	OR4DnP	6	8	77.48	IHGGVAGHVQVMNSLVI	87	M	AC019272.4	62255 ... 61317
284	OR2ARn P	0	3	30.89	MLGSC.....	71	M	AJ251154.1	56533 ... 57369
285	OR7E29 P	4	3	136.03	MAGGELLDLHIMPAFGL	56	M	AF073989.1	547 ... 1515
286	OR4CnP	3	11	51.12	AHGAIVGHIQFVNSICL	74	M	AF102522.1	40 ... 660
287	OR5PnP	2	11	6.93	LVGTCVGNTFCPSSIIV	74	M	AF121977.1	262 ... 1197
288	OR7EnP	5	3	136.04	MVACGVLDLHIIGSFGL	52	R	AF091580.1	7 ... 663
289	OR56An	0	11	4.73	MNLPSFRLPILQAGLLS	41	M	AF121975.1	50 ... 1012
290	OR56An P	9	11	4.73	KNQAFFRMPILQGGLLS	73	M	AF121981.1	89 ... 475
291	OR5Pn	0	11	6.89	LAATCVAISYSLSSIIV	63	M	AF121977.1	262 ... 1197
292	OR7E53 P	5	3	136.04	MAGGEFPDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
293	OR5Pn	0	11	6.89	LVGTCMGNTFCPSSIIA	83	M	AF121977.1	262 ... 1197
294	OR52Ln	0	11	4.73	MHSSSVRLPFLGMAVIL	59	M	AF121976.2	474 ... 1307
295	OR5E1	3	11	6.89	LGATXGYNIQLFSNLG	51	R	U50948.1	34 ... 978
296	OR56An P	3	11	4.73	MNLASFRMAILPPPPPP	39	M	AF121976.2	474 ... 1307
297	OR4KnP	2	8	88.25	IHTGMIVHSQFIDS...	57	M	AB030896.1	1 ... 906
298	OR52Ln	0	11	4.73	MHSSSVRLPFLGVAVVL	59	M	AF121976.2	474 ... 1307
299	OR7EnP	1	4	74.82	MVF.....	55	R	AF091580.1	7 ... 663
300	OR52Xn P	5	11	4.73	MHSASLXLSFLAVALGG	51	M	AF121976.2	474 ... 1307
301	ORnP	13	4	74.82	STGCKGRKXLKLVRFQ	24	R	M64386.1	130 ... 975
302	OR56An	0	11	4.73	MNLTSFRVPVLQAGLLS	84	M	AF121981.1	89 ... 475

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
303	OR56AnP	10	11	4.73	LI...GMMXNL...KKK	60	M	AF121981.1	89 ... 475
304	OR1R1P	5	17	3	MVGISAVHLHLIEGVVA	48	M	AF073967.1	2 ... 649
305	OR52EnP	2	11	3.79	MHTGSGRSPFLYGAILF	64	M	AF121979.1	53 ... 1106
306	OR51AnP	4	11	3.7	EHTVALKLPLLGAGSTL	46	R	AF079864.1	632 ... 1576
307	OR51An	0	11	3.7	EHSVSVKLPPTYFGCLV	48	R	AF079864.1	632 ... 1576
308	OR4CnP	1	11	51.12	VHGGVVGHVQFVNSICL	75	M	AF102522.1	40 ... 660
309	OR52JnP	9	11	3.79	MHTGACRFPI LGVVYLN	58	M	AF121979.1	53 ... 1106
310	OR4RnP	9	11	51.12GGGVXSVNGNYL	66	M	AF102522.1	40 ... 660
311	OR52JnP	0	11	3.79	MHTGACRLPMLGVVFN	58	M	AF121976.2	474 ... 1307
312	OR4CnP	3	11	51.12	VHGGGVGHIQFINSICL	76	M	AF102522.1	40 ... 660
313	OR51AnP	2	11	3.79	EHSASAKLPPTYFVTGL	83	M	AF121985.1	2 ... 478
314	OR7EnP	15	12	93.55	IVVCDLLDLHIHSTFGL	55	M	AF073989.1	547 ... 1515
315	OR5MnP	2	11	52.17	CIVLHVYLMERMVASNQ	54	M	AF102528.1	52 ... 669
316	OR10ABnP	1	11	6.93	MLASCAVFCITILSVLG	47	M	AC073778.1	168744 ... 167803
317	OR52SnP	2	11	3.79	MHSTSARLPHLSVATGV	54	M	AF121976.2	474 ... 1307
318	OR5Mn	0	11	52.14	CIVHIFYTAAWMLANFY	49	R	AF091579.1	7 ... 663
319	OR10Sn	0	11	138.1	LHASCIIHIHLSIVAG	61	M	AF259072.1	32953 ... 32000
320	OR5MnP	4	11	52.14	CIVHIFYTTAWMLANFY	48	R	AF091579.1	7 ... 663
321	OR10Gn	0	11	138.1	LHGSCGSHVQLIDIVAG	61	M	AF259072.1	55611 ... 54658
322	ORnP	20	11	29.15	ILGIYEGSAHYFIILFL	33	M	AL365337.1	192661 ... 191711
323	OR5MnP	2	11	52.19	CIVIYGYSMEWMVANLS	54	M	AF102528.1	52 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
324	OR10GnP	10	11	138.1	LYGSCWGHLPYVIKFT	30	M	L14567.1	17 ... 667
325	OR10TnP	1	1	154.34	LVACCACTIVLILSVLV	57	M	X92969.1	8035 ... 8961
326	ORnP	16	11	52.17	LAAPLLLVFVLAASAAA	33	R	M64376.1	1 ... 999
327	OR10RnP	11	1	154.5	MLAVFTICVFLIGGALV	47	M	AC023611.2	108224 ... 107271
328	OR5MnP	2	11	52.16	CIVHLVYTMWMMVANFY	49	R	AF091579.1	7 ... 663
329	OR7EnP	4	8	6.68	MLACGVLDLHIDSFGL	55	M	AF102536.1	22 ... 669
330	OR10Tn	0	1	154.27	LLACCLTIVALLLSVIV	58	M	AC012302.5	54283 ... 55224
331	OR1E1	0	17	3.04	MLGDSLLHLHLIMGILI	83	R	Y07557.1	1 ... 942
332	OR5BKnP	4	12	42.11	STGGAIAIMDFLSQWGL	46	M	AF073965.1	2 ... 643
333	OR5MnP	3	11	52.17	CIVHIVYTMWMMVANLF	48	R	AF091579.1	7 ... 663
334	OR3A3	0	17	3.06	LHAGCACNTHALAAMAA	49	M	AF073967.1	2 ... 649
335	OR10ADnP	1	12	42.11	TFGVCTFNFLIIDAVIS	44	M	AF247657.1	1 ... 945
336	OR10Rn	0	1	154.5	MLAICAGATVLICGVLV	56	M	AC073778.1	168744 ... 167803
337	OR5TnP	4	11	51.94	MCGTCAAHIHAFFVIEV	51	M	AF121977.1	262 ... 1197
338	OR4GnP	15	7	0.23	ICRKMAVHSQFVNSISA	42	M	AB030892.1	1 ... 939
339	OR6Yn	0	1	154.5	LVVCYGCTIKFDLAVII	61	M	NM_010983.1	178 ... 975
340	OR1E2	0	17	3.15	MLSDSLLHLHLIMGILI	80	R	Y07557.1	1 ... 942
341	OR8Hn	0	11	51.94	MVGACGINVNWILATLV	51	M	NM_013728.1	1 ... 948
342	OR4Fn	0	7	0.23	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
343	OR10Kn	0	1	154.27	MLGCSACVIIILCVLI	83	M	AC073778.1	168744 ... 167803
344	OR7LnP	11	X	140.17	MLGVCGHGTNLXFFFFI	32	M	AL133160.1	63932 ... 64759
345	OR8InP	7	11	51.94	MVVCCMINVSVSLATLG	44	R	M64386.1	130 ... 975

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
346	OR10Rn P	0	1	154.5	MLAVCTSI VGFIFGV LV	54	M	AC073778.1	168744 ... 167803
347	OR2AFn P	11	X	140.17	MLGTCGHVTLAGISTLL	43	R	L34074.1	73 ... 1011
348	OR8Kn	0	11	51.94	LEIILVYVFLKIFSNLF	55	M	AF102528.1	52 ... 669
349	ORnP	7	10	127.57	S.CCCLLTYYIIHHHHH	31	M	AC020958.1	164590 ... 163746
350	OR8KnP	10	11	51.94	MIIILYQMVKIFSNLF	35	M	AC073945.4	152209 ... 153150
351	OR51Hn	0	11	3.6	MHGISSRPVPLGVVTL	49	R	AF079864.1	632 ... 1576
352	OR7EnP	5	3	136.03	MVACGVLDLHIIDSFGL	51	M	AF073989.1	547 ... 1515
353	ORnP	8	3	56.17	LLLLFLIEQH.....I	32	R	M64376.1	1 ... 999
354	OR5BMn P	20	3	103.93	KXNKCTLSSSLMVFIQF	30	M	AF146372.1	509 ... 1456
355	OR10Gn P	0	11	138.1	LHGCGGHHFQFTDILAT	63	M	AF259072.1	55611 ... 54658
356	OR2Yn	0	5	209.23	LLGSCAANIQLMARVVV	74	M	AC044846.2	139468 ... 138536
357	OR10Dn P	1	11	138.1	LHGCGGHHVLLSNVVAM	66	M	AC074177.4	128803 ... 129726
358	OR3BnP	7	X	158.48	IHAPSILNTYLLSFVAA	37	M	AL136158.1 4	29455 ... 30402
359	OR8Dn	0	11	138.1	LCVICAVDIHICIIGNMA	62	R	X80671.1	203 ... 1129
360	OR5RnP	0	11	52.13	LLMICVYVFHIIIFADMS	68	M	AF102528.1	52 ... 669
361	OR10Gn	0	11	138.1	LHGSCGSHVQLINIVAG	58	M	AF259072.1	55611 ... 54658
362	OR5BDn P	12	11	53.74	MTGTCVVIHRALSSITP	39	M	NM_013728. 1	1 ... 948
363	OR5ALn P	1	11	52.13	VIVVLSYVQALIANTC	52	M	AC073947.3	29192 ... 30115
364	OR52Hn P	3	11	4.15	LHFVSGRVPCLGVPVT	59	M	AF121975.1	50 ... 1012
365	OR10Gn	0	11	138.1	LHGCGSSHVQLITVVAG	56	M	AF259072.1	55611 ... 54658

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
366	OR5Mn	0	11	52.17	CIVHIVYTMWVMVANLF	52	M	AF146372.1	509 ... 1456
367	OR51Mn	0	11	4.15	MHSFSIRAPILGVVTVL	50	M	NM_013617.1	1 ... 921
368	OR6Tn	0	11	138.1	SFGTFAAWCPLALSVLG	52	M	NM_010991.1	1 ... 939
369	OR6DnP	5	10		SLGSFVVLGLKALVVLT	69	R	AF034903.1	85 ... 1053
370	OR4B1	0	11	45.36	IHGVIGGHIQVVSFSF	62	M	AF102522.1	40 ... 660
371	OR5ALnP	4	11	52.13	VISVVGYMIQALIANVC	50	M	AF146372.1	509 ... 1456
372	OR51Qn	0	11	4.15	FHSFSACAPSLGLAIIV	49	M	NM_013617.1	1 ... 921
373	OR4Dn	0	11	138.1	LHGGIAGHVQLMNNVTM	63	M	AC019272.4	62255 ... 61317
374	OR52Nn	0	11	4.58	MHTGSLRLPSLGAIGF	52	M	NM_013619.1	118 ... 969
375	OR4Xn	0	11	45.36	MHGGAIHGQQLINGISV	58	M	AB030896.1	1 ... 906
376	OR8Jn	0	11	52.03	LLIVVLYTVVYVSANVG	77	M	X89682.1	2 ... 472
377	OR51JnP	2	11	4.15	MHSMSIKLPLLGIVTFL	46	M	AF071080.2	15931 ... 16851
378	OR10Gn	0	11	138.1	LHGSCSSHVQLIDIVAG	60	M	AF259072.1	55611 ... 54658
379	OR52En	0	11	4.58	MHTGTVRLPFLGVIIID	66	M	AF121979.1	53 ... 1106
380	OR4Xn	0	11	45.36	LHGGIIGHAQLINGLSI	64	M	AB030895.1	1 ... 924
381	OR10A2	1	11	5.69	MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
382	OR5Mn	0	11	52.14	CIVHVYVICWMIANFY	49	R	AF091579.1	7 ... 663
383	OR52En	0	11	4.58	MHTGSVRFPFLISVVGI	59	M	AF121979.1	53 ... 1106
384	OR8Kn	0	11	51.94	LLIGLIYILVKIFADLS	53	M	AF146372.1	509 ... 1456
385	OR10An	0	11	5.66	MFGACASVVQWAATFIF	89	M	AF247657.1	1 ... 945
386	OR8LnP	3	11	52.13	LIVMSYVLQLLANTF	51	M	AF102528.1	52 ... 669
387	OR5BPnP	8	11	52.82	VVVVVGSI VPPVGLHL	43	R	U50948.1	34 ... 978
388	OR52Nn	0	11	4.58	MHTGSARLPFLGAIGF	54	M	AF121976.2	474 ... 1307

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
389	ORnP	7	11	45.36	WWWIALLR.AAAAAK	28	M	X89686.1	32 ... 472
390	OR8JnP	1	11	51.94	LLIVILQTTVCVFSNLF	99	M	X89682.1	2 ... 472
391	OR5Mn	0	11	52.24	CIVIFVYNSQLMVATLS	50	R	AF091579.1	7 ... 663
392	OR52En	0	11	4.58	MHTVSIRMPLLGSILL	66	M	AF121979.1	53 ... 1106
393	OR5Tn	0	11	51.94	VCGTCAAHIALFVIEV	52	M	AF146372.1	509 ... 1456
394	OR52NnP	5	11	4.58	MHTGSVQLPFLGAAIGF	51	M	NM_013619.1	118 ... 969
395	OR4B2P	6	11	45.36	IFGIIGRHVQVNSELS	53	M	AB030896.1	1 ... 906
396	OR51KnP	6	11	4.15	MHSCSGKLP LLGIVNFL	51	M	NM_013617.1	1 ... 921
397	OR52QnP	10	11	4.58	MYTGSVRFPFLFVAVGI	45	M	AF121979.1	53 ... 1106
398	OR4Fn	0	15	86.21	IHGGMIIHIQFVNSISA	50	M	AF102522.1	40 ... 660
399	OR11MnP	1	12	41.92	FSAACGSSFTL.....	48	M	AL359381.1	175785 ... 176720
400	OR52Nn	0	11	4.44	MHTGSARLPFLGVAIGF	57	M	NM_013619.1	118 ... 969
401	OR56An	0	11	4.58	MNLASFRMPILQGGLLS	73	M	AF121981.1	89 ... 475
402	OR5AwnP	14	X		LXADFTSNLPTTSSNVV	39	R	X80671.1	203 ... 1129
403	OR52Nn	0	11	4.51	MHTGSARLPFLGVAIGF	55	M	AF121976.2	474 ... 1307
404	ORnP	15	X		ISCIFELTLPLPSNVNV	31	M	AC073947.3	29192 ... 30115
405	OR52EnP	6	11	4.58	VHSVSVRMPILGNIILL	62	M	AF121979.1	53 ... 1106
406	OR5BHnP	9	X		MVASCGGKTVSLCGTLT	40	M	NM_013728.1	1 ... 948
407	OR4QnP	1	15	1.66	IHGAMAGHMQLMNSLSV	60	M	AC019272.4	62255 ... 61317
408	OR51En	0	11	3.04	MHSGSARLPFLGVIAIL	60	R	AF079864.1	632 ... 1576
409	OR11KnP	2	15	1.66	FSGYGFCITLLITFVFI	53	M	AF121972.1	171 ... 1109
410	OR12D1P	1	6	33.02	LHGSATIHLMSTGIAG	76	M	AL133159.4	16108 ... 15185

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
411	OR4NnP	3	15	1.61	LHGGGAGHIQLMNSMTM	55	M	AC019272.4	62255 ... 61317
412	OR11A1	0	6	33.02	FGATCTSVLVLTLSCLI	76	M	AL359381.1	175785 ... 176720
413	OR10C1	0	6	33.02	MLGACSCVGHFIATLIC	59	M	AL365336.1	122764 ... 121784
414	OR2H1	0	6	33.02	LLGTCVMQVQSLSSFVV	88	M	AL078630.1	48786 ... 47851
415	OR9RnP	8	12	59.71	LAVGGGCNIQFLLSITT	54	R	AF091579.1	7 ... 663
416	OR4FnP	0	7	0.53VLHFQFVNSICG	50	M	AB030896.1	1 ... 906
417	OR7D4	3	19	11.31	VMAGTAIFVHLLATLGF	67	R	AF091580.1	7 ... 663
418	OR7E25 P	3	19	11.31	MIACSVLDLHIVIGFGL	61	R	AF091580.1	7 ... 663
419	OR2D2	0	11	5.69	LLGCCGSVVDFITGILI	65	M	AF073987.1	2 ... 649
420	OR10An	0	11	5.69	MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
421	OR2WnP	3	1	254.49	LLGGCVCQGHVVLAVVS	54	R	L34074.1	73 ... 1011
422	OR7E16 P	8	19	11.31	IAGCDLLDLHIMLALGL	60	M	AF102536.1	22 ... 669
423	OR52Pn	0	11	4.44	MHCMSARLPCLGAIVIV	59	M	AF121976.2	474 ... 1307
424	OR6AnP	4	11	5.66	LLGCCGGIVKLDLAILG	94	R	M64386.1	130 ... 975
425	OR7D2	0	19	11.24	VMPITVITLHLIMTLGF	61	R	AF091580.1	7 ... 663
426	OR52Un P	3	11	4.44	LHSASVRFPMLGVAVAY	52	M	AF121976.2	474 ... 1307
427	OR2AGn	0	11	5.6	MLGGDTLSIYYVMGFLP	55	M	AF102527.1	22 ... 669
428	OR7G3	0	19	11.24	ILVGNLVDLHMVVT LGV	64	R	AF091580.1	7 ... 663
429	OR56Bn P	3	11	4.44	IHVGSFRFPVLQLAGMS	41	M	AF133300.1	25713 ... 26573
430	OR2AGn P	1	11	5.51	MLGSDTLIGHYITGFL	55	M	AF102527.1	22 ... 669
431	OR56Bn	0	11	4.44	MHVASFRCSVLQLALMS	39	M	NM_013619. 1	118 ... 969
432	OR6AnP	5	11	5.51	LLGCCGGIVKLDLAILG	93	R	M64386.1	130 ... 975
433	OR4FnP	4	19	63.23	IHGGMVLHFQFVNSICG	49	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
434	OR6Wn	0	7	148.04	SFGSFAVSSPQDLSFVT	47	M	NM_010991.1	1 ... 939
435	OR4Mn	0	15	1.59	LHGAMLGHIQLMSSISV	52	M	AF259072.1	104176 ... 105099
436	OR52Yn P	13	11	3.6	VVVVVLQWPVMGMAVDF	29	M	AF133300.1	46551 ... 47498
437	OR11Hn P	2	15	1.78	FFGTCLCWIPCLSVIG	61	M	AF121972.1	171 ... 1109
438	OR9An	0	7	148.04	LSGTFVFSWPALMAILG	46	M	NM_010991.1	1 ... 939
439	OR5Mn	0	11	52.19	CILLFFYDFQLMSANLS	50	M	AC069563.9	129775 ... 130725
440	OR6Vn	0	7	148.04	FFGSFAAAPTSDMAFVS	45	M	NM_010991.1	1 ... 939
441	OR4Nn	0	15	1.61	LHGGGAGHIQLMNSMTL	53	M	AC019272.4	62255 ... 61317
442	OR51An P	4	11	3.6	EHTDSLILPFTGLACMS	43	M	NM_013617.1	1 ... 921
443	OR9PnP	10	7	148.04	FGSNSFEHLVFIHSLLM	39	M	NM_010983.1	178 ... 975
444	OR4H6P	3	15	1.66	MHGCI LGHVQLVNSISG	59	M	AF259072.1	104176 ... 105099
445	OR51Fn P	2	11	3.6	MHTFSLRLPLGLDTTI	48	R	AF079864.1	632 ... 1576
446	OR7E1P	3	11	68.1	MVACGVLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
447	OR51Tn	0	11	3.6	MHSLSVRFPLAGLQNT	44	R	AF079864.1	632 ... 1576
448	OR2Vn	0	13	104.15	IVVGGSFDIQVICMLF	84	M	AF102535.1	16 ... 669
449	OR51Hn P	7	11	3.6	MHGGSARAPVLGAVIIL	51	R	AF079864.1	632 ... 1576
450	OR51An	0	11	3.6	EHTVSIRLPFTGIAC TL	48	M	AF071080.2	26330 ... 27262
451	OR2AIn P	2	5	209.13	YLGSCLSNFHLMARILL	55	M	AC044846.2	112743 ... 113748
452	OR2F2	0	7	148.74	LLGGFTSNVQIISLLT	54	M	AF073974.1	41 ... 649
453	OR1F12	0	6	31.61	MMANNAINLHMVTVIFV	58	M	AC023167.7	60743 ... 61663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
454	OR7G1P	0	19	11.24	ILAGSLMDVQMIASFGI	60	R	AF091580.1	7 ... 663
455	OR7G2	0	19	11.24	ILAGNLTNLLMIAAFGV	61	R	AF091580.1	7 ... 663
456	OR1M1	0	19	11.24	MHGISAFITHLIVAVIT	89	M	X89689.1	32 ... 472
457	OR51UnP	1	11	2.89	VTDDN.....	48	R	AF079864.1	632 ... 1576
458	OR52Hn	0	11	4.19	MHFVSGRIPDLGVPTVS	59	M	AF121975.1	50 ... 1012
459	OR1F1	0	16	6.15	MFVDNGVNLHLIEGVM	75	R	M64377.1	1 ... 939
460	OR10FnP	0	16	87.09	MIGICTTTTHLVATFII	48	M	AF247657.1	1 ... 945
461	OR4FnP	4	19	7.9	IHGGMVLHFQFVNSICG	49	M	AB030896.1	1 ... 906
462	OR2T1	0	1	254.77	HLVGFGDGLIMCCMLI	92	M	AF102527.1	22 ... 669
463	OR7EnP	9	19	22.8	VAGCDLLDLHIMLAFGL	60	M	AF102536.1	22 ... 669
464	OR51Gn	0	11	3.6	LHSFSVRLPLMGVITVI	57	M	NM_013617.1	1 ... 921
465	OR2Tn	0	1	254.77	MVAGFGLDTFIMCCMLI	67	M	AF102527.1	22 ... 669
466	OR5BGnP	2	11	51.27	AAAAAGGSIHNLFAVEI	52	R	U50948.1	34 ... 978
467	OR5WnP	3	11	51.27	MGADCLVDIHCMFVVAC	51	M	AF146372.1	509 ... 1456
468	OR51Sn	0	11	3.6	MHSVSARLPLLLVLMGD	42	M	AF071080.2	26330 ... 27262
469	OR5WnP	1	11	51.27LVFIES	55	M	AC074177.4	107189 ... 107708
470	OR51AnP	3	11	3.6	EHTDSLILLPTGVAMMD	46	M	NM_013617.1	1 ... 921
471	OR5Dn	0	11	51.21	FCGVTGWCILFCIANES	46	M	AF146372.1	509 ... 1456
472	OR7EnP	4	4	5.55	MVACGVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
473	OR51Fn	0	11	3.6	MHTFSSRPVFGALTTF	53	R	AF079864.1	632 ... 1576
474	OR5Dn	0	11	51.21	YCVVSGWGVLYLFANEC	48	M	NM_013728.1	1 ... 948
475	OR52Rn	0	11	3.6	VHSSSIRWPFMGVAVAF	58	M	AF121976.2	474 ... 1307
476	ORnP	27	11	51.21	FCFAAGQSPGFLCFFFF	23	M	AB030893.1	37 ... 930

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
477	OR7EnP	6	3	121.47	MVACDVLDLHIIDSFSL	57	M	AF073989.1	547 ... 1515
478	OR6Qn	0	11	54.04	LTGACAVTLPLDVSULA	52	M	NM_010983.1	178 ... 975
479	OR4Fn	0	6	185.89	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
480	OR7EnP	3	13	40.31	FFSP.AAALHIMPAFGL	65	M	X89686.1	32 ... 472
481	OR7En	0	2	95.17	MVACDVLDLHIIDSFGL	57	M	AF073989.1	547 ... 1515
482	OR4Nn	0	14	0.27	LHGAMVGHVQLMNSLSL	58	M	AC019272.4	62255 ... 61317
483	OR2ASn P	7	1	254.77GGGGMICGLLP	43	M	AF102535.1	16 ... 669
484	OR11Hn	0	14	0.33	FFGTCFIGIPYFSVLF	90	M	AF121972.1	171 ... 1109
485	OR2Tn	0	1	254.77	MLAGFGLDMLIMCCMLI	69	M	AF102527.1	22 ... 669
486	OR2TnP	1	1	254.77	CMMGFSGDLLIMCCMLI	77	M	AF102527.1	22 ... 669
487	OR2AKn P	3	1	254.55	TLGGACSNIHVSGILL	50	M	AF102533.1	16 ... 669
488	ORnP	16	12	4.38	VLKSKCWQLPFYMPLLM	25	R	Y07557.1	1 ... 942
489	OR5DnP	4	11	51.21	FCAVTGWSTLFCIANES	48	R	U50948.1	34 ... 978
490	OR7EnP	1	4	5.55	FVACDVLDLHIIDNFG	54	M	AF102536.1	22 ... 669
491	OR5L2	0	11	51.27	FCGVVCCCIHLLVANEV	53	M	AF146372.1	509 ... 1456
492	OR5Dn	0	11	51.27	FCVVLVWCTLSLVANES	48	M	NM_013728.1	1 ... 948
493	ORnP	4	9	81.99	..CCCLFFQSIASGTYY	23	M	AL359381.1	82137 ... 81544
494	OR10Qn	0	11	54.08	MVGSCGLPQLLLVSVLI	50	M	AL365336.1	123248 ... 124093
495	OR9MnP	1	11	51.27	LCVDSGGSIHNLFAVEI	54	M	AC069559.8	73704 ... 74636
496	OR7E62 P	5	2	73.96	MAACDVLDLHTIDSFRL	56	M	AF073989.1	547 ... 1515
497	OR9LnP	13	11	54.06	MFVGCTLVAYGILTMIA	32	M	AC069561.1 0	147203 ... 146274

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
498	OR7E46P	10	2	73.96	MAGVEFCDLHIMPAFGL	54	M	AF102536.1	22 ... 669
499	OR1S1	0	11	54.08	MIVVNILITHLLVGVI	56	M	AC073769.1	133488 ... 132556
500	OR5DnP	0	11	51.21	FCVIMGWCTLSCISSEC	45	M	AC069563.9	111696 ... 112671
501	OR9InP	4	11	54.06	FTASCGGNICCSAVIT	46	R	AF091579.1	7 ... 663
502	OR5Dn	0	11	51.21	FCVVSGWCELSLLANES	53	M	AF146372.1	509 ... 1456
503	OR9QnP	4	11	54.08	FTASCGASVRTIFAVMA	47	M	AL365337.1	192661 ... 191711
504	OR51CnP	0	11	3.04	MKTVSARMPMLGAMTVV	51	R	AF079864.1	632 ... 1576
505	OR5WnP	1	11	51.27	FCADCGVDIHL.....	53	M	AC069561.1 0	127636 ... 126698
506	OR9InP	2	11	54.06	FTAGCSCGLHCICAMFA	46	M	AC074177.4	106297 ... 105361
507	OR51AnP	4	11	3.04	MHSVSARVPVPGVVTGL	72	M	X89685.1	2 ... 481
508	OR5L1	0	11	51.21	FCVVVCCCIHLLVANEV	55	M	AF146372.1	509 ... 1456
509	OR7EnP	5	13	50.42VVDLHIMPAFGL	66	M	X89686.1	32 ... 472
510	OR5BLnP	18	11	54.08	ILGNXLENQCIFAMIT	29	R	M64392.1	1 ... 942
511	OR51En	0	11	3.04	MHSASVRFPPLGAIVMV	95	R	AF079864.1	632 ... 1576
512	OR51Dn	0	11	3.04	MHSASSRFPLIGIIVMV	61	R	AF079864.1	632 ... 1576
513	OR52In	0	11	3.04	MHTATARFPLMSGSMVS	46	M	AF121975.1	50 ... 1012
514	OR4KnP	2	18	19.04	IHTGMIVHSQFIDSLSS	56	M	AB030896.1	1 ... 906
515	OR52In	0	11	2.99	MHTATARAPLMSGSMVS	47	M	AF121975.1	50 ... 1012
516	OR4KnP	2	18	19.04	IHNGIIVHSQFMTSIAI	55	M	AB030896.1	1 ... 906
517	OR52MnP	1	11	3.04	MHATSVRYLPIGIGVLL	51	R	AF079864.1	632 ... 1576

SEQ ID #	Symbol	D	C	Mb coord	CDR	#	S	Acc	Range
518	ORnP	7	6	31.58	FLVSCLLLLLLLEGIHW	30	M	AF073964.1	41 ... 649
519	ORnP	9	8	88.25	IXVVVLNIVNMTTIFL	24	M	AC074177.4	149899 ... 148964
520	ORnP	9	10	70.63	YSIVMFYHAHFICELLN	26	M	AC068902.1 1	144125 ... 143193
521	ORnP	9	9	70.7	WWWWWSWYGNFDD SITX	26	R	AF091563.1	7 ... 669
522	ORnP	9	5	202.43	FFFFFF.PPPPP.....	27	R	AF034902.1	4197 ... 5177
523	ORnP	10	11	137.77	LLLLWSQFQFLAVVVV	29	R	M64376.1	1 ... 999
524	ORnP	3	11	16.31	NNNNNLLXMNILTLLAI	27	M	AL136158.1 4	29455 ... 30402
525	ORnP	17	11	55.6	LAGNNIYCYHM..LLLL	26	R	M64377.1	1 ... 939
526	OR6Pn	0	1	154.6	LIACCASSMKFDLAMIL	60	M	NM_010983. 1	178 ... 975
527	OR7EnP	3	14	33.48	MVACDVLDLHIIDSFGL	54	R	AF091580.1	7 ... 663
528	ORnP	12	11	138.51	LMCHS.FFFFFFFMMMMM	29	R	AF091573.1	7 ... 663
529	OR7EnP	5	14	33.48	MAGGDFLDLYILPDFGL	55	M	AF073989.1	547 ... 1515
530	ORnP	7	10	127.4	S.CCCLLYIIHHHHHH	31	M	AC020958.1	164590 ... 163746
531	OR10XnP	2	1	154.6	MLGGCSAITELIISGLG	49	M	AC073778.1	168744 ... 167803
532	OR10Zn	0	1	154.71	MAACCTTFGMVILSVLV	56	M	AC025913.3	108128 ... 109067
533	OR6KnP	2	1	154.73	MYGIVGCTPEWVVHEIT	40	R	M64386.1	130 ... 975
534	OR6Kn	0	1	154.73	MHGIVSCTPEWVIHEIT	44	M	AC027184.3	54955 ... 54017
535	OR1FnP	1	4	97.57IEGVMT	73	R	M64377.1	1 ... 939
536	OR1ABnP	3	19	19.44	MIGISAFNTHLV.....	64	M	AC073769.1	133488 ... 132556
537	OR52MnP	1	11	2.89	MHATSARYLPIGIGVLL	49	M	AF121975.1	50 ... 1012
538	OR1XnP	6	5	202.43	MIANTLGIVHIFAALFA	71	M	AF102530.1	1 ... 666

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
539	OR4FnP	8	16	83.04	QQQQQVIHSQFVNSLTC	46	M	AC019272.4	62255 ... 61317
540	OR52Mn P	5	11	2.89	MHATSVRYLPIGIGVLM	45	R	AF079864.1	632 ... 1576
541	OR2Vn	0	5	209.61	IVVGGSFDIQVICMLF	83	M	AF102535.1	16 ... 669
542	OR2V1P	4	5	209.61	IVVGGSFDIQALCCMLL	90	M	AF102537.1	16 ... 669
543	OR2Zn	0	19	65.55	ITGVGSVNIQILSGILL	76	M	AC073769.1	54319 ... 55289
544	OR52Kn P	5	11	2.89AMFIEL	52	M	AF121975.1	50 ... 1012
545	OR10Hn	0	19	19.7	MFGFSWGMVIGLVTAI	75	M	AC023604.2	214343 ... 213396
546	OR2Dn	0	11	5.77	ILGCCRSVVDIFIMGILA	85	M	AF073987.1	2 ... 649
547	OR7EnP	6	2	161.49	VVGCCSSDLHIMPAFGL	64	M	X89686.1	32 ... 472
548	OR11Gn P	4	14	0.27	FFGSCSLWIPVSLSLLI	68	M	AC027184.3	54955 ... 54017
549	ORn P	12	14	0.27	GSCGNSLHHYLMVNIIL	28	M	AF121972.1	171 ... 1109
550	OR11Gn	0	14	0.33	FFGSCNLWIPNFLSPVM	67	M	AF121972.1	171 ... 1109
551	OR11Hn P	5	14	0.33	FTGTAFSFSVSQFLSIIL	68	M	AF121972.1	171 ... 1109
552	OR6Kn	0	1	154.73	MHENGGFIPEDHATII	46	R	AF034897.1	354 ... 1199
553	OR11Hn	0	14	0.33	FFGTCVGCVPCLCFNIIG	71	M	AF121972.1	171 ... 1109
554	OR6KnP	0	1	154.73	MHGNGGFVPEWDHAAIF	46	M	AL365336.1	122764 ... 121784
555	OR11Hn P	2	14	0.33	FFGTCLIGISFFVSFIL	70	M	AF121972.1	171 ... 1109
556	OR6KnP	2	1	154.82	MHGVAGFMPECDRASIT	43	M	AC027184.3	54955 ... 54017
557	OR6Kn	0	1	154.84	MHGISGCLPEWVIHEIA	45	R	AF034900.1	1 ... 963
558	OR2Ln	0	1	254.55	SSGGAGINAHYVSTFLF	53	M	AF102527.1	22 ... 669
559	OR4GnP	8	16	83.04	ICRKMAVHSQFVNSISA	45	M	AB030892.1	1 ... 939

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
560	OR6Nn	0	1	154.84	IHGACGGGVELDINKIA	50	R	M64386.1	130 ... 975
561	OR2LnP	2	1	254.55	SLAVGGINAHY....W	52	M	AF102535.1	16 ... 669
562	OR9A1	0	7	146.91	LLGTLVLSWPALMAIIG	45	M	L14567.1	17 ... 667
563	OR6Nn	0	1	155.69	THGACACCSELDINIII	51	M	AL136158.1 4	29455 ... 30402
564	OR10Hn	0	19		MFGFSCGMVVAGLV TAL	86	M	AC023604.2	245345 ... 246298
565	OR7EnP	4	9	71.72	MVACDVLDLHIMNSFGL	57	M	AF073989.1	547 ... 1515
566	OR2AQn P	5	1	155.69	FCHSCLLLSLLPFFFF	31	M	AL359352.1	55588 ... 56546
567	OR2LnP	3	1	254.55	SMAGAGINAHYVSSFLF	50	M	AF102537.1	16 ... 669
568	OR5ARn	0	11	52.46	FVVDCGASAHLLLCIES	53	R	AF091579.1	7 ... 663
569	OR7EnP	4	9	71.79	TAGGETLDLHIMPAFGL	57	M	AF102536.1	22 ... 669
570	OR10AA nP	2	1	155.69	THGMCAAAPLHVITATC	84	M	AC005992.1 5	9114 ... 8173
571	OR10Jn P	4	1	157.7	MIAICGVVVQSNVSVIV	72	M	X92969.1	8035 ... 8961
572	OR5A1P	0	11	55.81	FVGLCGSIQSNVVVGT	81	M	Y15525.1	1 ... 705
573	OR2AHn P	5	11	52.46	MLGSCISSVILVFSIVI	51	M	AF247657.1	1 ... 945
574	OR10Jn P	4	1	157.7	LLGICGIMVQSNVSVLL	68	M	X92969.1	8035 ... 8961
575	OR56Bn P	2	11	4.93	IHMCSSRLPVLQLVVVS	39	M	AF121975.1	50 ... 1012
576	OR5M1	0	11	52.35	CIVIFIYSSQLMVANLS	49	R	AF091579.1	7 ... 663
577	OR52Wn P	0	11	4.93	MHTASLLAVPLGLSISM	48	M	AF121976.2	474 ... 1307
578	OR5AMn P	5	11	52.35	FIVIIYAYNVQLMVANLC	35	M	AC068904.1 5	113793 ... 114719
579	OR52Bn P	3	11	4.93	MHFVSTQTPVLGVPSVV	89	M	AF121975.1	50 ... 1012
580	OR5MnP	1	11	52.35	CVLLYFWVMQLLSANLV	48	R	X80671.1	203 ... 1129

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
581	OR5APn P	6	11	52.35	FGAGGALNIHFIFANES	55	R	X80671.1	203 ... 1129
582	OR56Bn	0	11	4.95	IHFCSFRLPVLQLALVS	41	M	AF121975.1	50 ... 1012
583	OR5APn	0	11	52.35	FGLGCTANIHMIFSIVS	55	M	AF121977.1	262 ... 1197
584	OR52Bn	0	11	4.93	GHFVSARIPVLGVPMVL	73	M	AF121975.1	50 ... 1012
585	OR9Gn	0	11	52.5	FAAYCVGNIIKMLLNVC	45	M	AC074177.4	106297 ... 105361
586	OR52Kn	0	11	2.86	MHSISARLPLLGVASVL	53	M	NM_013619. 1	118 ... 969
587	OR5MnP	1	11	52.35	FIVIIYAYNSQLMVANLC	51	M	AC074177.4	106297 ... 105361
588	OR52Kn	0	11	2.86	MHSISARLPLLGVAIVL	52	M	NM_013619. 1	118 ... 969
589	OR52Kn P	3	11	2.82	MHSISARLPLLGVAIGL	53	M	NM_013619. 1	118 ... 969
590	OR52Bn P	4	11	2.78	IHFISARVPDLGVLTVL	57	M	AF121975.1	50 ... 1012
591	OR2B6P	0	6	31.62	LLGAYATNWLLLVSFHI	79	R	L34074.1	73 ... 1011
592	OR2WnP	7	6	31.61	LLRGCASNVMLAFAIVL	58	M	AF102516.1	52 ... 669
593	OR2AnP	5	7	148.83	TMAHCTCLVHLISSILG	72	M	AF102521.1	22 ... 669
594	ORnP	16	6	31.61	FLVSCMDFMYIVLNNVI	39	M	AF102516.1	52 ... 669
595	OR2LnP	0	1	254.55	STAVAGINAHYVSAFLF	50	M	AF102527.1	22 ... 669
596	OR2W2P	5	6	31.61	LLGGCVCQSYWVLSIVM	55	R	L34074.1	73 ... 1011
597	OR2LnP	1	1	254.55	SLAGA.....	61	M	AF102535.1	16 ... 669
598	OR2B7P	1	6	31.61	LLGGCTTNIQLIVSFLV	59	M	AC044846.2	105668 ... 104736
599	OR2Ln	0	1	254.43	SLGGAGINAHYVSAFLF	53	M	AF102527.1	22 ... 669
600	OR5BFn	0	1	254.77	VVVYLASYMHSISAVGG	46	M	AL359352.1	9138 ... 8177

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
601	OR2LnP	4	1	254.55	SVAGMSMDAHYVSTFLF	47	M	AF102527.1	22 ... 669
602	OR7EnP	3	10	17.14	MVACCVLDLHI.....	51	R	AF091580.1	7 ... 663
603	OR1H1	2	9	106.04	LGADNVIHVHLLVALLA	57	M	AC073769.1	133488 ... 132556
604	ORnP	14	1	254.49	TTTKKSERIYIVSSFLI	24	M	AF102527.1	22 ... 669
605	OR4Dn	0	11	55.81	IHGGIASHIQLMNNVTL	64	M	AC019272.4	183633 ... 182701
606	OR1Ln	0	9	106.04	MYGNSFFHLHLQEAVLT	54	M	AC023167.7	60743 ... 61663
607	OR5AXn	0	1	254.2	L TSAIVIFAYGGVGLSS	47	M	AL136158.1 4	154973 ... 155908
608	OR5An	0	11	55.77	YCGLCGS SIESTVSVGV	64	M	Y15525.1	1 ... 705
609	OR5AYn	0	1	254.2	LVAGILNLLYGSIGYAS	50	M	AL359352.1	126933 ... 127889
610	OR13Gn	0	1	255.42	LTLGMMINVHLVADLAG	59	M	AF102540.1	16 ... 669
611	OR5BBn P	0	11	55.77	YASLCGGSVHPLEAVGG	54	M	Y15525.1	1 ... 705
612	OR9GnP	6	11	52.49	FVXNCAGNIIELMLNIT	47	M	AF121977.1	262 ... 1197
613	OR2TnP	4	1	254.77	HLAGFAGNLLVMCCMLI	75	M	AF102527.1	22 ... 669
614	ORnP	7	1	255.42	PVAGKGAF LHSVESLGS	38	M	AL365337.1	192661 ... 191711
615	OR1Jn	0	9	95.9	MITDSVLSSHLMVG VIL	66	M	AF102524.1	52 ... 669
616	OR2CnP	1	16	6.47	LLGACIGNIQFLVCFTV	85	M	M84005.1	1 ... 936
617	OR9GnP	2	11	52.49	FAAYCYGNILNLLLNVS	49	M	AL365337.1	192661 ... 191711
618	OR2C1	0	16	6.4	LLGACIGNIQFLVCFTV	85	M	M84005.1	1 ... 936
619	OR51An P	2	11	4.22	52	M	AF071080.2	26330 ... 27262
620	OR9Gn	0	11	52.49	LCAYCGGNAHNLVVTVS	53	M	AC068904.1 5	165039 ... 165965

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
621	OR52Bn	0	11	2.78	LHFISTRTPILGILTVL	61	M	AF121975.1	50 ... 1012
622	OR1K1	0	9	105.89	MFGVSMVHLYLIEGVVT	58	R	M64377.1	1 ... 939
623	OR51Rn P	3	11	2.78	MHTYSARLPGLGSISLL	47	R	AF079864.1	632 ... 1576
624	OR7EnP	2	13	54.83	MVACDVLDLHILDSFGL	57	M	AF073989.1	547 ... 1515
625	OR52Pn P	3	11	2.82	MHSASARLPPLGAAVVT	55	M	AF121975.1	50 ... 1012
626	OR7EnP	5	9	70.7	MVACDVQYVHSMDSFGL	48	M	AF102536.1	22 ... 669
627	OR7EnP	5	9	70.7	TAGGD.CCCCC.....	43	M	AF073989.1	547 ... 1515
628	OR4KnP	1	21	8.12	IHTGMIVHSQFIDSLSS	57	M	AF259072.1	104176 ... 105099
629	OR4KnP	2	21	8.12	IHNGIVVHSQFMTSTAT	54	M	AB030896.1	1 ... 906
630	OR7EnP	6	9	70.7VFLVHVPFAFGL	58	M	X89686.1	32 ... 472
631	OR51In	0	11	4.15	MHSFSGKTPFVGIVITYM	51	R	AF079864.1	632 ... 1576
632	OR51In	0	11	4.15	MHSMSGRTPLLGVLTFM	56	R	AF079864.1	632 ... 1576
633	OR2AnP	1	7	148.83	TLAICTFL.....	63	M	AF102521.1	22 ... 669
634	OR2A2	2	7	148.83	TLAVCTCLVHLITCVLG	68	M	AF102521.1	22 ... 669
635	OR2AnP	8	7	148.83	TFAACTCLVHLITCVLG	68	M	AF102521.1	22 ... 669
636	OR2Gn	0	1	256.63	LHGSCMSTVQLLASFLV	59	M	NM_008762. 1	1 ... 936
637	OR2AnP	0	7	148.83	TLAHCAFFFFL.....	57	M	AF102521.1	22 ... 669
638	OR6Fn	0	1	254.2	MFGCYGCAVPLAIAVIS	71	R	M64378.1	1 ... 933
639	OR2AnP	4	7	148.83	TLAHCAFLVHLISCILG	68	M	AF102521.1	22 ... 669
640	OR2Gn	0	1	256.02	LLGSCISSIHFLVSEVI	63	M	M84005.1	1 ... 936
641	OR7E37 P	5	13	26.5	MAGGEFLDLHIMPAFGL	57	M	AF073989.1	547 ... 1515
642	OR5AVn	0	1	256.02	AMATVMSCMHA VFGLVI	51	M	AL359352.1	9138 ... 8177

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
643	OR2AJn P	7	1	254.43	VLLGCGINVHYVSAFLI	55	M	AF102527.1	22 ... 669
644	OR13En P	1	9	39.89	MLGSCLTNLQLLATLTA	79	M	AJ251155.1	15491 ... 16423
645	OR2Cn	0	1	257.85	FHGACAGTVGLMASFVL	63	M	M84005.1	1 ... 936
646	OR2TnP	0	1	254.43	IPGGCSLDLQAMCCMLV	59	M	AF102537.1	16 ... 669
647	OR2WnP	2			LMGSCVCNIMQTLGLLV	56	M	M84005.1	1 ... 936
648	OR13Jn	0	9	39.89	MLGSCALKTEILGSLLV	82	M	AJ251155.1	6062 ... 6997
649	OR6RnP	2	1	254.39	SFGCFLGLPSLDSSLIS	45	M	NM_010983. 1	178 ... 975
650	OR5ATn	0	1	254.39	VLASLVYIMHGLINLDC	50	M	AL359352.1	111313 ... 112242
651	OR2Zn	0	19	10.64	ITGVGSVNIQILSGILL	76	M	AC073769.1	54319 ... 55289
652	OR4Ln	0	14	0.08	MHGGMLIHSQVLDSLST	53	M	AB030893.1	37 ... 930
653	OR4UnP	14	14	0.15	RHSGMAMHSQVLDSLST	46	M	AB030895.1	1 ... 924
654	OR4Fn	0	6	185.98	IHGGMIIHIQFVNSISA	50	M	AF102522.1	40 ... 660
655	OR4FnP	2	6	185.98	IHGGMAIHVQFVNSISS	50	M	AB030896.1	1 ... 906
656	OR4Fn	0	6	185.98	IHGGMATHVQFVNSISG	50	M	AB030896.1	1 ... 906
657	OR4Fn	0	6	185.98	IHGGMTIHVQFVNSISG	50	M	AB030896.1	1 ... 906
658	OR4AnP	5	11	50.28	IHGGILGHVQFVNDICV	65	M	AF102522.1	40 ... 660
659	OR4LnP	1	14	0.21	KHGSMLIHSQVLDSLST	53	M	AB030893.1	37 ... 930
660	OR7E33 P	6	13	54.79	MAGGEFLDLRILPAFGL	56	M	AF073989.1	547 ... 1515
661	OR2Cn	0	1	257.85	FHGACAGTVGLMASFVL	63	M	M84005.1	1 ... 936
662	OR4Kn	0	14	0.15	MHGGMSVHSQFVDSLST	53	M	AF259072.1	104176 ... 105099
663	OR5U1	0	6	33.45	VIASVAASMHIIFTAAI	84	M	AL359352.1	111313 ... 112242
664	OR4Kn	0	14	0.08	IHGGMAVHSQFMDLSS	58	M	AF259072.1	104176 ... 105099

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
665	OR5V1	0	6	33.45	LVVGCSANVHLLTGIGT	84	M	AL365337.1	192661 ... 191711
666	OR4QnP	1	14	0.08	LHGAMAGHVQLMNSISI	62	M	AF259072.1	104176 ... 105099
667	OR12D3	0	6	33.45	LHGSAAIYMHMLVTISG	70	M	AL359381.1	128169 ... 127234
668	OR4Kn	0	14	0.08	IHTGMIVHSQFIDSLSS	59	M	AF259072.1	104176 ... 105099
669	OR51CnP	3			MKTVSARMPMLGAMTVV	53	R	AF079864.1	632 ... 1576
670	OR1J2	0	9	105.94	MITDSVLSSHLMVGVIL	66	M	AF102524.1	52 ... 669
671	OR5BJnP	3			SIGSAAVNTKFPSC LGV	46	M	AF073965.1	2 ... 643
672	OR1J1	0	9	105.82	TIADSGICLHLIAAAIL	63	M	AF102524.1	52 ... 669
673	OR13En	0			MLGSCLTNLQLLATLTA	83	M	AJ251155.1	15491 ... 16423
674	OR4KnP	5	14	0.08	IHGGMVIHTHFVNSLSM	53	M	AB030893.1	37 ... 930
675	OR1LnP	5	9	105.84	MYGNSFFHLHLQEAVLT	54	M	AC023167.7	60743 ... 61663
676	OR2CnP	2			FHGACAGTVGLMASFVL	59	M	M84005.1	1 ... 936
677	OR4TnP	9	14	0.21	MLSELLSHSQFVKSLSI	47	M	AC019272.4	62255 ... 61317
678	OR5BnP	1			FVITSGCNIHNIVVND	51	M	AF121977.1	262 ... 1197
679	OR4Kn	0	14	0.21	IHGGMTLHFQFINSISS	53	M	AB030896.1	1 ... 906
680	OR11Ln	0	1	254.43	LVGACVTTLHMILSVLI	50	M	AF121972.1	171 ... 1109
681	OR7E68P	5	10	17.21	MAGGELLDLHIMPAFGL	56	M	AF102536.1	22 ... 669
682	OR7EnP	2	10	17.21	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
683	OR7E31P	6	9	70.71	TAGGELLDLHIMPAFGL	55	M	AF073989.1	547 ... 1515
684	OR7EnP	3	9	70.71	MVACDVLDLHIMDSFGL	58	M	AF073989.1	547 ... 1515

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
685	OR5AKn P	3	11	52.82	LAATCGMNVHFLFVNLF	79	R	U50948.1	34 ... 978
686	OR5AKn	0	11	52.83	FAATCGMNVQFLFVNLF	79	R	U50948.1	34 ... 978
687	OR5AKn	0	11	52.83	FAATCGINVHFDVDFDLF	79	R	U50948.1	34 ... 978
688	OR5BQn P	9	11	52.82	TTTTTLLLLMLTFFFF	42	R	U50948.1	34 ... 978
689	OR1Nn	0	9	105.94	LLGGNVLPMLHMGFLV	56	R	AF091566.1	1 ... 663
690	OR1J4	0	9	105.94	MITDNVLNSHLIVGVIL	69	M	AF102524.1	52 ... 669
691	OR1Nn	0	9	105.94	MLGDSLLVTHLVGLV	85	R	AB038167.1	1 ... 933
692	OR2AnP	4	3	94.41	TLAVCTIMVHHLGSIVG	65	M	AF102521.1	22 ... 669
693	OR2ANn P	17	9	93.78VVVLEFMVNLLI	23	M	AC074177.4	128803 ... 129726
694	OR5K1	0	3	104.47	FCETCGAHIHLLFSVQF	51	R	AF091575.1	52 ... 663
695	OR2K2	0	9	93.78	MLGSCVTTLEFMVSLLI	60	M	AJ251154.1	35662 ... 36615
696	OR8Hn	0	11	51.76	MAGTCGIDVNSIIVTLV	51	M	AC069559.8	36251 ... 35322
697	ORnP	15	11	51.76	LIFKNLFSPLXXHYIL	28	M	X89682.1	2 ... 472
698	OR4AnP	14	11	50.28	FGRRVVGHIQLYGHNYV	38	M	AB030895.1	1 ... 924
699	OR4An	0	11	50.28	LHGGVVGQFQIVNGSCI	59	M	AB030895.1	1 ... 924
700	OR6Sn	0	14	0.58	FFGAFAGPGPADLAIVS	50	R	M64378.1	1 ... 933
701	OR4RnP	16	11	50.28	NLGAIMEHVXSVNGNYL	52	M	AF102522.1	40 ... 660
702	OR13Cn	0	9	86.77	MLGTCGINVQFLTTFLT	65	M	AJ133425.1	61 ... 1014
703	OR13Dn P	4	9	86.77	MYGSCVLNTELGNFLS	64	M	AC023789.5	371264 ... 372220
704	OR7EnP	3	11	2.13	MIACGVLDLHIINSEGL	54	R	AF091580.1	7 ... 663
705	OR10Pn P	1	12	59.88	MIGICTTTTHLVATFII	49	M	AF247657.1	1 ... 945
706	OR8In	0	11	51.76	MVVCCMISISVSLATLS	50	M	AC069559.8	137090 ... 138039
707	OR8G1	0			..IIIGICVHCIVGNIV	75	R	AF091576.1	52 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
708	ORnP	7	12	59.88	CFPGEAFFTLL.....	34	M	AL359352.1	145887 ... 145042
709	OR5F1	0	11	51.76	MIATCGANVNHSLANIG	50	M	Y15525.1	1 ... 705
710	OR5FnP	1	11	51.76	MIATCGANVNYFFANKG	52	M	Y15525.1	1 ... 705
711	OR6BnP	6	2	251.7	LSVCCFSIIKFDLAILF	70	M	L14567.1	17 ... 667
712	OR2D1	0			LLGCCASVDFITGILI	64	M	AF073987.1	2 ... 649
713	OR5ASn	0	11	51.76	MAADCLSTVHLLLCIQS	52	M	AC068904.1 5	165039 ... 165965
714	OR5SnP	8	2	251.7	FSSTTGRSVQLKLCMMN	64	R	AF091579.1	7 ... 663
715	OR5AQn P	0	11	51.76	SAVTDAGNTHGPFSAIF	51	R	X80671.1	203 ... 1129
716	OR6BnP	3	2	251.7	LSVCCFSIIKFDLAILF	67	M	L14567.1	17 ... 667
717	OR5JnP	2	11	51.76	YVLTGGGNTHGLFSIAL	52	R	X80671.1	203 ... 1129
718	OR9AnP	4	7	146.91	QLGTLVFFWPALMAIIG	44	M	NM_010991. 1	1 ... 939
719	OR5BEn P	2	11	51.76	YSLTCVLNTHSFLSTST	45	R	AF091564.1	7 ... 663
720	OR9An	0	7	146.91	LLGTFVFFWPVLMVAVLG	47	M	NM_010991. 1	1 ... 939
721	OR8Hn	0	11	51.76	MVGTCGIDVNSIIATLV	51	M	AC069559.8	36251 ... 35322
722	OR5BNn P	14	11	51.76	LLMTCAYMSHS.....P	54	M	AF102528.1	52 ... 669
723	OR8Jn	0	11	51.76	LLIVVLYTVVCVSANLF	80	M	X89682.1	2 ... 472
724	OR9NnP	9	7	146.91	LFGTFIIIIIL.AAAAA	36	M	NM_010991. 1	1 ... 939
725	OR7EnP	4	7		MVACGMLDLHITHSFAL	51	R	AF091580.1	7 ... 663
726	OR7E9P	3	7		MVACDVLDLHVIDSFGL	51	M	AF073989.1	547 ... 1515
727	OR8KnP	8	11	51.76	MMITLICQIIDILTNP	36	M	AC069563.9	28460 ... 29383
728	OR2AnP	1	7	148.97	ILAHC.....	44	M	AF102521.1	22 ... 669
729	OR8Kn	0	11	51.76	LLIIFIYQMFKSFSNLS	56	M	AF102528.1	52 ... 669
730	OR7E39 P	4			MVGGEFLFHLHIMPAFGL	55	R	AF091580.1	7 ... 663

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
731	OR7E27 P	3			MAGGELLDLHIMPAFGL	57	M	AF102536.1	22 ... 669
732	OR2Hn	0	6		FLGTCVMEVQSLASILV	81	M	AL078630.1	41097 ... 40165
733	OR13Cn P	2	9	40.16	MLGACGATVQLMANFLV	87	M	AJ133428.1	61 ... 1017
734	OR13Cn	0	9	40.16	MFGACGAAVQLMTNFLV	89	M	AJ133424.1	61 ... 1017
735	OR2S1P	4	9	40.16	MFGACGANVQLMTNFLV	89	M	AJ251154.1	2703 ... 1747
736	OR2AMn P	1	9	40.16RRRRRV.MMMM	63	M	AJ251154.1	2703 ... 1747
737	OR1N1	0	1		MLGDSLLVTHLVGLV	85	R	AB038167.1	1 ... 933
738	OR2S2	0	9	40.13	MFAGCSIAVHLMTNFLV	83	M	AJ251154.1	2703 ... 1747
739	OR7E26 P	4	1		MAGGELLDLHIMPAFGL	56	M	AF102536.1	22 ... 669
740	OR1F11	0			LAGNNGVNLHLIEGVM	99	R	M64377.1	1 ... 939
741	OR5ACn P	3	3	103.97	FGATCIIHILFSIQF	66	R	AF091575.1	52 ... 663
742	OR5B10 P	2	13		MVATNGCNLRDLMSNV	46	M	AF102528.1	52 ... 669
743	OR2AnP	1	12	85.7	TLAVCAFLVHLIACILG	76	M	AF102521.1	22 ... 669
744	OR1E5	0	13		MLGDSLLHLHLIMGILI	83	R	Y07557.1	1 ... 942
745	OR4Fn	0	6	185.71	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
746	OR5CnP	0	9	40.53	MAADC.....	47	M	Y15525.1	1 ... 705
747	OR2WnP	0	6	31.62	LLGGCVSNIMQALAI	64	M	AF102516.1	52 ... 669
748	OR2L2	0			..IIIGINAHYVSSFLL	48	M	AF102537.1	16 ... 669
749	OR4H8P	2	14		MHGCILGHVQLVNSISG	56	M	AF259072.1	104176 ... 105099
750	OR5D10 P	5			LCVVTTWCTLFTSANES	44	R	AF010293.1	211 ... 1143
751	OR7A12 P	1	14		MVIVSAMNIEMMSALGG	68	M	AF283558.1	1 ... 927
752	OR2L1	0			..IIIGINAHYVSTFLF	48	M	AF102527.1	22 ... 669
753	OR2F3P	0	14		LLGGFTSSVQIISSLLT	55	M	AF073974.1	41 ... 649

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
754	OR4H10P	2	15		MHGCILGHVQLVNSISG	57	M	AF259072.1	104176 ... 105099
755	OR5H1	0			..IIILGHIHFVFSIQF	56	R	AF091575.1	52 ... 663
756	OR2K1	0			..IIIIITTLVCMVSLLI	58	M	AJ133428.1	61 ... 1017
757	OR7E11P	7	11		MAGGEFLDLHILPAFGL	52	M	AF073989.1	547 ... 1515
758	OR7A3P	1	11		MVIVSAMNIEMMSALGG	68	M	AF283558.1	1 ... 927
759	OR6A1	0	11		LLGCCGGIVKLDLAILG	91	R	M64386.1	130 ... 975
760	OR5I1	0	11		FCADSLGSHVFLYGVFI	52	M	Y15525.1	1 ... 705
761	OR2H3	0	6		ILGTCVIGVQSVASILV	86	M	AL078630.1	41097 ... 40165
762	OR10J1	0			MVGICGIVTQSTISVLV	73	M	X92969.1	8035 ... 8961
763	OR7E3P	3	11		MFACGVLDLHIIDSFGL	54	M	AF102536.1	22 ... 669
764	OR1D6P	1	11		LVVANLFYIHLTGIFI	48	R	Y07557.1	1 ... 942
765	OR5D10P	2	18		LCVVTWCTLTFSASES	45	R	U50948.1	34 ... 978
766	OR5D5P	2	18		LCVVTWCTLTFSANES	46	M	AC073947.3	29192 ... 30115
767	OR52A1	0	11		MHQGSMAVCLIGVAVAF	72	M	NM_013620.1	1 ... 945
768	OR2AEn	0	7	98.36	HLGGCMGNIHIVSSLLL	48	M	AC073769.1	143294 ... 142353
769	OR6LnP	7	10	149.44	LLSSCSSAVSLRAAILA	40	M	NM_010983.1	178 ... 975
770	OR6LnP	7	10	149.44	LLSSCSSAVSLRAAILA	41	M	NM_010983.1	178 ... 975
771	OR7MnP	7	10	149.44NVYVSL.....	29	M	AC073947.3	43325 ... 42733
772	OR13Cn	0	9	86.77	MFGACGTDVQFMSNVLI	69	M	AJ133428.1	61 ... 1017
773	OR13Cn	0	9	86.85	MLGTCGANVQFMATFTM	71	M	AJ133425.1	61 ... 1014
774	OR2InP	6			LLGSC.....	79	M	AL078630.1	151152 ... 150391

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
775	OR4An	0	11	50.28	LHGGVVGHFQVVNSICV	58	M	AB030895.1	1 ... 924
776	OR2InP	3		RRRRRMARILL	77	M	AL078630.1	151152 ... 150391
777	OR4AnP	4	11	50.28	LHGGVVGSGFQVVNGICV	53	M	AB030896.1	1 ... 906
778	OR4AnP	7	11	50.28	PHGGAVAHFQVVNGICV	57	M	AB030896.1	1 ... 906
779	OR8C1P	2	11		LCVHCGMGVHCMIVVVV	72	M	AC068905.1 2	76922 ... 75948
780	OR4AnP	1	11	50.28	LHGDVVGHFQVVNGICV	56	M	AB030896.1	1 ... 906
781	OR7E15 P	5	11		MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515
782	OR10A1	0	11		MFGVCAPVVQWAGTVVI	76	M	AF247657.1	1 ... 945
783	OR2An	0			TSAVCTCLVHLI.....	70	M	AF102521.1	22 ... 669
784	OR7EnP	6			MAGGELFHLHIMPAFGL	57	M	AF073989.1	547 ... 1515
785	OR7En	0			MAGGDFLDLHIVPAFVL	54	R	AF091580.1	7 ... 663
786	OR51A1 P	5	11		MHTLSARLPLLAVITFL	43	R	AF079864.1	632 ... 1576
787	OR7E47 P	4			KAGTNLLDLYIMPTFGL	56	M	AF073989.1	547 ... 1515
788	OR5B5P	2	3		MAATNICNIHELVANIS	48	M	AF146372.1	509 ... 1456
789	OR1F10	0	3		MFVDNGVNLHLIEGVM	72	R	M64377.1	1 ... 939
790	OR8G2	0			...IIIGLGIHFVLSNIT	75	M	AF102518.1	52 ... 669
791	OR1Sn	0	11	54.08	MIVVNILITHLLVGIVF	55	M	AC073769.1	133488 ... 132556
792	OR4AnP	3	11	50.73	LHGGAVGHFQVVSGLCV	56	M	AB030896.1	1 ... 906
793	OR4AnP	7	11	50.76	LHGGILGHFQVVNGMCV	58	M	AB030896.1	1 ... 906
794	OR4AnP	5	11	50.66	LHGGVLGHFQVVNGMRV	56	M	AB030896.1	1 ... 906
795	OR4AnP	7	11	50.73	PHGGVVGRFQVVKVICV	54	M	AB030896.1	1 ... 906
796	OR4AnP	1	11	50.81	LHGGIVGHFQVVS GMCV	60	M	AB030896.1	1 ... 906
797	OR4AnP	10	11	50.81	LHGGVVGNFQVVNGICV	55	M	AF102522.1	40 ... 660
798	OR4An	0	11	50.73	LHAGVAGHVQFMNGICV	62	M	AB030895.1	1 ... 924
799	OR4An	0	11	50.73	LHGGVVGHVQFVNGICV	57	M	AB030896.1	1 ... 906
800	OR7E42 P	4			MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
801	OR2M3P	2			ITLGCFLDIDALCCMIF	55	M	AF102537.1	16 ... 669
802	OR4H11P	2	4		MHGCI LGHVQLVNSISG	57	M	AF259072.1	104176 ... 105099
803	OR7E57P	5			MAXGEFLDLHILPAFGL	51	M	AF102536.1	22 ... 669
804	OR2B1P	0	5		LLGAYATNWLLLVSFHI	78	R	L34074.1	73 ... 1011
805	OR7E34P	2			MAGGDSLDLHIMPAFGL	56	M	AF073989.1	547 ... 1515
806	OR7E56P	4			MAGDELFFLHILPAFGL	52	M	AF073989.1	547 ... 1515
807	OR3AnP	1	5		LHAGCACNTHALAAMAA	49	M	AF073967.1	2 ... 649
808	OR4H5P	2	5		MHGCI LGHVQLVNSISG	56	M	AF259072.1	104176 ... 105099
809	OR1En	0	5		MLGDSLLHLHIMGILI	82	R	Y07557.1	1 ... 942
810	OR51CnP	2	11		3MKTVSYYYIXQ.....	48	M	AF121975.1	50 ... 1012
811	OR2WnP	2	6	30.51	LLGGCVSNIMQALAIIA	64	M	AF102516.1	52 ... 669
812	OR51B1P	5	11		AHSVSGRSPVRPLITIL	68	M	AF071080.2	15931 ... 16851
813	OR7E81P	3			MAGGEFFSLHIMPAFGL	54	M	AF102536.1	22 ... 669
814	OR7E44P	1			MAGGELFDLHIMLAFL	53	M	AF073989.1	547 ... 1515
815	OR5B7P	2	6		MAATNICNIHEL VANIS	47	M	NM_013728.1	1 ... 948
816	OR7E36P	4			MAGGELFFLHIMPAFGL	58	M	AF073989.1	547 ... 1515
817	OR2A5	0	7		TMAHCTCLVHLIASILG	74	M	AF102521.1	22 ... 669
818	OR5B1P	2	8		MAATNICNIHEL VANIS	47	M	AF146372.1	509 ... 1456
819	OR8B8	0	11	137.68	LLVSGMGAHCVVVDIV	72	M	AC069559.8	120212 ... 119283
820	OR8B4P	0	11	137.71	LCVNCGVGAHSFVVITL	87	M	AC068910.2	133103 ... 132162

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
821	ORnP	15	11	137.77	LCVENRRRTATHCKSHII	35	M	AC069563.9	60295 ... 59327
822	OR8B3	0	11	137.77	LLVICAMGAHCVVVNIV	85	M	AC069563.9	129775 ... 130725
823	OR2Bn	0	6	30.51	LLGSCASNQWLISFLI	89	R	L34074.1	73 ... 1011
824	OR8B6P	6	11	137.77	LAFFCGLSAHCVAAAVI	73	M	AC069559.8	96224 ... 95292
825	OR8B5P	6	11	137.77	LFFFFXGLGAHCVVANTV	73	M	AC069559.8	96224 ... 95292
826	OR4E2	0	14	1.7	LHACIAGHGQLINSISS	90	M	AF259072.1	104176 ... 105099
827	OR8B7P	4	11	137.77	FCVICGWGAHCVAAIFV	71	M	AC069559.8	96224 ... 95292
828	OR11Jn P	3	15	1.82	FSCAGFGSMPLCVSIII	56	M	AF121972.1	171 ... 1109
829	OR4E1P	3	14	1.7	MHACIAGHALLINSISV	92	M	AB030893.1	37 ... 930
830	OR10Dn P	7	11	137.96HHHILLGNVLSI	85	M	AC074177.4	12106 ... 13038
831	ORnP	10	14	1.7	VFRGGFHKFFF.....	23	M	AF102536.1	22 ... 669
832	OR8D2	0	11	137.77	LLVIGVLWVHRLIGNTA	70	M	AC073947.3	29192 ... 30115
833	OR11In P	1	1	126.31	FGAACGCLITLATSVTI	51	M	AL359381.1	175785 ... 176720
834	OR11Jn P	1	15	1.82	FSCACFGWTPLCISIIL	56	M	AF121972.1	171 ... 1109
835	OR10An P	3	11	5.64	MFGVCTPVVQWAGTVVI	74	M	AF247657.1	1 ... 945
836	OR8C3P	5	11	137.77	LCVHCGMGVHCMIVVVV	73	M	AC068905.1 2	76922 ... 75948
837	OR2DnP	6	11	5.64	LLGCCGSVVDFITGILI	62	M	AF073987.1	2 ... 649
838	OR4PnP	0	11	51.03	LHGGIVGHSQ.....	59	M	AB030895.1	1 ... 924
839	OR7E21 P	5			MAGGEFIDLHIMPAFGL	50	M	AF073989.1	547 ... 1515
840	OR2M1	0			IVLGCFLDIYAICSMLE	55	M	AF102537.1	16 ... 669
841	OR7AnP	4	19		NLAGVVMNLQM.....	63	M	AF073970.1	41 ... 649

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
842	OR5D11 P	1	8		LCVVTTWCTLFTSANES	44	R	AF010293.1	211 ... 1143
843	OR7E50 P	7	8		IVVCDMLDLHVFLDIFL	57	M	AF102536.1	22 ... 669
844	OR7E45 P	3			MAGGELFDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
845	OR7E77 P	6			MAGGEFLDLHIMPAFGL	51	M	AF073989.1	547 ... 1515
846	OR8B2	0	11	137.77	LLVICAMGAHCVVNVIV	84	M	AC069563.9	129775 ... 130725
847	OR8D1	0	11	137.77	LVVVGALSTHALIANTV	87	M	AC073947.3	29192 ... 30115
848	OR8B1P	4	11	137.77	LLLVCGMGAHCVVNVIV	84	M	AC069559.8	96224 ... 95292
849	OR7A1P	2	19		MIVVSVVYLQMTSLGG	72	R	M64376.1	1 ... 999
850	OR7E8P	4	8	13.72	MVACGVLDLHIIDSFGL	53	M	AF102536.1	22 ... 669
851	OR4DnP	7	11	55.86	MHGGVAGHVQLMNNISL	58	M	AC019272.4	183633 ... 182701
852	OR7E80 P	7	8	13.72	MAGGELQDVHIMPAFGL	54	M	AF073989.1	547 ... 1515
853	OR4DnP	5	11	55.86	MHGGGAAGHVQLMNNLTL	62	M	AC019272.4	183633 ... 182701
854	OR7E10 P	8	8	13.72	IVACDLLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
855	OR10B1 P	3	19	17.91	MLGCCLSVIEMILSVVM	85	M	AC012302.5	54283 ... 55224
856	OR2InP	3		 LLLLMARILL	75	M	AL078630.1	151152 ... 150391
857	OR4Dn	0	11	55.86	MHGGVGGAQLMNNVSF	65	M	AC019272.4	183633 ... 182701
858	OR5ACn	0			.VVVVIIHVHLIFGIQP	65	R	AF091575.1	52 ... 663
859	OR2I1	0	6	33.63	LLGSCASNAQLMARILL	79	M	AL078630.1	151152 ... 150391
860	OR10H1	0	19	19.86	MFGFSCGMVVAGLVTAL	88	M	AC023604.2	245345 ... 246298

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
861	OR7E59 P	5			CPEARVFLHIMPAFGL	53	M	AF102536.1	22 ... 669
862	OR7E28 P	4			MAGGELDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
863	OR5B3	0			MVATNGCNIHDLVVNII	51	R	U50948.1	34 ... 978
864	OR2A6	0			TLAHCAFLVPLIACILG	75	M	AF102521.1	22 ... 669
865	OR6Cn	0			.VVVCAIPPLVMAALI	47	M	NM_010991.1	1 ... 939
866	OR7E54 P	5			MAGGEFLDLHIMPAFGL	52	M	AF073989.1	547 ... 1515
867	OR7E48 P	3			MAGGEFLDLHIMPAFGL	57	R	AF091580.1	7 ... 663
868	OR67An P	3	11	76.42	MHSCAGTLPAQGIIVSL	83	R	AF091561.1	52 ... 663
869	OR4Dn P	1	11	55.86	MHGGVAGHVQLMNNLTL	63	M	AC019272.4	183633 ... 182701
870	OR4Cn P	1	11	50.91	VHGCILGHAQLNSICS	57	M	AB030896.1	1 ... 906
871	OR4Dn P	2	11	55.86	IHGGIAGHVQLMNNVTL	65	M	AC019272.4	183633 ... 182701
872	OR10H2	0	19	19.94	MFGFSCGMVVAGLVMAL	85	M	AC023604.2	245345 ... 246298
873	OR10H3	0	19	19.94	MFGFSWGMVMGLVTAI	75	M	AC023604.2	214343 ... 213396
874	OR55Cn P	2	11	2.65	VYLLYLQPGGG.....	45	M	AF121980.1	160 ... 1053
875	OR55Bn P	3	11	2.65	.VVVVLQVPLGMCTVS	53	M	AF121980.1	160 ... 1053
876	OR52Vn P	4	11	4.19	LHNHIMVYXFLGTTSP	48	M	NM_013619.1	118 ... 969
877	OR2B3	0	6	33.64	LLGACFINLQLFSILI	75	R	L34074.1	73 ... 1011
878	OR52Tn P	6	11	4.22	FGHFLIFLDFLDILTIS	45	M	AF121975.1	50 ... 1012
879	OR2J1P	5	6	33.64	LLGTCASTLHFLMSFVI	57	R	L34074.1	73 ... 1011
880	OR52Hn P	3	11	4.19	LHFVSGRVPCLGVPTVT	60	M	AF121975.1	50 ... 1012

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
881	OR2J3	0	6	33.64	LLGTCASNLHFLTSFVI	58	R	L34074.1	73 ... 1011
882	OR52An	0			FHSVS.....VVRLFS	75	R	AF079864.1	632 ... 1576
883	OR4Qn	0			.VVVVAGHMQLVNSLSV	56	M	AB030893.1	37 ... 930
884	OR52Bn P	2	11	4.22	LHFVSVRTSILGVPSVL	60	M	AF121975.1	50 ... 1012
885	OR2N1P	9	6	33.64	LHGGCPIYSEALVCM LV	81	M	AJ132195.1	79 ... 906
886	OR51En P	1			FHSASVRFP LLGAIAMV	90	R	AF079864.1	632 ... 1576
887	OR2J2	0	6	33.64	LLGICAIILHFLMSFVI	57	R	L34074.1	73 ... 1011
888	OR2In	0		RRRRRRMARILR	77	M	AL078630.1	151152 ... 150391
889	OR2J4P	5	6	33.64	LLGTCASNLHFLTSFVL	56	R	L34074.1	73 ... 1011
890	OR7E40 P	4			MAGGDILDLYILPDFGL	55	M	AF073989.1	547 ... 1515
891	OR2H4P	3	6	33.64	LLGAYLTQIQAMASLLM	63	M	AL078630.1	41097 ... 40165
892	OR7E52 P	5			IVVCDVLDLHVCDIFGL	61	M	AF073989.1	547 ... 1515
893	OR2InP	9			LLGSC.....	80	M	AL078630.1	151152 ... 150391
894	OR6C1	0			LIGVFTVIPALGCATLF	52	M	NM_010991.1	1 ... 939
895	OR7E30 P	3			MAGGEFLDLHIMPAFGL	56	M	AF073989.1	547 ... 1515
896	OR5BAn P	0	11	53.69	LVVTSVENIQNLFSVTL	51	R	AF091579.1	7 ... 663
897	OR7H1P	3	19	11.38	MMGGTVLYIQLLVALDV	74	M	AF073989.1	547 ... 1515
898	OR5B2	0	11	54.45	MVATNGCNFHLTSNIF	47	R	U50948.1	34 ... 978
899	OR5AZn P	1	11	53.69	MIGTCTVNLLCILCLIF	48	R	AF091579.1	7 ... 663
900	OR5Bn	0	11	54.45	MVATNGCNIHDLVVNII	51	R	U50948.1	34 ... 978

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
901	OR52Bn	0	11	4.22	KILFSARIPSLGAASTL	64	M	NM_013619.1	118 ... 969
902	OR5BnP	2	11	54.45	MAATNICNIHELVANIS	49	R	U50948.1	34 ... 978
903	OR52Dn	0	11	4.19	MHYASVRIPFLGVAAML	66	M	AF121976.2	474 ... 1307
904	OR7A11	1	19	17.72	MVEASAIIDLHMAVLGV	67	M	AF283558.1	1 ... 927
905	OR5BnP	9	11	54.45	MAATSALTVDLLQFFL	41	M	NM_013728.1	1 ... 948
906	OR51AnP	5	11	4.19	THSWFSRMPLLGIVAFV	50	R	AF079864.1	632 ... 1576
907	OR7A15P	4	19	17.72	MIVGSVTHLHMAALGG	74	R	M64376.1	1 ... 999
908	OR7C2	0	19	17.72	IIGCNGIGLETMTVLGF	98	R	AF091580.1	7 ... 663
909	OR7E23P	7	21	20.89	MAGGELFHLQIMPAFGL	57	M	AF073989.1	547 ... 1515
910	OR2E1	8	6	32.05	AHACCTINLQI.RRRRR	43	M	AL078630.1	106872 ... 105934
911	OR1I1	0	19	17.87	MHGTSAIQIHLIFGVGS	57	R	AF091566.1	1 ... 663
912	OR1RnP	3	17	3.12	MVGISAVHLHLIEGVVA	45	R	M64377.1	1 ... 939
913	OR4F3	0	8	0.07	IHGGMVLHFQFVNSICG	51	M	AB030896.1	1 ... 906
914	OR2AEn	0	7	98.7	HLGGCMGNIHIVSSLLL	49	M	AC073769.1	143294 ... 142353
915	OR2InP	7		TTTTMARILL	72	M	AL078630.1	151152 ... 150391
916	OR52AnP	2			IHSASVRFP LLGXPPPP	94	R	AF079864.1	632 ... 1576
917	OR7C1	0	19		ITGCNGIGLETIATLGI	81	R	AF091580.1	7 ... 663
918	OR2A3P	2	7	149.11	MLAACTCLINLVGGVLG	63	M	AF102521.1	22 ... 669
919	OR7A5	0	19		MIAGNAMYLMITVLGG	74	M	AF283558.1	1 ... 927
920	OR2InP	3		MARILL	67	M	AL078630.1	151152 ... 150391
921	OR7A10	0	19		MLVGNAMNLQMAVLGG	76	R	M64376.1	1 ... 999
922	OR2An	0			81	M	AF102521.1	22 ... 669
923	OR2M2	0			IISGCFLDIDAICMLF	57	M	AF102537.1	16 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
924	OR7A8P	2	19		MLAVSSLNLQMIATLGG	71	M	AF283558.1	1 ... 927
925	OR2An	0			TSVCTTLIHL.....	78	M	L14566.1	62 ... 667
926	OR7E20P	4			MAGGELLFLHIMPAFGL	56	M	AF073989.1	547 ... 1515
927	OR2AnP	3			TLAHCTCLVHL.....	65	M	AF102521.1	22 ... 669
928	OR5BhnP	7			MVASC GGKTVS.....	34	M	Y15525.1	1 ... 705
929	OR1En	0			LMGDSLLHLHLIMGISI	92	M	AC068902.1 1	196434 ... 195499
930	OR1EnP	1			MLGDSLLHLHLIIGVVL	98	M	AF073976.1	32 ... 649
931	OR5Bn	0	11	54.45	FVITSGCNIHNIVVND	51	R	U50948.1	34 ... 978
932	OR8RnP	12	11	73.74	LFLSYGGGAHH.....	52	M	AC069561.1 0	7848 ... 8783
933	OR5ANn	0	11	55.69	YSGLSGTAFQATLTFGA	55	R	AF091564.1	7 ... 663
934	OR5ANn P	1	11	55.69	YSGLCGTGIQATLTFGT	59	M	Y15525.1	1 ... 705
935	OR5BRn P	8	11	55.69	MSNVCGTVIQATLTFGT	33	M	Y15525.1	1 ... 705
936	OR2A1	0	7	149.18	TLGHCTCLAHLIACFLG	77	M	AF102521.1	22 ... 669
937	OR10An	0	11	6.81	MLGGCFLVQWAGTIIV	54	M	AF247657.1	1 ... 945
938	OR2A9	3	7	149.18	TLAHCTCLVHLIACILG	78	M	AF102521.1	22 ... 669
939	OR2A7	0	7	149.18	TSVCTTLIHLVAGLG	81	M	L14566.1	62 ... 667
940	OR10A3	0	11	6.81	MLGGCFSVVQWAGTIV	58	M	AF247657.1	1 ... 945
941	OR10Cn	0	6	33.36	MLGACSCVGHFIATLIC	59	M	AL365336.1	122764 ... 121784
942	OR7A2P	0	19		MVIVSVMNLQVMAALDG	73	M	AF283558.1	1 ... 927
943	OR10Wn P	2	11	54.3	MIGSCASLQLFVAAAIV	47	M	AC012302.5	54283 ... 55224
944	OR7A17	0	19		MVGGSAINSOMMAALAG	76	M	AF283558.1	1 ... 927
945	OR5Bn	0	11	54.3	MAATNGINIQLDISNVF	47	M	AF102528.1	52 ... 669
946	OR5BnP	5	11	54.3	MVATNGCNLRDLMSNVL	47	M	AF102528.1	52 ... 669

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
947	OR1Q1	0	9	106.13	TIAVNMLHLHLIEGVIG	54	M	AF073967.1	2 ... 649
948	OR2Hn	0	6	33.33	LLGTCVMQVQSLSSFVV	88	M	AL078630.1	48786 ... 47851
949	OR7EnP	5	3	90.04	MVACDVLDLHIIDSFGL	54	M	AF073989.1	547 ... 1515
950	OR7A14	0	19	17.72	MVIVSAMNI.....	71	M	AC073772.1	227187 ... 226252
951	OR1B1	0	9	106.13	FYGVTLVHLRLIEGLMG	49	M	AC068902.1 1	83719 ... 84647
952	OR12D2	0	6	33.23	LHGSSTIHLHMLVTIAG	81	M	AL359381.1	105330 ... 104407
953	OR7EnP	4	3	11.92	MVACDVLDLHIIDSFGL	55	M	AF073989.1	547 ... 1515
954	OR8BnP	5	15	74.31	LXVVEGMAHCVVVNIV	82	M	AC069559.8	96224 ... 95292
955	OR1L1	0	9	106.13	MLGNSLIHLHLVEGVIT	57	M	AC023167.7	60743 ... 61663
956	OR11An	0	6	33.36	FGATCTSVLVLTLCLI	76	M	AL359381.1	175785 ... 176720
957	OR7AnP	4	12	44.29HLLDCYIRTTLSG	55	M	AF102534.1	52 ... 669
958	OR1C1	0	1	254.35	LVVNSGVHLHLIVGLAT	56	M	AC073769.1	133488 ... 132556
959	OR1D2	0	17	2.99	LVVANLLYIHLLTGIFI	50	M	AF073967.1	2 ... 649
960	OR1L3	0	9	106.13	MLGNSFFHLHLAEGSVA	53	M	AC023167.7	14677 ... 15636
961	OR12DnP	1	6	33.36	LHGSATIHLMSTGIAG	76	M	AL359381.1	105330 ... 104407
962	OR4G1P	4	16	83.04	KHGGMAIHSQFVNSISG	47	M	AB030896.1	1 ... 906
963	OR2B4P	1	6	33.53	LLGSCGSNVQLLLGLLM	90	M	AL359352.1	95024 ... 95965
964	OR11H1	0	22		FFGTCLCWIPLCLSVIG	61	M	AC027184.3	54955 ... 54017
965	OR4Fn	0	16	83.04	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
966	OR56AnP	5	11	4.73	MNLPSFQLPVLQAGFLS	38	M	AF121975.1	50 ... 1012

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
967	OR8NnP	7	4	164.13	REIIRVDAFLKKTANMI	34	M	AF102528.1	52 ... 669
968	OR7EnP	5			MVACDVLDLHIFDFGL	54	R	AF091580.1	7 ... 663
969	OR4Pn	0	11	50.95	LHGGIVGHSQLVNSIAV	56	M	AB030895.1	1 ... 924
970	OR6Cn	0			LIGVFCSTPPLGFATLF	51	M	NM_010991.1	1 ... 939
971	OR5BCnP	2	11	54.3GCQIHFLLANIF	41	M	AC069561.10	51687 ... 50743
972	OR10QnP	4	11	54.3	MLGGCGLLQLLVSVLV	48	M	AC012302.5	54283 ... 55224
973	OR5BnP	6	11	54.3	TDASNGGNIHELVTNIF	45	R	U50948.1	34 ... 978
974	OR10PnP	2	12	115.61	MIGICTTTTHLVATFII	46	M	AF247657.1	1 ... 945
975	OR1L4	0	9	106.22	MMGNSGIHFLVETVIT	62	M	AF073967.1	2 ... 649
976	OR2APnP	3	12	115.61	YMGAFLLLLLL.....	49	M	AF073987.1	2 ... 649
977	OR1L6	0	9	106.22	MMGNSGIHFLVETVIT	63	M	AF073967.1	2 ... 649
978	OR6UnP	6	12	115.61	DIGAFTLFMPLDLAALG	52	M	NM_010991.1	1 ... 939
979	OR5C1	0	9	106.06	MAADCAGSVHLLICIQA	50	R	X80671.1	203 ... 1129
980	OR11InP	1	15	70.72	FGAACGLITLATSVTI	51	M	AL359381.1	175785 ... 176720
981	OR4AnP	6	11	50.78	LYGGVVGHFQVNVGVCV	57	M	AB030896.1	1 ... 906
982	OR4GnP	14	2	114.45	ICRKMAVHSQFVNSISA	42	M	AB030892.1	1 ... 939
983	OR10Vn	0	11	56.15	MVGCGLLPLLLISVLI	48	M	AL136158.14	29455 ... 30402
984	OR4G2P	2	2	114.45	KHGGMAIHSQFVNSISG	48	M	AB030896.1	1 ... 906
985	OR10VnP	3	11	56.15	MIGRCGLLQLLMVSFLV	45	M	X92969.1	8035 ... 8961
986	OR4F4	0	2	114.45	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
987	OR4G3P	14	19	63.51	ICRKMAVHSQFVNSISA	42	M	AB030892.1	1 ... 939
988	OR5AKnP	4	11	52.82	LGATCSMNINFLFVNLC	65	R	U50948.1	34 ... 978
989	OR10YnP	14	11	56.15	MIRGCGLLFLLLCGHHL	43	M	AF247657.1	1 ... 945
990	OR4GnP	2	19	63.51	KHGGMAIHSQFVNSISG	48	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
991	ORnP	9	5	111.92	IMCSRTTYVXQLHGFFT	23	M	AF073989.1	547 ... 1515
992	OR4Fn	0	19	63.51	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
993	OR8A1	0	11	137.56	LLVICVIGIELVSANIV	61	M	AC069559.8	96224 ... 95292
994	OR8Bn	0	11	137.56	LCVVSGMGAHSVVDVM	66	M	AC069559.8	120212 ... 119283
995	OR6DnP	3	10	47.91	AYVSSLLLRTH.....	55	R	AF034901.1	2110 ... 3078
996	OR7E14 P	7	11	16.31	MAGGELDLHIMPAFGL	58	R	AF091580.1	7 ... 663
997	OR2M4	0			IVLGCALDIVALCCMLF	57	M	AF102537.1	16 ... 669
998	OR4WnP	3	X		LLLLL.....LLFFII	36	M	AC069559.8	73704 ... 74636
999	OR4Fn	0	19	63.51	IHGGMVIHSQFVNSLTC	50	M	AC019272.4	62255 ... 61317
1000	OR7EnP	3			MAGGESLDLHIMPAFGL	57	M	AF073989.1	547 ... 1515
1001	OR4GnP	4	19	63.51	KHGGMAIHSQFVNSISG	47	M	AB030896.1	1 ... 906
1002	OR10Jn P	1			LLGVCGITIQTISVLL	60	M	X92969.1	8035 ... 8961
1003	OR52En	0	11	4.58	MHTASIRMPLLGNILL	71	M	AF121979.1	53 ... 1106
1004	OR4RnP	24	11		VHGAIMGHVXS FANNCL	54	M	AF102522.1	40 ... 660
1005	OR4Cn	0	11		AHGAIVGHIQFVNSICL	75	M	AF102522.1	40 ... 660
1006	OR4AnP	10	11		GLGGIVGHIQL.....	44	M	AF102522.1	40 ... 660
1007	OR4AnP	4	11		LHGGVAGHFQVVG GCI	55	M	AB030895.1	1 ... 924
1008	OR4AnP	8	11		LHGGVAGHSHSVNGICV	54	M	AF102522.1	40 ... 660
1009	OR9Gn	0	11	52.54	FAAYCVGNIIKMLLNVC	46	M	AC074177.4	106297 ... 105361
1010	OR10An	0	12	59.65	MFGSCGSVLQWASTFIF	64	M	AF247657.1	1 ... 945
1011	OR4Cn	0	11		VHRGVVGHIQFINSICL	73	M	AF102522.1	40 ... 660

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1012	OR10Vn P	8	11	56.15	.FFFFIIXNEXSVVVLV	37	M	AC073945.4	110931 ... 111893
1013	OR10Un P	3	12	59.65	MAGLCATVAQLMLSFIS	56	R	AF034898.1	1 ... 981
1014	OR7E2P	3	11	90.37	MVACDVLDLHICDIFGL	59	M	AF073989.1	547 ... 1515
1015	OR7E35 P	6	4	11.87	MAGGEFLDLHIVPAFVL	53	M	AF102536.1	22 ... 669
1016	OR9KnP	0	12	59.71	LAIVGGCSLQVSLSIIP	49	R	AF091579.1	7 ... 663
1017	OR7E13 P	5	11	90.37	MAGGEFLDLHIMLAFGL	54	R	AF091580.1	7 ... 663
1018	OR7EnP	4	8	6.5	MLACGVLDLHIIDSFGL	55	M	AF102536.1	22 ... 669
1019	OR9Kn	0	12	59.71	LAIVGGCSIQMSLSIIP	49	M	NM_013728. 1	1 ... 948
1020	ORnP	13	11	137.56	PCVIYIGIDVHSLXEPAY	34	M	AC069559.8	36251 ... 35322
1021	OR7EnP	8	11	72.11	MAGGNLFFSLLMPAFGL	54	M	AF073989.1	547 ... 1515
1022	OR7EnP	5	3	140.64	MAGGKFLDLHIMPAFGL	53	M	AF073989.1	547 ... 1515
1023	OR3A4P	0	17	3.12	LHAGCMFNTQALAAMGA	44	M	AC073769.1	133488 ... 132556
1024	OR8QnP	9	11	137.56	LSIIIVETEFVFTXIVT	33	M	AC069559.8	137090 ... 138039
1025	OR7EnP	2	11	72.11	ILACGVLDLHIMHNFGFL	55	M	AF073989.1	547 ... 1515
1026	OR7EnP	3	3	140.64	MVACGVLDLHIHSFGL	56	M	AF073989.1	547 ... 1515
1027	OR3A1	0	17	3.07	LHVGCACNTHALVGMAT	50	M	AF073967.1	2 ... 649
1028	OR5Gn	0	11	52.52	MGEACGMSTHFLLAIGL	69	M	AF146372.1	509 ... 1456
1029	OR5MnP	7	4	42.45	LIIIVYVNAQRIIIMLE	39	M	AF073987.1	2 ... 649
1030	OR7EnP	1	3	136.02	MVACDVLDLHIIDNFGFL	54	M	AF073989.1	547 ... 1515
1031	OR5G1P	2	11	52.51	QGVACGINTHNVVAVGF	68	M	AF146372.1	509 ... 1456
1032	OR5PnP	3	11	6.93	LVGTCAGNSFCPSSVLS	70	M	AF121977.1	262 ... 1197

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1033	OR10AEnP	8	1	157.36	IIIIIGIMVIVQIHCVV	40	M	X92969.1	8035 ... 8961
1034	OR3A2	0	17	3.07	LHAGCACNTHALVGMAT	50	M	AC073769.1	133488 ... 132556
1035	OR10Jn	0	1	157.4	MVATCGIMLHANVSVIV	88	M	X92969.1	8035 ... 8961
1036	OR1D3P	2	17	2.94	LVVANLFYIHLLTGIFI	50	R	Y07557.1	1 ... 942
1037	OR10Jn	0	1	157.36	TVAICGIMVQSNVRVIV	72	M	X92969.1	8035 ... 8961
1038	OR1D4	0	17	2.99	LVVTNLLYLLLLTGIFT	49	R	Y07557.1	1 ... 942
1039	OR5GnP	8	11	52.51	QGVVYVANTHAVVAVLV	55	M	NM_013728.1	1 ... 948
1040	OR4SnP	1	11	50.99	LHGCIGGHIQLVNSIAG	61	M	AB030895.1	1 ... 924
1041	OR5GnP	4	11	52.51	LGVVCGVSTHFLVLGL	75	M	AF146372.1	509 ... 1456
1042	OR9HnP	2	1	254.35	FSGIAGWNAQMLLCIIS	59	R	AF091579.1	7 ... 663
1043	OR1A1	0	17	2.99	MIGNSGINPHLMGVIFV	86	M	AF073966.1	41 ... 643
1044	OR1A2	0	17	2.99	MIAKSGISPHMLGVFL	80	M	AF073966.1	41 ... 643
1045	OR8AnP	6	11	137.68	FLVICVMVIELVFANLI	50	M	AC069561.1 0	51687 ... 50743
1046	OR1P1P	1	17	2.99	LLGDIALLTRLLLGVII	82	M	AF102538.1	139 ... 675
1047	OR7E12P	7	11	1.92	MAGGEFFSLHIMPAFGL	55	M	AF073989.1	547 ... 1515
1048	OR4A1P	4	11		LHGGVVGHFQVVNGICV	57	M	AB030896.1	1 ... 906
1049	OR10G3	0	14	1.7	LHGSCGAHLQLTDIVVS	91	M	AF259072.1	19582 ... 18644
1050	OR10G1P	3	14	1.7	LHGSCGAHIQLTDIVAS	93	M	AF259072.1	55611 ... 54658
1051	OR10G2	0	14	1.7	LHGSCGAHIQLTDVVAS	91	M	AF259072.1	55611 ... 54658
1052	OR5Tn	0	11	51.94	MVGTCAAHIHALFVIEV	52	M	AF121977.1	262 ... 1197
1053	OR7EnP	8	3	136.02	MVACGVLDLHIIGSFGL	53	R	AF091580.1	7 ... 663
1054	OR7EnP	5	3	136.02	MAGGKFLDLHIMPAFGL	54	M	AF073989.1	547 ... 1515
1055	OR4AnP	2	11	50.93	LHAGVVGHVQFMNGICV	61	M	AB030895.1	1 ... 924
1056	OR4C1	1	11	50.93	LHGGIIGHVQFVNSMCL	66	M	AB030896.1	1 ... 906

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1057	OR1EnP	7	17	2.9MMMYTLIMGILI	80	M	AF073961.1	32 ... 649
1058	OR7KnP	11	14	5.99	MIGCNFIELYMMIGIFG	49	R	AF091580.1	7 ... 663
1059	OR4CnP	3	11	50.93	LHDGIEGHIQFVNSMCA	61	M	AF102522.1	40 ... 660
1060	OR1RnP	11	17	2.9	MVGISAVHLHLIEGVVA	44	R	M64377.1	1 ... 939
1061	OR5AUn	0	14	1.22	MAATCGANIHCLFANLS	51	M	AC069559.8	85584 ... 84655
1062	OR4Cn	0	11	50.96	LHAGVVGHIQFVNSICI	69	M	AF102522.1	40 ... 660
1063	OR4Cn	0	11	50.96	VHGCIVGHVQLLSICV	57	M	AB030895.1	1 ... 924
1064	OR13Dn P	2	9	86.89	MLGSCWITLRLFTVIVL	58	M	AJ251154.1	2703 ... 1747
1065	OR5n				ASASLTSYVHNEEEVFV	44	M	AL359352.1	111313 ... 112242
1066	OR2Hn				LLGTCVMQVQSLSSLV	83	M	AL078630.1	48786 ... 47851
1067	ORn				25	M	AC074177.4	88434 ... 88916
1068	ORn			EINLLLARGKAL	29	M	AF283814.1	1 ... 930
1069	ORn				NNNNNFXXSLHLCCILI	29	M	AC074177.4	128803 ... 129726
1070	ORn				TLLLLTFQHHL.....	27	M	L14569.1	62 ... 667
1071	OR6Fn				..CCCWPIPTSAIAVIS	46	R	M64386.1	130 ... 975
1072	ORn			ILLLLL	33	R	U50947.1	418 ... 1350
1073	ORn				..CCCLIPFFFTSGYSW	24	R	M64392.1	1 ... 942
1074	OR10An				PLGECDPPEEQMYVGLVM	51	M	AF247657.1	1 ... 945
1075	ORn				IPNASRRRRR....PP	25	R	M64388.1	1 ... 942
1076	OR2Ln				FLAGAGINAHYVSTFLF	51	M	AF102527.1	22 ... 669
1077	OR10Jn				LTGICGIMVQSNVSVLL	57	M	X92969.1	8035 ... 8961
1078	OR1Kn				LLLLLMVNLYLIKGVVT	50	R	M64377.1	1 ... 939
1079	OR10Dn				LHGSCGLHILLSNVISG	69	M	AC074177.4	12106 ... 13038
1080	ORn			CCCI	41	R	M64376.1	1 ... 999

SEQ ID #	Symbol	D	C	Mb coord	CDR	%	S	Acc	Range
1081	OR2Ln				SLACGGLNAHFVRTLSF	52	M	AF102537.1	16 ... 669
1082	ORn				HHHHHRLESSSLLLLLL	38	M	AC073945.4	152209 ... 153150
1083	ORn			LLLLLS	27	M	AL365336.1	41087 ... 41711
1084	OR2n			GGGGGG	57	M	AF102521.1	22 ... 669

5 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be apparent to those skilled in the art that various changes and modifications can be practiced without departing from the spirit of the invention. Therefore the foregoing descriptions and examples should not be construed as limiting the scope of the invention.

10

 All patents, patent applications, and publications cited herein are hereby incorporated by reference in their entirety. In particular, the following documents are hereby incorporated by reference in their entirety: United States Provisional Patent Applications Serial Nos. 60/145,412, filed July 23, 1999; 60/155,126, filed September 22, 1999; 60/158,495, filed October 8, 1999; 60/158,615, filed October 8, 1999; 60/181,113, filed February 8, 2000; 60/181,115, filed February 8, 2000; 60/184,809, filed February 24, 2000; 60/188,332, filed March 9, 2000; and United States Patent Applications Serial Nos. 09/620,753, filed July 21, 2000; and 09/621,122, filed July 21, 2000.

CLAIMS

What is claimed is:

- 5 1. An isolated and purified polynucleotide sequence encoding an olfactory receptor and having the nucleotide sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a nucleotide sequence that is at least about 95% homologous to a nucleotide sequence of the group consisting of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through
10 SEQ ID NO:152 and encoding a polypeptide having olfactory receptor function.
2. An expression vector comprising a polynucleotide sequence of claim 1.
3. A host cell comprising the expression vector of claim 2.
- 15 4. An isolated and purified olfactory receptor polypeptide comprising the translated sequence of SEQ ID NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of the translated sequence of SEQ ID
20 NO:1 through SEQ ID NO: 73 and SEQ ID NO:111 through SEQ ID NO:152 and having olfactory receptor function.
5. A host cell expressing a polypeptide of claim 4 or a functional fragment thereof.
- 25 6. A phage expressing a polypeptide of claim 4 or a functional fragment thereof.
7. A preparation containing a polypeptide of claim 4, further comprising
30 biological or synthetic molecules which maintain the functional structure of the polypeptide.

8. An isolated and purified polynucleotide sequence encoding an olfactory receptor and having the nucleotide sequence selected from the group consisting of SEQ ID NO: 153 through SEQ ID NO: 1084 or a nucleotide sequence having a sequence at least about 95% homologous to a nucleotide sequence of the group consisting of SEQ ID NO: 153 through SEQ ID NO: 1084 and encoding a polypeptide having olfactory receptor function.
9. An expression vector comprising a polynucleotide sequence of claim 8.
10. A host cell comprising the expression vector of claim 9.
11. An isolated and purified olfactory receptor polypeptide comprising the sequence of SEQ ID NO: 1085 through SEQ ID NO: 2008, or a polypeptide sequence that is at least about 95% homologous to a polypeptide sequence of the group consisting of SEQ ID NO: 1085 through SEQ ID NO: 2008 and having olfactory receptor function.
12. A host cell expressing a polypeptide of claim 11 or a functional fragment thereof.
13. A phage expressing a polypeptide of claim 11 or a functional fragment thereof.
14. A preparation containing a polypeptide of claim 11, further comprising biological or synthetic molecules which maintain the functional structure of the polypeptide.
15. A library of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising the expression products of at least two polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

16. A library of olfactory receptors according to claim 15, wherein the library comprises the expression products of at least 50 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through
5 SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

17. A library of olfactory receptors according to claim 15, wherein the library comprises the expression products of at least 100 polynucleotides of SEQ ID NO:1 through
10 SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

18. A library of olfactory receptors according to claim 15, wherein the library
15 comprises the expression products of at least 200 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

20 19. A library of olfactory receptors according to claim 15, wherein the library comprises the expression products of at least 500 polynucleotides of SEQ ID NO:1 through SEQ ID NO: 73, SEQ ID NO:111 through SEQ ID NO:152, and SEQ ID NO: 153 through SEQ ID NO: 1084 wherein said polynucleotides encode functional olfactory receptors; or functional fragments of said expression products.

25 20. A library of olfactory receptors suitable for determining the interaction pattern of a composition with the receptors, comprising at least two polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008, wherein said polypeptides are functional olfactory receptors; or functional fragments of said polypeptides.

30 21. A library of olfactory receptors according to claim 20, wherein the library comprises at least 50 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,

wherein said polypeptides are functional olfactory receptors; or functional fragments of said polypeptides.

22. A library of olfactory receptors according to claim 20, wherein the library
5 comprises at least 100 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,
wherein said polypeptides are functional olfactory receptors; or functional fragments of
said polypeptides.

23. A library of olfactory receptors according to claim 20, wherein the library
10 comprises at least 200 polypeptides of SEQ ID NOS of SEQ ID NO: 1085 through SEQ
ID NO: 2008, wherein said polypeptides are functional olfactory receptors; or functional
fragments of said polypeptides.

24. A library of olfactory receptors according to claim 20, wherein the library
15 comprises at least 500 polypeptides of SEQ ID NO: 1085 through SEQ ID NO: 2008,
wherein said polypeptides are functional olfactory receptors; or functional fragments of
said polypeptides.

25. A method for determining the binding pattern of a composition with
20 olfactory receptors, comprising the steps of:
 exposing the composition to a library according to claim 21; and
 determining whether the composition binds to each olfactory receptor, thereby
determining the overall binding pattern of the composition.

26. The method of claim 25, wherein the composition consists essentially of one
25 compound or chemical.

27. The method of claim 25, wherein the composition comprises at least two
compounds or chemicals.

28. The method of claim 25, wherein the step of determining whether the
30 composition binds to each olfactory receptor further comprises a determination of the

approximate binding constant with which the composition binds to each receptor or functional fragment thereof.

29. The method of claim 25, further comprising the step of determining whether
5 a receptor or functional fragment thereof to which the composition binds is activated.

30. The method of claim 29, further comprising the step of determining the
absolute or relative amount by which the receptor or functional fragment thereof is
activated.

10

31. A DNA array or a DNA chip comprising DNA segments derived from SEQ ID
NO: 153 through SEQ ID NO: 1084.

32. A method of determining differences among individuals with respect to their
15 olfactory faculties, comprising the steps of comparing the olfactory DNA of the individual
against the array or chip of claim 31.

33. A method to determine single nucleotide polymorphisms in olfactory receptors,
comprising the steps of uniquely amplifying olfactory receptor sequences from DNA
20 obtained from one or more individuals, based on primers designed according to the first 25
bases and the last 25 bases of any combination of, or each of, SEQ ID NO: 153 through
SEQ ID NO: 1084, and determining the similarities and differences between said amplified
DNA and the corresponding receptor from SEQ ID NO: 153 through SEQ ID NO: 1084.

FIGURE 1

SEQ. ID NO:1

1 GGNTTATNCC NCGTTGNACT GCAGGGGNNC AACNCACAGN ACGCCCGNTG CTGAGGCTAT AAATGANCGG
 71 NNTAAGGAGA GGAGTGAAGA CAGTAAAAAA ACACAGAGAT AAATTTATCA ATTGGGAAGC TTTCAAAGGG
 141 CCAAAATATAG ATGAATATTA ATGGGCCAAA GAAGAGAAGC ACAACAGTAA TGTGGGCAGA CAGAGTGGAA
 211 AGGGCCTTGG ACATCCCATC AGAGGCTTGG CGATGCACAG TAGCAAGGAT GATAGTGTCA GAAATGAGCA
 281 AAAGGAGGAA ACACATAAGT GAGAGCAGAC CACTGTTAGT GAGCACCAGT ATCTCAAAAC CATAGGTGTC
 351 TAAGCAGGCA AGCTTGATCA CTAGGAGGAG GTCACAGAAA AAATTGTCTA CCTGTTGGG TCCACAGAAA
 421 GGCAGATTGA CTTTGAATGC CAGGTGGGTG GCTGAGTGTG AGATGCCAAT GGCCAGGAA ACCCCCACCA
 491 GAACAGTTCA CACCCTCCGG TTCATGATGG TTATGTAGTG CAGAGGTTTG CATATAGCAA TGTATCTATC
 561 ATAGGCCATG GCAACAAGAA GCACCATCTC ACTACCCCA AAAACATGCA AGN

SEQ. ID NO:2

1 GGNNNTNAC ACGGACTCCA AGCAGTGGTA ACAACGCAGA GTACGCCCGT TCCTGAGTGA GTAGATGAAG
 71 GGGTTCAGCA TGGGATTGAT GACAGTGTG AAAATTCCAA CAGCTTTATC CTTGTCTGAA AGCTTGGTTG
 141 AACCAGTCG CATATAGTTA AAGATACCTG AACCATAGAA TATGGCAACC ACAGTGAGGT GGGAGCCACA
 211 TGTGGAGAAG GCTTCTTCC TGCCCTCTAC AGAGCGAATT CGCAGGACTG CAGCTGCCAC GTGGATATAG
 281 GAGATGACAA TGAGAGCCAT GGGGGTACCT GCCATTATAA AACCACAGC AAAAAGCAGC AGCTCATTGA
 351 GTTGGGTGCT GGAGCAGGAG AGCTGGAAGA GCTGTGGGAG GTCACAGTAG AAGTGATTGA TCACATTGGG
 421 GCCACAGAAG TTGAGCGTGG ACATGGCCAC AGTGTGGGTC AGTGCGTTGG TGAAAGCACA AGCCAGGAC
 491 GCAGCCATCA ACATCCTCTG GACTGTCTGA CTCATGCGGG TGCTTGTAGG TGAGGGGCC GGCAGATGGG
 561 CAGGAATCGG TCATAGGG

SEQ. ID NO:3

1 TGGNNTTTTA TCNCCNTTGG AGCTCCNAAG CAGTGGTAAC AACGCAGAGT ACGCCCGTTG CGAAGCGTGT
 71 AGATTAGGGG GTTCAGTAGG GGAGTGATGA CAGTGTAGGT CACCGAGATC AGCTGGTCAT GTTCTCTGGT
 141 GTTCTCTGAC TTGGGCTTGA GGTAGGCAAT GGAGGCACAG CTGTAGTGGA CAATGACCAC AGTGAGGTGG
 211 GATGCACAGG TGGCAAAAGC CTTCTTCCGG CCCTCAACTG AAGTAATCTT GAGGATTGTA GAGATAATGA
 281 GAACATAAGA AATGAAAACC AGACCCATAG GTACAACAAG CACCAGCACA CTGATAATCA AAGTCAGGAT
 351 TTCATTGACA GTGGTGTCAA TGCAGGAGAG CTTTCATCACA GGGCGGATGT CACAGAAGAA GTGGGGCACC
 421 TTTTCTAGCA CAGAAGGGTA ACCTGAATAC AGATGTCACT TGCGTTATTG CTACAATCAG CCAATGCTG
 491 CAAGGCCCCC AGGACAAGTT GGATACGCAG CCTCTTGTTT ATAATAACCA TGTATCTCAA GGGGGTTGCA
 561 AGATGGCCAC ATAGCNGNTC ATATTCCN

SEQ. ID NO:4

1 GTNGTTNTTA ACNCCATTGG AGCTCCAAAG CAGTGGTAAC AACGCAGAGT ACGCCCCCAA TGTATTTTTT
 71 TTTGAGAAAC TTGTCTTTCT TAGATTTTTG TTACATCTCT GTCACAAATC CAAAATCTAT TGTTAGTTCC
 141 TTGACTCATG ATACTTCCAT TTCTTTCTTT GGGTGTGCTC TGCAAGCCTT CTTTTTCATG GACTTGGCAA
 211 CTACGGAGGT AGCCATCCTT ACAGTGATGT CCTGTGACCG CTATATGGCC ATCTGCCGGC CTTTACATTA
 281 TGAGGTCATC ATAAACCAAG GTGTCTGTCT GAGGATGATG GCCATGTCGT GGCTCAGTGG GGTGATCTGT
 351 GGATTCATGC ATGTGATAGC AACATTCTCA TTACCATTCT GTGGCGCAA TAGAATACGT CAATTTTTCT
 421 GTAATATTCC ACAACTNCTA AGCCTCTTAG ACCCCAAAGT AATTACCATT GAGATTGGAG TCATNGGNTT
 491 TTGGTACAAG TCTTNGATA ATCCTCTTTG NTGNAATTAC TCTCTCTAC ATGTNCATTT TTTTTTGNCA
 561 TCATGAGGGA TTCCTTCTAA AGG

SEQ. ID NO:5

1 GNGGNTTNNT NCCNCCNTTG GACTCCAAAG CAGTGGTAAC AACGCAGAGT ACGCCCGTGT GTAAATGAAT
 71 GGGTTCAACA TGGGAGTCAT AACAGTGTAG GACAAATGATA GCAGCTTCGT GCCCTCAGGT GAATTATTTG
 141 ATTTAGGCCG GAAGTAGGTG AGGCTTAATG ATATATAGAA AAGAGAGACA ACAAGGAGGT GTGAGGAACA
 211 TGTAGAAAAG GCTTTATTCT TCCCTTTAGC TGATGGGATC TTGAGGATGG CAGCAGCAAT GCGAGTATAG
 281 GAACACAAGA TCAGCAAGCA GGGGATCATG ACCACCAGAA TGGTTCCGAC GATGGCGTAG ATCTCAAACA
 351 GTGCTGTGTC TGCACAGACC AGCCTCAGCA CAGGTGGGCT GTCACAGAAG AAGTGGTTCA CCTTGTGGT
 421 GCCACAGAAT GGAAACTGA AGAGCCATGT GGTCTGCACA GTAGCTACAG GAAAGCCTGG GAACCAGGAG
 491 GCAGCAGCCA GTTTGGCAG AGTCCTTTGG TTCATGATGA CTGGGTAGTG CAAGGGACTN GCAGATNNNC

561 NCATTCGGTC ATATGNCATG GNAG
 SEQ. ID NO: 6
 1 CNTTGGAGCT CCAAAGCAGT GGTAACAACG CAGAGTACGC CCGCTCCGCA GAGAATAGAT GAAAGGGTTC
 71 AGGGTCGGGG GCACGACTGT GTAGAACGCA GACAGGAAAA CATCCAGAAC GGGGGGAGAA TTTGAAATTG
 141 GCTTCACATA GGCAATGCTG CCAGATATCA TAAAGAGTGT TACAACCACA AGATGTGGAA TGCAGGTAGA
 211 AAATGTTTTT GATCTACCCCT CCTTAGAAGG AATCCTCATG ATGACAGAAA AAATGTACAT GTAGGAGAGA
 281 GTAATTACAA CAAAGGAGAT TATCACAAGA CTTGTACCAA AAACCATGAC TCCAATCTCA ATGGTAATTA
 351 CTTTGGGGTC TAAGAGGCTT AGGAGTTTGT GGAATATTAC AGAAAAATTG ACGTATTCTA TTGCGCCAC
 421 AGAATGGTAA TGAGAATGTT GCTATCACAT GCATGAATCC ACAGATCACC CCACTGAGCC ACGACATGGC
 491 CATCATCCTC AGACAGACAC CTTGGTTTAT GATGACCTCA TAATGTAAAG GCCGGCAGGA TGGCCATATA
 561 GCGGTCATAG GA

SEQ. ID NO: 7
 1 GCAGTGGTAA CAACGCAGAG TACCGCCCCC TATGTACTTT TTCTTGGGAA ACTTGTCTGT GTTTGACATG
 71 GGTTTCTCCT CAGTGACTTG TCCCAAAATG CTGCTCTACC TTATGGGGCT GGGCCGACTC ATCTCCTACA
 141 AAGACTGTGT CTGCCAGCTT TTCTTCTTCC ATTTCTCTCGG GAGCATTGAG TGCTTCTTGT TTACGGTGAT
 211 GGCCTATGAC CGCTTCACTG CCATCTGTTA TCCTCTGCGA TACACAGTCA TCATGAACCC AAGGATCTGT
 281 GTGGCCCTGG CTGTGGGCAC ATGGCTGTTA GGGTGCATTG ATTCCAGTAT CTTGACCTCC CTCACCTTCA
 351 CTTTGGCCACA CTGTGGTCCC AATGAAGTGG ATCACTTCTT CTGTGACATT CCAGCACTGT TGCCCTTGGC
 421 CTGTGCTGAC ACATCCTTAG CCCAGAGGGT GAGCTTCACC AACGTTGGCC TCATATCTCT GGCTGCTTTC
 491 TGCTAAATCT TTTATCCTAC ACTAGAATCA CAAATATCTA TCTTAAGCAT TCGTACAAC

SEQ. ID NO: 8
 1 GGAACAACGC AGAGTCGCCC CCGATGTACT TGTTCTTCTC CAACCTGTCC TTTGCTGACA TTTGTGTTAC
 71 TTCCACCACC ATTCCAAAAA TGCTGATGAA CATCCAGACA CAGAACAAAG TCATCACCTA CATAGCCTGC
 141 CTCATGCAGA TGTATTTTTT CATACTCTTT GCTGGATTTG AAAACTTCCT CCTGTCCGTG ATGGCCTATG
 211 ACCGGTTTGT GGCCATCTGT CACCCCTGTC ACTACATGGT CATTATGAAC CCTCACCTCT GTGGACTGCT
 281 GGTTCTGGCA TCCTGGACCA TGAGTGCTCT GTATTCTTG CTACAAATCT TAATGGTAGT ACGACTGTCC
 351 TTCTGACAGC CCTTAGAAAT CCCCACCTT TTCTGTGAAC TTAATCAGGT CATCCAACCT GCTTGTCTG
 421 ATAGCTTTCT TAATCACATG GTGATATATT TTACAGTTTG CGCTGCTGGG TGGAGGTCCC TGACTGGGAT
 491 CCTTTACTTC TTACTCTAAG ATAATTTCTT CATACATGCA ATCTCANCAA GNTCAGGG

SEQ. ID NO: 9
 1 GGGTTTTNAC CCNNTNGGAG CTCCNAGCAG TGGTAACAAC GCAGAGTACG CCCGTTTCGT AGGCTATAAA
 71 TGAAGGGGTT GAGTGAGGGA GTCACCACTC CATAGAAGAG GGCCATGAAC TTGGGTGAT CCCTTGAGAT
 141 GGAGGAGGGG GGCTGAAGGT ACATGCTGAT GGCTGGGCCA TAAATAAGA AACTACAAT AAGATGGGAG
 211 GAGCATGTCC CAAAGGCCTT TNTCCTTCCC TTGGAAGATT TGATCTTAAA TACAGCACTT NCAATACTAG
 281 CATAGGAAGC AAGAATTAAG CATANTGGGA CAGCTAACAT AAAAATGCAT ACCACAGAGA GTGTGAGCTC
 351 GTTAGAACCC TTTTCACCAC AGGCAATCTT TATCAGAACA GGAATCTCAC ACACCAAGTG GTCCAGCTTA
 421 TTGAGACCAC ACAGTGGNAA TTTGTATTGT GGCAGTGGCC CTCTGAGAAC GGCATAGATT ATACCAANTT
 491 AACCACNACN GCGGNAACTA ANGATTGAGA CGCNCCTGGAT TCATGATGAG GGTNTAGTGA AGAGGTNTNC
 561 AGAATGGCCA CATACCGNTC AAA

SEQ. ID NO: 10
 1 GCTGCTNCCA GCAGTGGTAA CAACGCANAG TACGCCCCCA ATGTATTTGT TCTTCGGCCA TCTGTCTCTC
 71 CTGGATGTCT GCTTCATCAC CACTACCATC CCACAGATGT TGATCCACCT CGTGGTCAGG GACCACATTG
 141 TCTCCTTTGT ATGTTGCATG ACCCAGATGT ACTNTGTCTT CTGTGTTGGT GTGGCCGAGA GCATCCTCTT
 211 GGCTTTTCATG GCCTATGACC GNTATGNTGC TATCTGCTAC CCACTTAACT ATGTCCCGAT CATAAGCCAT
 281 AAGGTCTGTG TCAGGCTTGT GGGAACTGCC TGGNTCTTTG GGCTGATCAA TGGCATCTTT NTCGGGTATA
 351 TTTCATTCTT AGAGCCCTTC CGCAGAGACA ACCACATAGA AAGCTTCTTC TGGCAGGCCC CCATAGTGAT
 421 TTGGCCTCTT TTGTGGGGGA CCCTNANANT AGTCTGTGGG CAAATCTTTN GCCGATGCCA TCGTGGTAAT
 491 TCTNAGNCCC ATNGGTGCTN ACTGNTACTT ACCTATNTGC ACATTCTGT CCACCATCCT AGNNAAAGTC
 561 CTCCTTCTN

SEQ. ID NO: 11

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1 GGNNTTTTAC CNCNATTGGA GCTCCAAAGC AGTGGTAACA ACGCAGAGTA CGCCCCCTAT GTACTTGTTC
71 TTGAGAAACT TGTCTTTCTT AGATTTTGT TACATCTCTG TCACAATTCC AAAATCTATT GTTAGTTCCCT
141 TGACTCATGA TACTTCCATT TCTTTCTTTG GGTGTGCTCT GCAAGCCTTC TTTTTCATGG ACTTGGCAAC
211 TACGGAGGTA GCCATCCTTA CAGTGATGTC CTATGACCGC TATATGGCCA TCTGCCGGCC TTTACATTAT
281 GAGGTCATCA TAAGCCAAGG TGTCTGTCTG AGGATGATGG CCATGTCGTG GCTCAGTGGG GTGATCTGTG
351 GATTCATGCA TGTGATAGCA ACATTCTCAT TACCATTCTG TGGGCGCAAT AGAATACGTC AATTTTTCTG
421 TAATATTCCA CAGCTCCTAA GCCTCTTAGA CCCCAAAGTA ATTACCATTG AGATTGGAGT CATGGTTTTT
491 GGTACAAGGC TTNGGATAAT CTNCTTTGGT GNAATTACTC TCTCCTACAT GTACATTTTT TCTGCATCAT
561 GAGGATTCCCT TCTAAGGAGG GG

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SEQ. ID NO:12

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1 GGNNTTGGACC ACGGAGCTCC AAGCAGTGGT AACAAACGAG AGTACGCCCT CTTGTCCTCG TGCCGATACA
71 TGATGGGGTT CAACATGGGA GTCATAACAG TGTAGGACAA TGATAGCAGC TTCTTGCCCT GAGGTGAATT
141 ATTTGATTTA GGCCGGAAGT AGGTGAGGCT TAATGATATA TAGAAAAGAG AGACAACAAG GAGGTGTGAG
211 GAACATGTAG AAAAGGCTTT ATTCTTCCCT TTAGCTGATG GGATCTTGAG GATGGCAGCA GCAATGTGAG
281 TATAGGAACA CAAGATCAGC AAGCAGGGGA TCATGACCAC CAGAATGGTT CCGACGATGG CGTAGATCTC
351 AAAGAGTGCT GTGTCTGCAC AGACCAGCCT CAGNACAGGT GGGCTGTCAC AGAAGAAGTG GTTCACCTTG
421 TTGGTGCCAC AGAATGGAAA ACTGAAGAGC CATGTGGTCT GCACAGTAGC TACAGGAAAG CCTGGGAACC
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561 ATGGCCACAT ANCGGTCNT

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SEQ. ID NO:13

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1 GNNNTTNNNN CCACTGGAGC TCCAAAGCAG TGGTAACAAC GCAGAGTACG CCCCCAATGT ATTTATTCTT
71 GCTCACCTCT CCTTAGTTGA TATCTGTTTT ACCACCAGTA TTGTCCCCCA GCTGCTGTGG AACCTAAAAG
141 GACCTGACAA AACAATCACA TTCCTGGGTT GTGTCATCCA GCTCTACATC TCCCTGGCAT TGGGCTCCAC
211 TGAGTGTGTC CTCCTGGCTG TAATGGCTTT TGATCGCTAT GCTGCAGTTT GCAAACCTCT CCACTATACC
281 GCCGTAATGA ACCCTCAGCT GTGCCAGGCT CTGGCAGGGG TTGCGTGGCT GAGTGGAGTG GGAACACTC
351 TTATCCAGGG CACTGTCACC CTCTGGCTTC CTCGCTGTGG ACACCGATTG CACTAACATT TCTTCGTGAG
421 GTACCCCTCA TGATTAAGCT TGCACTGTGT GACATCCATG ATAATGAGGT TCAGCTCTTT GTTGCTTCAC
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561 TCAAGTCAGT CCAGCCT

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SEQ. ID NO:14

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1 GGNNTNTNAC TCCATGGACT CCAAGCAGTG GTAACAACGC AGAGTACGCC CATACATGAT GGGGTTCAGT
71 AGGGGAGTGA TGACAGTGTA GGTCAACGAG ATCAGCTGGT CATGTTCTCT GGTGTTCTCT GACTTGGGCT
141 TGAGCTAGGC AATGGAGGCA CAGCTGTAGT GGACAATGAC CACAGTGAGG TGGGATGCAC AGGTGGCAAA
211 AGCCTTCTTC CGGCCCTCAA CTGAAGCAAT CTTGAGGATT GNAGAGATAA TGAGAACATA AGAATGAAA
281 ACCAGACCCA TAGGTACAAC AAGCACCAGC ACACTGATAA TCAAAGTCAG GATTTTCATTG ACAGTGGTGT
351 CAATGCAGGA GAGCTTCATC ACAGNGCGGA TGTACAGAA GAAGTGGGGC ACCTTTCTAG CACAGAAGGG
421 TAACCTGAAT ACAGATGTCA CTTGCGTTAT TGTACAATC AGCCCAATGC TGCNGGCCCC CAGGACAAGT
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561 ANACCATTCG TGNGAGC

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SEQ. ID NO:15

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1 GNCNTNTTA ACNCCATTGG AGCTCCAAAG CAGTGGTAAC AACGCAGAGT ACGCCCATTA CGAAAAGTGT
71 AGATGAAGGG GTTCAAGAGG GGTGTGATGA TGCAGCTCAG GACGGAGGCA CCTTTGTTGA GCAGTTTGGA
141 CTGAGCCTCT GACATACGAA TGATAGAGAA GATGGAAGTG CCATAGATGA TGACCACCAC TGTAAGATGC
211 GAGGCGCAAG TGGAAAACGC TTTCTTTCGC TCAGCAGCTG TAGGGGCCCT GAGAACAGTG GCAAGAATGC
281 AGGCATAGGA AACTGAGGTC AGAGCCAGTG AGCCAGTAA CACCAACGTA GAGAGCATGA AAGCCACCAG
351 TTTCAGCAGG TGGGTGTCCC CACAAGAAAG CCTGAGCAAG GGCCAACTGT CACGAAAGAA GTGGTCAATA
421 CCATTGNGGC CACAGAAAGG CATGGCTGGC CATGAGGACA GTGGGGCAAA GGACCCAGAG GAATNCANCT
491 AGCCAGGAGG CCACACTAGT TTGTGAACAG ACATGGCCAT TNATTAGGGT CTCATAGCGG AGTTGTCGNC
561 AGATTTGCNT GGTNACGATT CAN

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SEQ. ID NO:16

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1 GGNNTTTTAC CNCNATTGGA CTCCAAAGCA GTGGTAACAA CGCAGAGTAC GCCCCCTATG TATTTATTCT
71 TGCTCACCTC TCCTTAGTTG ATATCTGTTT TACCACCACT ATTGTCCCC AGCTGCTGTG GAACCTAAAA
141 GGACCTGACA AAACAATCAC ATTCCTGGGT TGTGTCATCC AGCTCTACAT CTCCCTGGCA TTGGGCTCCA
211 CTGAGTGTGT CCTCCTGGCT GTAATGGCTT TTGATCGCTG TGCTGCAGTT TGCAAACCTC TCCACTATAC
281 CGCCGTAATG AACCCCTCAGC TGTGCCAGGC TCTGGCAGGG GTTGCGTGGC TGAGTGGAGT GGGAAACACT
351 CTTATCCAGG GCACTGTCAC CCTCTGGCTT CCCCCTGTG GACACCGATT GCTCCAACAT TTCTTCGTGA
421 GGTACCCTCC ATGATTAAGC TTGCATGTGT GGACATCCAT GATAATGAGG TTCAGCTCTT TGTGTCTTCA
491 CTGGTCTTGC TCCTCTTGCC CTTAGTGCTA ATACTGCTGC CTATGGACAT ATAGCCAANG TGGCATAAAG
561 GATCAAGTCA GTCCAGG

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SEQ. ID NO:17

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1 GNNNNTTNTT CANTCCATTG GGCCCTCTAG ATGCATGCTC GAGCGGCCGC CAGTGTGATG GATATCTGCA
71 GAATTCGCCC TTATTCCGGA GGGTATACAT GAAGGGATTG GTAAGTAGAC GTAAACTCGA AGCCAAGAAC
141 AGAATTTCTC TTAGAAAAGA GAATTGAAAC TAAAGAGAAA GAACTAGCAA AGAAGGAAAT ATTGAATATA
211 CAAGAGAGAG GAGACAGATG ATGGAACAAG ACTCTGAAAG AGGTGGAAGG GATTGAATAC AATCAAAAGT
281 ATGGTGACTG CTAGTTCCAA GATGGTGGCG TAGGGGCAAG CTGGCTTTGC TTACCCCCCT GGCAGAAAAC
351 CAAAAACAAA TAGCACCAG ATTATCACTA GCAATATCCC AGAACTCACA TATAAGGATG AGACAGTTCC
421 CAGGGCCCAG AGAAGATCAG AAGCACAAGT GGGAGAAGTC AGCTTTGGAT GCTACTTTGT TCTAAGGGAG
491 ACAAGTTGGG AGGATGATTG CAGATGTATA TTCAATGTTA TAAACAGCC CATAAAACAA AGATTGGAAA
561 ATGTTGAATT TTGCAACCAG GAGCAAATAC TGGGAAAGGC GAATTCAGC CACTTGCGNC C

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SEQ. ID NO:18

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1 GNNNNTTNAN TCANTGCCCT NGGGCCCTCT AGATGCATGC TCGAGCGGCC GCCAGTGTGA TGGATATCTG
71 CAGAATTCGC CTTGTGTGCG CAAGGTGTAA ATGAAAGGGT TTGCGCAGGA GTAAATGAAG GGATTACGCA
141 GGAGTAAATG AAGGGATTAC GCAGGAGTAA ATGAAGGGAT TACGCAGGAG TAAATGAAGG GATTACGCAG
211 GAGTAAATGA AGGGATTACG CAGGAGTAAA TGAAGGGATT ACGCAGGAGT AAATGAAGGG ATTACGCAGG
281 AGTAAATGAA GGGATTACGC AGGAGTAAAT GAAGGGATTA CGCAGGAGTA AATGAAGGGA TTACGCAGGA
351 GTAAATGAAG GGATTACGCA GGAGCAAATA CATAGGAAGG GCGAATTCCA GCACACTGGC GCGCGTTACT
421 AGTGGATCCG AGCTCGGTAC CAAGCTTGAT GCATAGCTTG AGTATTCTAA CGCGTCACTT AAATAGCTTG
491 GCGTAATCAT GGTCATAGCT GTTCTCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG
561 CCCGGAAGCA TAAAGTGTA AGNCTGGGGT GCCTAATGAG TGACTTACTC CATTG

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SEQ. ID NO:19

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1 GNNANTNATT CCATCCATTG TCCCTTCAGA TGCATGCTCG AGCGGCCGCC AGTGTGATGG ATATCTGCAG
71 AATTCGCCCT TCTTGGTTTT TGTGCTGATA GATCATGGGA TTCAGCATGG GGGTGACCAC AGTGATACATC
141 ACTGAGGCTG TTGCACTTGA GTGTGAGTTG CGGGTGGCAG CAGAACTAAG GTACACCCCT AGGATTGCAC
211 CATAAAATAA GGAGACAACT GAGAGGTGAG ATGCACAGGT GGAAGATGCC TTGTACTTCC CCTGAGCTGA
281 TGAGATNGCA TGTATGGAAN GAAATTATNT TANAAGTAAG AGTAAAGNAT NCCAGTCAGG GGNANCNTTC
351 ACCCATCAGN TGCAANTTGT AAAAATTATA TTCAANCNAT NTGNATTTAA NGAAAANCCT TATCANGTAN
421 AACTGCAAG GNTNTGNATT NANCCCTNGN ANTTAANNNT TCNACAAGAA AATAANGTGC GTTNNAACTT
491 TTNTAAGTCC CTNTCNCCAT TAANGTCNAN TCCNTCCNTA TCCCTTTTCN NATTTTGNAN TCNNGANTAC
561 NNTCTNNNGC NNTCNATTTT TNTNNTNNCT GACCTACTAA CCNATTNAGT TACNACAAGN CCNTTCNANT
631 CTCTATAATT NCTCGCANGT TNTCCCTCTT NNCANNNTCC CNTTNTNTC CCTNTTCCCC ATCTNC

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SEQ. ID NO:20

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1 CCATTGGCCC TCTAGATGCA TGCTCGAGCG GCCGCCAGTG TGATGGATAT CTGCAGAATT CGCCCTTCCT
71 ATGTATTTTC TCTTACTGGG CTTTCTGGT TCTCAAATC TTCAGCTCTC TCTCTTTATG CTTTCTCTGG
141 TGATGTACAT CCTCACAGTT AGTGGTAATG TGGCTATCTT GATGTTGGTG AGCACCTCCC ATCAGTTGCA
211 TACCCCATG TACTTCTTTC TGAGCAACCT CTCCTTCTG GAGATTGGT ATACCACAGC AGCAGTGCCC
281 AAAGCACTGG CCATCCTACT GGAGAGAAGT CAGACCATAT CATTTACAAG CTGTCTTTTG CAGATGTACT
351 TTGTTTTCTC ATTAGGCTGC ACAGAGTACT TCCTCCTGGC AGCCATGGCT TATGACCGCT GTCTTGCCAT
421 CTGCTATCCT TTACACTACG GAGCCATCAT GAGTAGCTG CTCTCAGCG AACTGGCCTT GGGCTTCTGG
491 GTGGNTGGGT TCGGGGGCAA TGCAGTGCCC ACAGGCCTTC AATCAAGTGG GCTGNTCCTT CTGGTGGCCC
561 CCGGTGCCAA TCAACCACTT TTTTTTGGG ACAATTGCAN CCCTGGAATT GGCC

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SEQ. ID NO:21

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1 GNNCTTANTT CAATCCCACC NANCCNTGCC GANGCATGCT CGNGCGGCCG CCAGTGTGAT GGATATCTGC
71 AGAATTCGCC CTTCTATGT ATTTACTCTT ACTGGGCTTT CCTGGNTCTC AAACCTCTCA GCTCTCTCTC
141 TTTATGCTTT TTCTGGTGAT GTACATCCTC ACAGTTAGTG GTAATGTGGC TATCTTGATG NTGGTGAGCA
211 CNTCCCATCA GNTGCATACC CCCATGTTNT TCTTTCTGAG CNACCTCTCC TTCTGGAGA TTTGGTATNC
281 CNCAAGCNGC ANNGCCCCAA GCTTTGCNCA TCTTATTGCN CAGANGCINN CCNNTACANN NACNCTCCTG
351 TTTNTGGCTN CCTTNCCTCT TNCTTCNCTC ANNTACTNCN TCTNCTNTAG TNTCTTTCTT CTCTNCTNCT
421 CNTNNCNCCT NTAATNTTCC NCCTNTTCTN NTTCTNTTT TCCCTNCTCT GTTTCACCCC TACCTCTTAT
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561 CTCNTTTTAT ATCGCCTCTT CTCNTNCTTC CNNTTCTCTC TCCTCANNCA TATCNANTNT NTTCTACTCT
631 CGTNCNNTAT CTANNCTCCT NTTTCNGTCC TNCTTCTCCT NTCATTTCTA TATTNCTTCT CANACANTNT
701 TCGCATCGTN GCANCATCTC CTCCCATCTC CTGTNCNCTN TTCCN

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SEQ. ID NO:22

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1 GNNNTTAANT CATTCCCCNC TCNATGCATG CTCGAGCGGC CGCCAGNGTG ATGGATATCT GCAGAATTCCG
71 CCCTTGTTTC GGAGGCAGTA GATGAATGGG TTGATGGAAT CTGAGACAGT GCTCTAGAAT CTGTGTTTCA
141 TACAGGATGA GATATAAATG AAACAAATGC TAAATAATGA CACAAGGTAC CTTGCCGAGA GAGGAATCAT
211 CCACCTGGAA GGGTAGGCTG TTTGTGAATA ATGTAGGGTG GGAGAGAAGG CTTTACTAAG GAGATGGGCT
281 TAAAGAATGT GAACGATGTG CTCACAGAGG CCACAGAAGA GAAATTATAG CCAGGAGAAC AACCTGAAAG
351 ACAAAGGACA CGGTGGCATG AGCGCATGTA ACACAATGTA CTCAGGAAAT GGTGGGCATC CTGAGATATG
421 GAGTGGAAAT CAGTACAGGG CTTTGTAAC TCAGCTTGGA GTCAGATCAC AGAAAGCCTT GACAAGGAAC
491 TGAAAATGGG TTCTGAAGGC CAGAAGCCCA TTCAAGATTC CCAAAGGGAA AAACACAAAT CAGCTTGTTT
561 TCAGGACGTA ATTCTTGGA GTTGCTAGAA TTACATCAGA AAGGAGGTTT ACNT

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SEQ. ID NO:23

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1 GNNNTNANTC ANNCANTGGG CCCTCTAGAT GCATGCTCGA GCGGCCGCCA GTGTGATGGA TATCTGCAGA
71 ATTCGCCCTT CCTATGTATT TCCTCTTACT GGGCTTTCCT GGTCTCAAA CTCTTCAGCT CTCTCTCTTT
141 ATGCTTTTTT TGGTGATGTA CATCCCCACA GTTAGTGGTA ATGTGGCTAT CTGATGTTG GTGAGCACCT
211 CCCATCAGTT GCATACCCCC ATGTACTTCT TTCTGAGCAA CCTCTCCTTC CTGGAGATTT GGTATACCAC
281 AGCAGCAGTG CCCAAAGCAC TGGCCATCCT ACTGGGGAGA AGTCAGACCA TATCATTTAC AAGCTGTCTT
351 TTGCAGATGT ACTTTGTTAT CTCATTAGGC TGCACAGAT ACTTCCTCCT GGCAGCCATG GCTTATGACC
421 GCTGTCTTGC CATCTGCTAT CCTTTACACT ACGGAGCCAT CATGAGTAGC CTGCTCTCAG CGCAGCTGGC
491 CCTGGGCTCC TGGGTGNGGG GGTTCGTGGC CATTGCAAGT GCCACAAGC CTAATCAGT GGCCCTGTCC
561 NTCTGGGGGC CCGGGGCCA TTNACCACTT TNTTCTGGGA CAATTGCACC CCTGGAATTG G

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SEQ. ID NO:24

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1 TNNTTAANTC ATTCCNTTGN CCCTCAGAT GCATGCTCGA GCGGCCGCCA GTGTGATGGA TATCTGCAGA
71 ATTCGCCCTT TCCTTGTTAC TGAGGGAGTA GATTAGGGGA TTGATGGAAT CTGAGACAGT GCTCTAGAAT
141 CTGTGTTTCA TACAGGATGA GATATAAATG AAACAAATGC TAAATAATGA CACAAGGTAC CTTGCCGAGA
211 GAGGAATCAT CCACCTGGAA GGGTAGGCTG TTTGTGAATA ATGTAGGGTG GGAGAGAAGG CTTTACTAAG
281 GAGATGGGCT TAAAGAATGT GAACGATGTG CTCACAGAGG CCACAGAAGA GAAATTATAG CCAGGAGAAC
351 AACCTGAAAG ACAAAGGACA CGGTGGCATA AGCGCATGTA ACACAATGTA CTCAGGAAAT GGCTGGCATC
421 CTGAGATATG GAGTGAATA CAGTACAGGG CTTTGTAAC TCAGCTTGGA GTCAGATCAC AGAAAGCCTT
491 GACAAGGAAC TGAAAATGGG TTCTGAAGGC CAGAAGCCAT TCAAGATTCC CAAAGGGAAA AACACANATC
561 ACTTGTTTTT AGGACGTATT CTTGGGCAGT TGCTAGAATT ACATCAGAAA GG

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SEQ. ID NO:25

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1 GNNNTTANT CCATGCCCCT CTAGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAATTC
71 GCCCTTGTTT CGCAGCCTAT AAATGAAGGG GTTGATGGAA TCTGAGACAG TGCTCTAGAA TCTGTGTTTC
141 ATACAGGATG AGATATAAAT GAAACAAATG CTAATAATG ACACAAGGTA CCTTGCCGAG AGAGGAATCA
211 TCCACCTGGA AGGGTAGGCT GTTTGTGAAT AATGTAGGGT GGGAGAGAGG GCTTTACTAA GGAGATGGGC
281 TTAAAGAATG TGAACGATGT GCTCACAGAG GCCACAGAAG AGAATTATA GCCAGGAGAA CAACCTGAAA
351 GACAAAGGAC ACCGGTGGCA TAAGCACATG TAACACAATG TACTCAGGAA ATGGCTGGCA TCTGAGGTA
421 TGGAGTGGAA TACAGTACCG GGGCTTTGTA AACTCAGCTT GGAGTCAGAT CCAGAAAGCC CTTGACAAGG
491 AACTGAAAT TGGGTTCTTG AAGGCCAGAA GCCATTCAAG GATTCCCCAA AGGGGAAAAA CACAAATCAA

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561 GCTTGTTTTT AGGGACCGTT AATTCTGGGG CCAGGTTGCT TGAATTACCT TCANGAAAGG GAGGTTTACA
631 CT

SEQ. ID NO:26

1 GNNCTTATTC ATCCCCCTCT AGATGCATGC TCGAGCGGCC GCCAGTGTGA TGGATATCTG CAGAATTCGC
71 CCTTCTTTG TTCCTCAGAG TGTAGATTAG GGGTTGATG GGGTTGATGG AATCTGAGAC AGTGCTCTAG
141 AATCTGTGTT TCATACAGGA TGAGATATAA ATGAAACAAA TGCTAAATAA TGACACAAGG TACCTTGCCG
211 AGAGAGGAAT CATCCACCTG GAAGGGTAGG CTGTTTGTGA ATAATGTAGG GTGGGAGAGA AGGCTTTACT
281 AAGGAGATGG GCTTAAAGAA TGTGAACGAT GTGCTCACAG AGGCCACAGA AGAGAAATTA TAGCCAGGAG
351 AACAACTGA AAGACAAAGG ACACGGTGGC ATAAGCGCAT GTAACACAAT GTACTCAGGA AATGGCTGNC
421 ATNCTNAGAT ATGGAGNGNG AATACCAGTA CANGGCTTTN TANACTCANC TTGGAGTNCA GAATCACANA
491 ANGCTTGCA AGGAACTGAA AATGGGTTCT GAAAGGCCAG AAGCCNTTNA AGATCCCCAA AGGGAAAAAA
561 CACAAATCAA GCTTTTTTNA AGNACNGTAA TTCNTGGNGC CAGTTGCTTA GAATTNCCAT CANAAANG

SEQ. ID NO:27

1 GGNNTAAGCC TTCCCCCTNC GATGCTGCTC GAGCGGCCGC CAGTGTGATG GATATCTGCA GAATTCGCCC
71 TTCCCATGTA TTTCTCTTA CTGGGCTTTC CTGGTTCTCA AACTCTTCAG CTCTCTCTCT TTATGCTTTT
141 TCTGGTGATG TACATCCTCA CAGTTAGNGG TAATGGGGCT ATCTTGATGN TGGTGAGCAC CNCCCATCAG
211 TTGCATACCC CCATGTACTT CTTTCTGAGC AACNNNTCCN TCCTGGAGAN TTTGGNATAC CACACGCAAN
281 NAGNGNCCNA AGGCACTTGG NCNTNCTACA GGNGGAGAAG GCTTGACCAT ANNATTTTAC CATGCCTNGC
351 CTTANGNCAN ACCCNCNTTN TNCCTNTTNT TCCNCTNNNN GGTNNNTCAN CCGCANNCTT NNATCNNNTG
421 NANCTTCATN GAATATGGNN TNNGTNTNTC TTGAGAGCCT CNNGATCNNA TTTTTTCCAN CNNCTAAAGN
491 GGNCTTNTC TCTCTNNNAT CTAGCTTNNT GGNCTCTTT TNNTNCTNA CCCGTGNTNT CCTATNTGNT
561 GTCTCTTCCT ACNNNCTGCN NTTATTNTAN ATCANNTCTN NCNTTGCTCT CNTNTACNAC ATNATCATNC
631 TCNCTCCCN CTNCTNCTCT CTATNNCNTA CCATCNCTCT CTTCTCATTC ANCTCTTNT CATTGNTTGT
701 TCANTTANNC ACTCTCCNTC NCATCTTCTA TNCACNTANT TTNTNTTTT NCTCTCTANT TCTNNTTCCA
771 NTGTNCACTC CNNTCTTNNC NNTTNCCCTA NCG

SEQ. ID NO:28

1 GTNNTTNANN NCATTGCCCC TCTNGATGCA TGCTCGAGCG GCCGCCAGTG TGATGGATAT CTGCAGAATT
71 CGCCCTTCCT ATGTACTTCC TCTTACCGGG CTTTCTGGT TCTCAAACTC TTCAGTCTC TCTCTTTATG
141 CTTTTTCTGG TGATGTACAT CCTCACGGTT AGTGGTAATG TGGCTATCTT GATGTTGGTG AGCACCTCCC
211 ATCAGTTGCA TACCCCATG TACTTCTTTC TGAGCAACCT CTCCTTCTG GAGATTGGT ATACCACAGC
281 AGCAGTGCCC AAAGCACTGG CCATCCTACT GGGGAGAAGT CAGACCATAT CATTTACAAG CTGTCTTTTG
351 CAGATGTACT TTGTTTTCTC ATTAGGCTGC ACAGAGTACT TCCTCCTGGC AGCCATGGCT TATGACCGCT
421 GTCTTGCCAT CTGCTATCCT TTACACTACG GAGCCATCAT GAGTAGCCTG CTCTCAGCGC AGCTGGCCCT
491 GGGCTTCTGG GTGGGTGGGT TTCGGGGCCA TTGCAAGTGC CCACAGCCCT TATCAAGTGG CCTGTCCCTC
561 TGNGGCCCCC GGGCCCATCA ACCACTTTTT TCTGGGGACA ATTGCACCCT GGAATGCCCC

SEQ. ID NO:29

1 GTNNTTNANN CCATNCCATT GGGCCCTCTA GATGCATGCT CGAGCGGCCG CCAGTGTGAT GGATATCTGC
71 AGAATTCGCC CTTTCATGGT TCCGGAACA GTAAATTATG GGGTTCAGTC ATGGTAACAG GAGGAGGCTG
141 AGTGATGGG CATGGATGGG GGCTGTGAAT GTGGCGGGAG CTCATGGATG TGCTCTTCTG AGTGCTTCAC
211 GTTCTGTAGT GAAATAAGAA GCAAGGTCAT CACCGAGAGG GAGGAGACAG GCTCGGGTGA GTTTAGTGGA
281 TATGAATCCA AGAGAGACCA TTCAACTTAG TTGTCTATTT TTTTCTCTC CAGTTATAGT CACTTGATG
351 AATGTAGATG TGGAGTACTT GATCATAAGA TCCATTTTAT GGCAGAAGAC ATTATTTTTC TGAGCCTTCT
421 GCTGTCAGTT TCTAAATAAG CAGGCCAGCC GGGCTGTGCA CCTAAATGTC TGTCTGGGAG GAGCAGGCTG
491 AGAAGTCTTG CAGTCTGCAG GACACCCGAG GAATCGTATT GTGGGAACCG TCCCCGAGAA CCACACGAGC
561 CGTGCTNCTC AGTNCTGACT GGAANAATGA AATTGNAAGC CAAGTNGTTC NNGGANCNNT

SEQ. ID NO:30

1 GNNNTTNANN CCATTGCGCC CTCTAGATGC ATGCTCGAGC GGCCGCCAGT GTGATGGATA TCTGCAGAAT
71 TCGCCCTTCC TATGTATTTT TCTTCTTAAC GATTGGAATG CCTGGGATTA GGCAGATGAT TTTCTTTTTT
141 CCCCATACCC CTCTATTATT TAGGTGATTG AGTTTAAATC CCTTTATCTA CACCCCTTCGG AACAAGGGCG
211 AATTCCAGCA CACTGGCGGC CGTTACTAGT GGATCCGAGC TCGGTACCAA GCTTGATGCA TAGCTTGAGT

281 ATTCTAACGC GTCACCTAAA TAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC
 351 CGCTCACAAT TCCACACAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT AATGAGTGAG
 421 CTAATCACA TTAATTGCGT TGCCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG CCAGCTGCAT
 491 TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTCGCGTA TTGGGCGCTC TTCCGCTTTC TCGCTCACTG
 561 ACTCGCTGGG CTTGCGTCGN TCGCTGCGG CGAGCGGGAT CAGCTCACTC AAAAGG

SEQ. ID NO:31

1 GNNNNNNNNT CANGCCATTG GGCCCTCTAG ATGCATGCTC GAGCGGCCGC CAGTGTGATG GATATCTGCA
 71 GAATTCGCCC TTCTATGTA TTTCTCTTCA CTTTCTCCGA CATCACTCAC AGCCACCCCA CCCTCAGCCT
 141 CTCCCTCCTC CCATGTATTT TCTCTTCAAT CTCTCCTTCT TTGATATCCT GAACTTTCTG TAGCTCTTTA
 211 TTTTCTCTTC CAATCCCTTC ATATACACGT TTCGTAACAA GGGCGAATTC CAGCACACTG GCGGCCGTTA
 281 CTAGTGGATC CGAGCTCGGT ACCAAGCTTG ATGCATAGCT TGAGTATTCT AACCGCTCAC CTAAATAGCT
 351 TGGCGTAATC ATGGTCATAG CTGTTTCCTG TGTGAAATTG TTATCCGCTC ACAATTCCAC ACAACATACG
 421 AGCCGGAAGC ATAAAGTGTA AAGCCTGGGG TGCCATAATGA GTGAGCTAAC TCACATTAAT TGCCTGCGCT
 491 CACTGGCCGC TTTCCANGTC GGGAAACCTG TCGGCCAGCT GCATTAAATG AATCGGCCAA CGCNCGGGGA
 561 GAGGCGGTTT GCGTATTGGG CGCTNTTTCG TTCTTCGNTN ACTGATCGNT GG

SEQ. ID NO:32

1 GNNNNNNNNT TCATNCCATT GGGCCCTCTA GATGCATGCT CGAGCGGCCG CCAGTGTGAT GGATATCTGC
 71 AGAATTCGCC CTTGTTGCTT AGAGTGTAAG TAAAGGGTT AACATTGGCT TAGAGGTGAA GAGTAAATAC
 141 ATAGGAAGGG CGAATTCCAG CACACTGGCG GCCGTTACTA GTGGATCCGA GCTCGGTACC AAGCTTGATG
 211 CATAGCTTGA GTATTCTAAC GCGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG TTTCTGTGT
 281 GAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGAGC CGGAAGCATA AAGTGTAAG CCTGGGGTGC
 351 CTAATGAGTG AGCTAACTCA CATTAAATTG GTTGGCTCA CTGCCCGCTT TCCAGTCGGG AAACCTGTCTG
 421 TGCCAGCTGC ATTAATGAAT CGGCCAACGC GCGGGGAGAG GCGGTTTGCG TATTGGGCGC TCTTCCGCTT
 491 CCTCGCTCAC TGACTCGCTG CGCTCGGTG NTCGGCTGCG GCGAGCGGTA TCAAGCTCAC TCAAAGGCGG
 561 TAATACGGTT ATCCACAGAA TCAGGGGGAT ACGCANGAAA GAACATGTGA GCAAAT

SEQ. ID NO:33

1 GNTNTNANTC ATGCCCCCNC CGATGCNTGC NCGAGCGGCC GCCAGTGTGA TGGATATCTG CAGAATTCGC
 71 CCTTGTGCGG GAGCGAATAT ATGAAGGGGT TAAGGGAAGA GAAAATACAT AGGAAGGGCG AATTCCAGCA
 141 CACTGGCGGC CGTTACTAGT GGATCCGAGC TCGGTACCAA GCTTGATGCA TAGCTTGAGT ATTCTAACGC
 211 GTCACCTAAA TAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC CGCTCACAAT
 281 TCCACACAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT AATGAGTGAG CTAATCACA
 351 TTAATTGCGT TGCGCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG CCAGCTGCAT TAATGAATCG
 421 GCCAACGCGC CGGGGAGAGG CGGTTTGCCT ATTGGGCGCT CTNCGCTTC CTCGCTCACT GACTCGCTTG
 491 CGCTCGGTCC GTTCGGCTGC GGCGAGCGGT ATCAANTCAC TCAAAAGGCG GGAATACGGG TTNACAGAG
 561 AATCAGGGGG ATAACGCNGG AAAGAACATG TGAGCCANAN GGCAGCAAAA GGCNAGGAA T

SEQ. ID NO:34

1 GNNNNNNNNT CANNCCATTG GGCCCTCTAG ATGCATGCTC GAGCGGCCGC CAGTGTGATG GATATCTGCA
 71 GAATTCGCCC TTGTTCCGAA GGCTATAGAT GAAGGGGTTT TAGGTTTTTA GGAACACAGG CTAAGGGGGA
 141 AGAGAAAATA CATGGGAAGG GCGAATTCCA GCACACTGGC GGCCGTTACT AGTGGATCCG AGCTCGGTAC
 211 CAAGCTTGAT GCATAGCTTG AGTATTCTAA CGCGTCACCT AAATAGCTTG GCGTAATCAT GGTATAGCT
 281 GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG CCGGAAGCAT AAAGTGTAAG
 351 GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG
 421 GAAACCTGTC GTGCCAGCTG CATTAAATGAA TCGGCCAACG CGCGGGGAGA GCGGTTTGC GTATTGGGCG
 491 CTCCTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC GTCGGCTGCG GCGAGCGGTA TCAGCTCACT
 561 CAAAGGCGGT AATACGGGTA TCCACAGAAT CANGGGATAA GCGAGGAAAA GACA

SEQ. ID NO:35

1 GGNNNTNANT CATTGCCCGC CTNGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAAATC
 71 GCCCTTCCGA TGTATTTTCT TCTACGTTAA GGTATTTTAA ATTGTTACTA ATGCATAAGG GCAACACATT
 141 CTGTAATGCT GACAAGATGA AAGAGCCAAA AGTAATTAAT GATGCTGTGA CCTCACAAT ATGTATGTGT
 211 GGATGTATAT ATATCTATTC AATATATGTA ACTATACATA TGTCTGTTTC TAATTGAAAA CACCAGGTAA

281 TTATCATCTG TAGAAACCCCT AGTGTCTCAG ATAAGTTGGC TAGTTTTTGG TTTCACATAA AGGAACAAAC
 351 ATTTATAGAT TTATATGTAT ATTAATAATG GTAAAAATTG GCTGGGTGCA GTGGTTCATG CCTATAATAC
 421 CAGCACTTTG GGAAGCCGAG GTGGGCGGAT TACTTGAGGT AAGGAGCCCA GCCTGACCAA CAAGGTGAAA
 491 CCCCATCCCT ACTAAAAATA CAAGAATTAG CCCGGGGATG GTGGTGGCCA CCTGTAATCC CAGCTACTTG
 561 GGAGACTGAA GCCAGGAAAA TCACTTGACC CAGGAAGCNG AGGTTGCAGG NGAG

SEQ. ID NO:36

1 NGNNNTTGAN TCAATTCNNN GNCGANGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAATTC
 71 GCCCTTCCTA TGTATTTCCCT TCTAGCCAAC CTCCCACTCA TTGATCTGTC TCTGTCTTCA GTCATAGCCC
 141 CCAAGATGAT TACTGACTTT TTCAGCCAGC GCAAAGTCAT CTCTTTCAAG GGCTGCCTTG TTCAGATATT
 211 TCTCCTTCAC TTCTTTGGTG GGAGTGAGAT GGTGATCCTC ATAGCCATGG GCTTTGACAG ATATATAGCA
 281 ATATGCAAAC CCCTACACTA CACTACAATT ATGTGTGGCA ACGCATGTGT CGGCATTATG GCTGTGCGAT
 351 GGGGAATTGG CTTTCTCCAT TCGGTGAGCC AGTTGGCCTT TGCCGTGCAC TTACCTTTCT GTGGTCCCAA
 421 TGAGGTCGAT AGTTTTTATT GTGACCTTCC TAGGGTAACC AAACCTGCCT GTACAGATAC CTACAGGCTA
 491 GATATTATGG TCATTGCTAA CAGTGGTGTG CTCACTGTGT GGTCTTTTGT CTTCTAATCA TCTCATACAC
 561 TATCATCTA ATGACCATCC AGCATTGCCC TTTAGATAAG TCGTNCAAAG G

SEQ. ID NO:37

1 GNNNTNANTC CNNNCCNCCN CTAGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC TGCAGAATTC
 71 GCCCTTCCCA TGTATTTGCT TCTCAGCAAC TTGTCCTTCT CTGACCTCTG CTTCTCTTCC GTGACCATTC
 141 CCAAGTTGTT ACAGAACATG CAGAACCAGG ACCCATCCAT CCCCTATGCG GACTGCCTGA CCCAAATGTA
 211 CTTCTTCTG TTATTTGGAG ACCTGGAGAA CTTCTCCTT GTGGCCATGG CCTATGACCG CTATGTGGCC
 281 ATCTGCTTCC CCCTGCACTA CACCGCCATC ATGAGCCCCA TGCTCTGTCT CGCCCTGGTG GCGCTGTCTT
 351 GGGTGCTGAC CACCTTCCAT GCCATGTTAC ACACTTTACT CATGGCCAGG TTGTGTTTTT GTGCGAGCAA
 421 TGTGATCCCC CACTTTTCT GNGATATGTC TGCTCTGCTG AAGCAGGCCT TCTCTGACAC TCGAGTTAAT
 491 GAATGGGTGA TATTTATCAT GGGAGGGCTC ATTCTTGTC TCCCATTCCT ACTCATTCTT GGGTCCTATG
 561 CAAGAATTGT CTCCTCATCC TCAAGTCCC TTTNTAANG GTATCTGCAA GGCCCT

SEQ. ID NO:38

1 NGNNNNNTNA NTCNANGCCN NGNGCCCTCT AGATGCATGC TCGAGCGGCC GCCAGTGTGA TGGATATCTG
 71 CAGAATTGCG CTTTCCAATG TATTTACTTC TCAGCCAGCT CTCCCTTATG GACCTGATGT ACATCTCCAC
 141 CACCGTCCCC AAGATGGCGT ACAACTTCCT GTCCGGCCAG AAAGGCATCT CTTTCTGGG ATGTGGTGTG
 211 CAAAGCTTCT TCTTCTGAC CATGGCGTGT TCTGAAGGCT TACTCCTGAC CTCCATGGCC TACGACCGTT
 281 ATTTGGCCAT CTGCCACTCT CTCTATTATC CTATCCGCAT GAGTAAAATG ATGTGTGTGA AGATGATTGG
 351 AGGCTCTTGG AACTTGGGGT CCATCAATC CTTGGCACAG ACAGTCTTTG CCCTTCATAT TCCCTACTGC
 421 AGGTCTAGGG CTATTGACCA TTTCTTCTGC GATGTCCAG CATGTTGCT TCTTGCTGTA CAGATACTTG
 491 GGTCTATGAA TATATGGTTT TTGTAAGGAC AAAGCCTCTT TCTTCTTTN CCTTTCATTG GCATCACTTC
 561 TTCTGNNGGC CGAGTCCTAA TTGCTGGCTA TATAATGCAC TCAAAGGAGG GGAGG

SEQ. ID NO:39

1 TAGNNNNNTT ANNTCANNGC CNNTGNNNGC TCAGATGCAT GCTCGAGCGG CCGCCAGTGT GATGGATATC
 71 TGCAGAATTC GCCCTTCCAA TGTATTTTCT TCTCAGCAGG AGAGATATTT ATCCTCACTG CCATGTCCTA
 141 TGACCGCTAT GTAGCCATCT GCTGTCCCCT GAACTACGAG GCTGCACAGA GTACTTCTC CTGGCAGCCA
 211 TGGCTTATGA CCGCTGTCTT GCCATCTGCT ATCCTTTACA CTACGGAGCC ATCATGAGTA GCCTGCTCTC
 281 AGCGCAGCTG GCCCTGGGCT CCTGGGTCTG TGGTTTCGTG GCCATTGCAG TGGCCACAGC CCTCATCAGT
 351 GGCCTGTCTT TCTGTGGCCC CCGTGCCATC AACCATTCTT TCTGTGACAT TGCACCCTGG ATTGCCCTGG
 421 CCTGCACCAA CACACAGGCA GTAGAGCTTG TGGCCTTTGT GATTGCTGNT GTGGTTATCC TGAGTTCATG
 491 CCTCATCACC CTTGTCTCCT ATGTGTACAT CATCAGCACC ATCCTTAGGA TCCCTCTGC AGTGGCCGGA
 561 GCAAAGCCTT CTCCCGTGCT CCTCGCATCT NAACNGGTG CTCATTGGT ATGGG

SEQ. ID NO:40

1 CATGCTCGAG CGGNCGCCAG NGNGATGGAT ATCTGCAGAA TTCGCCCTTC CTATGTATTT GCTTCTCAGC
 71 AGGAGAGATA TTTATCTTCA CTGCCATGTC CTATGACCGC TATGTAGCCA TCTGCTGTCC CCTGAACTAC

141 GAGGTGATTC ATGTGCCCAT TAGAGCTTGA GAAGCACTGC TTGGAAGCCC CTTCTGCCAT CAATGAGGCT
 211 GCACAGAGTA CTTCTCCTG GCAGCCATGG CTTATGACCG CTGCCTTGCC ATCTGCTATC CTTTACACTA
 281 CGGAGCCATC ATGAGTAGCC TGCTCTCAGC GCAGCTGGCC CTGGGCTCCT GGGTCTGTGG TTTCTGGCC
 351 ATTGCAGTGC CCACAGCCCT CATCAGTGGC CTGTCTTCT GTGGCCCCCG TGCCATCAAC CACTTCTTCT
 421 GTGACATTGC ACCCTGGATT GCCCTGGCCT GCACCAACAC ACAGGCAGTA GAAGCTTGNG GCCTTTGTGA
 491 ATTGCTGNTG TGGGTATCCC GAGTTCATGC CTCATCACCC TGNCTTCTA TGTGTACATC ATCAGGCACC
 561 ATTCTCAGGA TCCCTTCTGC AAGNGG

SEQ. ID NO: 41

1 ATGGNNNNNN NNTTTNNNA ANTTTTNCCC ANTTTGGGCG GNCCCCCCT TCTTTAAGGN AATGGGCCCCA
 71 TTGGGGCCCT CCCGGAAGGC CCGGGGGCNC CCGGCCCCAA AGGTTTGGGT TGGGAAATGG GGGGAATTTA
 141 AATTCCCTTG GGCCAAGGNA AAAATTTTCC NGCCCCCCT TTTTCCCTT TTTGGTTTT ANCCGGGGGA
 211 ANGGGGGGGT TGATTAATTA ATCGGGAAGN TNGGGGGGAA NTTTTTAAA AAAACCTTG GGGGAAGGTT
 281 CCAACCCAAC AAGGTTGGTT TTCCANGGGA CCGTTGGGAC CAGGCTTTTN GAATCAAGAA TCCCAAAGGG
 351 CATTCTTTTG GATTAAGGAA NGGTGCCGGG ACCGGTGAAA GGGAAAAAAC TGGTGGACCC CATACCAAAA
 421 TGAGAACCAC GGTGAGATGC CGAGGAGCAC GTGGAGAAAG GCTTTGCTTC CGGCCACTGG CAGAGGGGAT
 491 CCTGAGGATG GTGCTTGATG ATGTACACAT AGGAGACAA GGTGATGAG GCATGAATC AGGATAACCA
 561 CAACAGCNAT CACAAAGGCC ACAAGCTCT ACTGCCTGTG TGTGGGTGC AGGCCAGGGC AATCCAGGGG
 631 TGCAATGTCA CAAGAAAGAA AGTGGTTGAT GGCACGGNG GGCCACAGAA GGACAGGCCA CTTGATGAAG
 701 GGCTTGTTGG CACTGCAATG GCCACGAAAC CACCAGACCC AGGAACCCAN GGCCAAGCTT GCGCCTGAAG
 771 AGCAAGGCTA CTCATGAATG GCTTCCGTAG TNGTAAAGGA TAGCAAGATG GCAAAGGCAA GCCGGTCATN
 841 AAGCCATGGC TTGCCNG

SEQ. ID NO: 42

1 GNNNTTANNN CATTGCGCCC TCTAGATGCA TGCTCGAGCG GCNCGCCAGT GTGATGGATA TCTGCAGAAT
 71 TCGCCCTTGT TGCGCAAGGA GTAGATGAAC GGATTCAGGG CAAGGGAGTG CTGAGGAGAT AGACGGGTAT
 141 AACTGGGCA CAAGTCCATG AGTAATCAAG GCCTGTTATT TAAAAAAGG AAAAAAAGG CTTGAACAAT
 211 ATAGAATCCC ATTACCCAGA GATAGACTGG ATGGTGAATT AAATTTCTG GTGAATTTCT TTCCAGATAT
 281 CTCTCTATG ATATGTATAC ACAAGCAATT TTGGAAGAA AAGATACTTT ATAAGGATAA GCCTGAAAC
 351 TGCAACGAAT GCAATGTGGA GAATGAAGGC AAGATGTGGC GAAGAAGGGC ACCACAATCT GGTGGCTGAG
 421 AGAGTGCAAC TGCTACTACA GCTAAAAGGA GAGCTGGAGA AGCTGGTGAG GACAGTAAGA GATGAATCTG
 491 GTTTAAGACA CGCTGAGTCT CAAATGCCAT GGCTCCCCTA GGTGCTCTCT TCAGATGTAA ATCTTAAGCT
 561 CAAAGCAGGT GGATGAGAAA TCACATTTCA TAGTCCCTGC ACAGACGGCT NTNTTGAGCT

SEQ. ID NO: 43

1 GNNNTTANNN TCATTGCCCC GNNNGANGCA TGCTCGAGCG GCCGCCAGTG TGATGGATAT CTGCAGAATT
 71 CGCCCTTCCC ATGTATTTGC TTCTCAGCAA CTGTCTCTTC TCTGACCTCT GCTTCTCTTC CGTGACCATT
 141 CCAAGTTGT TACAGAACAT GCAGAACCAG GACCCATCCA TCCCCTATGC GGACTGCCTG ACCCAAATGT
 211 ACTTCTTCTT GTTATTTGGA GACCTGGAGA GCTTCTCTCT TGTGGCCATG GCCTATGACC GCTATGTGGC
 281 CATCTGCTTC CCCCTGCACT ACACCGCCAT CATGAGCCCC ATGCTCTGTC TCGCCTGGT GGCCTGTCC
 351 TGGGTGCTGA CCACCTTCCA TGCCATGTTA CACACTTTAC TCATGGCCAG GTTGCTTTTT TGTGCAGACA
 421 ATGTGATCCC CCACTTTTTC TGTGATATGT CTGCTCTGCT GAAGCTGGCC TTCTCTGACA CTCGAGTTAA
 491 TGAATGGGTG ATATTTATCA TGGGAGGGCT CATCTTGCA TCCATTCCTA CTCATCCTTG GGTCTATGC
 561 AAGAAATGCT CCTCATCCTC AAGGCCCTTC TNTAAGGGTA TCTGCAAG

SEQ. ID NO: 44

1 GNNNTNANT CNTGCCCTGN CCCNCGCNC NNGCGCCGCG GCGGATGGAT ATCTGCAGAA TTCGCCCTTG
 71 TTTACTAAGAG TATAGATGAA CGGATTCAGG GCAAGGGAGT GCTGAGGAGA TAGACGGGTA TACACTGGGC
 141 ACAAGTCCAT GAGTAATCAA GGCTGTATT TTAAGGAGG AAAAAAGCT TGAACAATAT AGAATCCCAT
 211 TACCCAGAGA TAGACTGGAT GGTGAATTAA ACTTCTTGGT GAATTTCTTT CCAGATATCT CTCTATGCAT
 281 GTGTATACAC AAGCAATTTT TGGGAAGAAA GATACTTTAT AAGGATAAGC CTGAAAAGCT CAACGAATGC
 351 AATGTGGAGA ATGAAGGCAA GATGTGGCGA AGAAGGGCAC CACAACTCTG TGGCTGAGAG AGTGCAACTG
 421 TCACTACAGC TAAAGGAGA GCTGGAGAAG CTGGTGAGGA CAGTAAGAGA TGAATCTGGN TTAAGACACG
 491 CTGAGTCTCA GATGCCATGG CTTCCCTAGG TTGCTCTTN CAGATGTAAA TCTTAAGCTC AAAGCANGTG
 561 GATGAGAAAT ACACATTTNA TAGTCACCTG CACAGACGGT TTTTGTAT

SEQ. ID NO: 45

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1 CATGCCCGT CCCNCNAGNT NCNNGCNCCG CGGCCGCNAN GGATATCTGN ANAATTCGCC CTTCTATGT
71 ATTTACTTCT CCAACTTCTC CTTCCCATCT CTATCATTAG AACCATTCA TATACACCCT ACGAAACAAG
141 GGCGAATTCC AGCACACTGG CGGCCGTTAC TAGTGGATCC GAGCTCGGTA CCAAGCTTGA TGCATAGCTT
211 GAGTATTCTA ACGCGTCACC TAAATAGCTT GGCGTAATCA TGGTCATAGC TGTTTCCTGT GTGAAATTGT
281 TATCCGCTCA CAATTCCACA CAACATACGA GCCGGAAGCA TAAAGTGTAA AGCCTGGGGT GCCTAATGAG
351 TGAGCTAACT CACATTAATT GCGTTGCGCT CACTGCCCGC TTTCCAGTCG GGAAACCTGT CGTGCCAGCT
421 GCATTAATGA ATCGGCCAAC GCGCGGGGAG AGGCGGTTTG CGTATTGGGC GCTCTTCCGC TTCTCGCTCA
491 CTGACTCGCT GCGCTCGGTC GTTCGGCTGN GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG NAATACGGTT
561 ATCCACAAGA ATCAGGGGGA TAACGCAAGA AAAGACATGT GA

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SEQ. ID NO: 46

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1 GNNNTNATTN ATTGCATTGG GCCCTCTAGA TGCATGCTCG AGCGGCCGCC AGTGTGATGG ATATCTGCAG
71 AATTCGCCCT TAGTGAGTAG ATGAAAGGGT TCAGCATGGG GGTCAACACA GTGTACATCA TAGCCATGAC
141 AGTGTCCTTT AGAGTAGAAC TATTAGCTGA TGAGCATAAG TAGAGACCAA TAACGGTTCC ATAGAACAGT
211 GACACCACAG ATAGGTGGGA GCCACAAGTA GAGAAGGCCCT TGCAGACACC CTTAGAAGAA GGGACCTTGA
281 GGATGGAGGA GACAATTCTT GCATAGGACC CAAGGATGAG TAGGAATGGG ATGACAAGAA TGAGCCCTCC
351 CATGATAAAC ATCACCATT CATTAACTCG AGTGTGAGAG AAGGCCAGCT TCAGCAGAGC AGACATATCA
421 CAGAAAAGGT GGGGGATCAC ATTGTCTGCA CAAAAACACA ACCTGGCCAT GAGTAAAGTG TGTAACATGG
491 CATGGAAGGT GGTGAGCACC CAGGACAGCG CCACCAGGGC GAGACAGAGC ATGGGGCTCA TGAGGGCGGT
561 GTAGTGCAGG GGAAGCAGA TGGCCACATA GCGGTCATAG GCCATGGCCA CAAGGAGGAA

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SEQ. ID NO: 47

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1 CNATGGGCC TCTAGATGCA TGCTCGAGCG GCCGCCAGTG TGATGGATAT CTGCAGAATT CGCCCTTCCA
71 ATGTATTTGC TTCTCAGCAA CTTGTCTTTC TCTGACCTCT GCTTCTCTTC CGTGACCATT CCCAAGTTGT
141 TACAGAACAT GCAGAACCAG GACCCATCCA TCCCCTATGC GGAATGCCTG ACCCAAATGT ACTTCTTCTT
211 GTTATTTGGA GACCTGGAGA GCTTCCTCCT TGTGGCCATG GCCTATGACC GCTATGTGGC CATCTGCTTC
281 CCCCTGCACT ACACCGCCAT CATGAGCCCC ATGCTCTGTC TCGCCCTGGT GGCGCTGTCC TGGGTGCTGA
351 CCACCTTCCA TGCCATGTTA CACACTTTAC TCATGGCCAG GTTGTGTTTT TGTGCAGACA ATGTGATCCC
421 CCACTTTTTC TGTGATTTGT CTGCTCTGCT GAAGCTGGCC TTCCCTGACA CTCGAGTTAA TGAATGGGTG
491 ATATTTTATCA TGGGAGGGCT CATTCTTGTC ATCCCATTCC TACTCAATCC TTGGGTCTAT GCAAGAAATT
561 GTCTTCTTCA TNCTCAANGG CCCTTTCTTC TAANGGTATC TTGCAAG

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SEQ. ID NO: 48

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1 ANNNCCNTNG GAGCTCCAAA GCAGTGGTAA CAACGCAGAG TACGCCCCCT ATGTACTTAC TTTTGTTAAG
71 TCCAACCTCC ATCCTCCTTG GCCTTTTGAT TCAATTGATC ACTCCTTCTT CCTCAAAACA CCTTGTTTCA
141 TCATCCTTTC TCAGTCTCCT TTGTGGATTG TTCCTCATTT ATTTGACCTC TTGCTGGTGA ACCCTTTCAT
211 ATACACTCTC CGTAACAAAG AGGGCGTACT TCTGTCTGCT TGAGCGNACT GATGGNACCC AGCTTTTGTT
281 CCCTTTAGTG AGGGNTAATT GCGCGCTTGG CGNAATCATG GNCATAGCTG NTTNCTGNNGN GAAANTGNTA
351 TTTCGNTNAC AATTNCACAC AACATACNAG CCGGGAGCAT AAAGGGNNAA GNCCTGGGGN GCCTAATGAG
421 GGAGCTTACT CACAATAATT GGGGTGNGCC CACTGGCCCC TTTCAGGCG GGAAACCTN GCGGGGCCAG
491 CTGGAATAAA TGAATCGGGC CACGCGCCGG GGAGGAGGGC GGGTTNNGGA ATTGGGCGCT TTTCCNTTT
561 CTNGGTTAAT GGAATNGGTN GGCNNNGTCC GTTCGGTTGG GGGGANCGGN NNT

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SEQ. ID NO: 49

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1 AACGCAGAGT ACCGCCCACT ACGTAATCTG TACATGAAAG GGTTTAAAG AGACTGGGAA GAGAGGAATT
71 GGCAAGATCA AGCAGAGGCA ACTCCTTCTA GTCCTTCTAG TACCGCAAGG GGCAGATAAA TGGAATGGGT
141 AACACCTAGA GGAAAGTATA CTTGCCAAAA GCAAAATNCAT AGGGGGGAGT ACATTATCGG GTTGAAAAA
211 GTATTCCATG CAGATAAAAA CAAAAGCAA ATACATCGGG GCGTACTTTC TGTCGTCTTT GAGCGTACTG
281 ATGGTACCCA GCTTTTGNTC CTTTAGTGAG GGTAAATTGC GCGCTTGGCG TAATCATGGT CATAGCTGGT
351 TTCTGTGTGA AATTGTTATC CCGCTCACA TTCACACAAC ATACGAGCCC GGGAGCATAA AGTGTAAGC
421 CTGGGGTGCC TAATGAGTGG AGCTTACTTA CATTAAATTG CGTTGCGCTC ACTGGCCGCT TTTCCAAGTC
491 GGGAAACCTG TCGTGNCAGC TTCANTAATG AATCGGCCAA CGCCGCGGGG AGAGGCGGGT TGCGTATTGG
561 GCGCTCTTCC GCTTCTTNGT TNACTGACTT CGG

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SEQ. ID NO:50

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1  GNNNTTTAAC  NCCGGNGCTN  CNAGCAGTGG  AACAAACGCAG  AGTACGCCCC  CGATGTACTT  TCTTTTTTCAG
71 TCTCAAGTCT  TCCTCTTCTC  CAAAGATTTT  GTCTTTTCTA  CTACCTGAGC  TACCAAATCC  CTTGTCAATCA
141 ATTTCAATAA  CTGTATTCTC  TTCATCATT  CAACTTCAA  CGTGTCACT  CAGAACAAGC  TTCATGTTAC
211 TTCCAATTTT  ATCCTTCTTG  TTTGCTGATT  CCAAGAATTC  CAGTCCCATC  TAGGCCCCGA  ATGCATTGTT
281 CCTGCCACCC  TTTTCATATC  CTCAATTCCC  TTGTATCATC  ACTTTCCTTT  TATATAGCAC  AGATTCCATG
351 ATTCATAACA  ATAATTATGT  TTTTTTTTGC  ATGTGCTCTT  AATTTCCCTT  CTTGCTCCTA  TTATCTTCTA
421 TCATACTTTT  CTGGAAACAC  TAATTCTGGT  GAAATATACT  CTTTGTGGAC  TTTGCACTTA  TGCTCAGTCA
491 GCTGAAGATG  ATGGCTAGAC  AAATACTCAC  AATCATGCTG  ACTGGCCCAA  TTTATAGTCA  TGACCACCGA
561 TTACAAACCC  CTTCAATTTAT  TCTCCGCAAC  AGGGGCGTCT  TCTGCGCTTG  AGCGTCCGGT  GGGG

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SEQ. ID NO:51

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1  GCAGTGGTAA  CAACGCAGAG  TACGCCCCGT  ACGGAGGCTG  TAAATAAAGG  GGTGAGGAA  GTAAAGTACT
71 TCACAGTACT  GGAGCACACA  GCATGTGAAT  TTCAGCCAAA  GGACAAATGC  CTCCAAAAA  AGTTAATTCA
141 CAGTGCAGCA  GGGCGAGGCA  CTTGTCTTAT  TCCTGGTTC  TCACATTGAC  CCTGAAAGGA  CTTTTTTTGT
211 TTAATCCCAT  TTTCACAGAT  GGGAAAGGGA  CTCTGTATGG  TTGTCACTTT  TATCCAAAGT  CTCATAGCCA
281 GTAAGAAGCT  GCCCTCAAAG  TCCCTACCTT  GTCTTCCATT  CGACTATTCT  GAGGTTTCT  CCCAGAAACC
351 CCATACCTCT  GCCTTATATT  TTAATGAAAA  GTATGTCTCC  AGGTTTATGT  GGAGAATAAC  CAAGACCTCA
421 GAAACATTTA  GTGAAATCA  GAGCTAGAAG  GAATCTGTTT  TTTTGGGAGT  TCAGAGAAAC  TGACTTGGAT
491 AAGACATCAA  AGTTGTCTTG  TGCAGCAAAT  TCTCCTCCGG  CACATAGTAG  GCACTCTGAT  AAATCAAAA
561 AGGCTTCTAA  GAAGAGGCAG  AAGN

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SEQ. ID NO:52

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1  GTGAANCCAN  NNTAANNCCN  ATTGGAGCTC  CAAGCAGTGG  TAACAACGCA  GAGTACGCCC  CCGATGTAGT
71 TTCTTCTTTC  CTTCTTCTCC  TCCTTCTTTC  CTCTTCTCT  TTCTCTCTCT  CTCCCTCTCC  CTCTCCCTCT
141 CCCTCTCTCT  CTCCTTTTTT  TTCTCCTTCC  TCCTCTCTCC  CCAATCCGT  TCATGACTTC  TTCTTCTTCC
211 TCTTCTTCTT  CTTTCTTTCT  TTCTTCTTTT  TCTCTAAGCA  GGATCCTGGG  CTGTTCAAAC  CAGAGAGCTG
281 TAAGTCTTTT  CTTTCCCAT  TACTGTTAGA  TCCGTTGAAT  CGGCTCCAGA  AACCACAAAC  GTTAACCTTT
351 GCATTTACAC  GTTTCGTAAC  GGGCGTACTT  CTGTCGTCTT  GAGCGTACTG  ATGGTACCCA  GCTTTTGTTC
421 CCTTTAGTGA  GGGTTAATTG  CGCGCTTGGC  GTAATCATGG  TCATAGCTGT  TTCCTGTGGG  AAATTGTTAT
491 CCGCTCACAA  TTCCACACAA  CATACGAGCC  GGGAGCATAA  AAGTGTAAG  CCTGGGGTGC  CTNATGAGTG
561 AGCTAACTCA  CATTAAATTG  GTTGCCTTA  CTGNCCGTTT  TCAGTCNGGA  AAN

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SEQ. ID NO:53

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1  TNANNCNNNT  TAANNCCCAT  TGGAGCTCCA  AAGCAGTGGT  AACAAACGCAG  AGTACGCCCC  CGATGTACTT
71 GCTTCTTCTT  CTTTGGAGTG  GCTGAATGCT  TCCTCCTGGC  TACCATGGCA  TATGACCGCT  ATGTGGCCAT
141 CTGCAGTCCC  TTGCACTACC  CAGTCATCAT  GAACCAAAGG  ACTCGTGCCA  AACTGGCTGC  TGCTCCTGG
211 TTCCCAGGCT  TTCCTGTAGC  TACTGTGCAG  ACCACATGGC  TCTTCAGTTT  TCCATTCTGT  GGCACCAACA
281 AGGTGAACCA  CTTCTTCTGT  GACAGCCAC  CTGTGCTGAG  GCTGGTCTGT  GCAGACACAG  CACTGTTTGA
351 GATCTACGCC  ATCGTCGGAA  CCATTCTGGT  GGTCATGATC  CCCTGCTTGC  TGATCTTGTG  TTCCTATACT
421 CGCATTGCTG  CTGCCATCCT  CAAGATCCCA  TCAGCTAAAG  GGAAGAATAA  AGCCTTTTCT  ACATGTTTCT
491 CACACCTCCT  TGGTGGCTCT  CTTTTCTATA  TATCATTAAG  CCTCACCTAC  TTCCGGCCTA  AATCAAATAA
561 TTCACCTGAG  GGCACGAAGC  TGCTATCATT  GCCTACACTG  NTATGACTCC  A

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SEQ. ID NO:54

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1  GTTNTTCCAT  GGAATCCCAA  GCAGTGGTAA  CAACGCAGAG  TACGCCCCCT  ATGTACTTAC  TTCTTGCTGG
71 CTTATCATTT  ATAGATATCA  TTTATTCTTC  ATCCATTTC  CACAGATCGA  TTTGAGACTT  GTTCTTTGGG
141 AATAATTCCA  TATCCTTCCC  ATCTTGCTTG  GCCAGCTCT  TTACAGAGCG  CTTTTTGGT  GGGTCAGAGG
211 TCTTTCTTCT  GTTGGTGATG  GCCTATGACC  TTGCATTACT  TGGTTATCAT  GAGACAATGG  GTGTGTGTTT
281 TGCTGCTGGT  AGTGTCTCTG  GTTGGAGGAT  TTCTGCACTC  AGTATTTCAA  CTTAGTGTTA  TTTATGGGCT
351 CCCATTCTGT  GACCTCAATG  TCATTGATCA  TTTTTCTGT  GATATGCACC  CTTTATTGAA  ACTGGTCTGT
421 ACCGATACCC  ATGTTATTGG  CCTCTTAGTG  GTGGCAATGG  AGGACTAGGT  TGCACTATTG  GGNTTCTGCT
491 CTTACTCATC  TCTTATGGNN  CATCTGCACT  CTCTAAAGAA  CCTTAGTCAG  AAAGGGAGGT  GAAAAGCCCT
561 CTCAACCTGC  AGTTCCACAT  AACTGGGGGG  TGGTTTCTTC  TTTGTN

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SEQ. ID NO:55

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1 TTANNCCNNT TNAATNCCNT TGGAGCTCCA AAGCAGTGGT AACAAACGCAG AGTACGCCCC CAATGTACTT
71 GCTTCTTCTT TTTTGGGGCT GCTGAGTGCT GCCTCTGGC CACCATGGCA TATGACCGCT ACGTGGCCAT
141 CTGTGACCCC TTGCACTACC CAGTCATCAT GGGCCACATA TCCTGTGCCC AGCTGGCAAG CTGCCTCTTG
211 GTTCTCAGGG TTTTCAGTGG CCACTGTGCA AACCACATGG ATTTTCAGTT TCCCTTTTGTG TGGCCCCAAC
281 AGGGTGAACC ACTTNTNTNG TGACAGCCCT CCTGTTATTG NACTGGTCTG TGCTGACACC TCTGTGTTTT
351 GAACTGGAGG CTCTTGACAG CCACTGCCTA ATTCAATTCTC TTTCCTTTCT TGCTGATCCT GGGATCCTAT
421 TTCGCATTCT CTTCATATC TTTAAGGATG CCGTCAGCTG AGGGGAAACA TNAGCATTCT NCACCTGTTC
491 CGCCACCTC TTGGGTGGCT CTCTCTTCTA TAGCACTGGC AATCCTTAAC GTATTTTCCG ACCCCAATTC
561 AAGTGCCTTT TTNTGAGAAG CAAAGAACT GGTGTCACT TTTTTTCAC AAGGGGNGAC TTCCAATGTT

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SEQ. ID NO:56

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1 GNGNTTTNNN CCATGGAGCT CCAAAGCAGT GGTAACAACG CAGAGTACGC CCCCCATGTA CTTTCTTCTT
71 CTTTGGAGTG GCTGAATGCT TCCTCTGGC TACCATGGCA TATGACCGCT ATGTGGCCAT CTGCAGTCCC
141 TTGCACTACC CAGTCATCAT GAACCAAGG ACTCGTGCCA AACTGGCTGC TACCTCTGG TTCCCAGGCT
211 TTCCTGTAGC TACTGTGCAG ACCACATGGC TCTTCAGTTT TCCATTCTGT GGCACCAACA AGGTGAACCA
281 CTCTTCTGT GACAGCCAC CTGTGCTGAG GCTGGTCTGT GCAGACACAG CACTCTTTGA GATCTACGCC
351 ATCGTCGGAA CCATTCTGGT GGTGATGATC CCCTGCTTGC TGATCTGTG TTCCTATACT CACATTGCTG
421 CTGCCATCCT CAAGGTCCCA TCAGCTAAAG GGAAGAATAA AGCCTTTTCT ACATGTTCTT CACACCTCCT
491 TGNTGTCTCT CTTTCTATA TATCATTAAG CCTCACCTAC TTCCGGCCTA AATCAAATAA TTCACCTGAG
561 GGCAAGAAGC TGCTATCATT GNCCTACACT GTTATGACTC CATGTTGAAC CCCATAATTT ATTCATTGAG
631 C

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SEQ. ID NO:57

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1 TTATNNCCAT TGGAGCTCCA AAGCAGTGGT AACAAACGCA GAGTACGCC CCCATGTATT TTCTTTTCTT
71 TGGGGNAGCT GNATGCTTCC TNCTGGCTAC CATGGNATAT GACCGCTAT GNGNCATCT GCAGTCCCTT
141 GNNCTCCCAG TCATTATGAA CCAAAGGACA CGGGCCAAAC TGGCTGGTGN TTCCTGGGTC CCAAGCTTTC
211 CTGNAGCTAC TNGCAAGAC CACAATGGCT CTNAGNTTT CCATTCTGNG GCACCAACAA GGTGAACCAC
281 TTNTTCTGN GACAGCCGGC TGTGCTGAAA GCTGGTCTGN TGCAAGACAC AGCACTGTTT GAGATCTACG
351 CCATCGTCGG AACCATTCTG GTGGTCAATG AACCCTGCT TGCTGATCTT GNGTTCCTAT ACTCGNATTG
421 GTGCTGCTAT CCCTCAAGAA CCCATCAAGC TAAANGGGA GCAATAAAGN CCTTTCTCTA CGTGCTCCTT
491 AACACCTCCC TTGGTGGCCT CTCTTTTCTA ATATAATCNT CTAAGCCTCA ACCTACTTCT TGGGCCCTNAA
561 NTCAAATAAA TTCTTCTGGA GAGGCAAGAA GGTGTATTTC ATTTATNCTA CACTGGTNGN GACTCCATGN
631 TGGAAT

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SEQ. ID NO:58

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1 GTNATNCCNT TTAATNCCNT TGGAGCTCCA AGCAGTGGTA ACAACGCAGA GTACGCCCGT TCCTCAGACA
71 GTATATGAAT GGGTTAAAAA TGGGCCAGAG CAGATGCAGG AAGATCAAAT AGGAGGCTAC TGCAGTAGAG
141 TCAAATCTAG GGCTGATGGT TTCTTGGGAT GCATAGTAAT AGGTAGATAG AGAAAGTCTT TAGGAGGTAG
211 AATGGACAGG ACTTCACAAT GCATTAAATG TAGGGAGAAA AAAAAATGATT CCTGGGTTTC TAGCTTGAGC
281 TAGTAGGGAT AGTGGTAGAA TTTACTGATA TGGAAAACG GAGGAAAAAG AGTTTGGAAG AGAAAGATGG
351 CAAGTTAAAT ACCTGTGGGA AATATAATCA CAGACACTAA ATAGGCAGCT GTGTGGGTGG CAAAGGAGAG
421 CCATGGGCTA GGAACATACA GTGGGATTCC CTGGCATGTC ATTGTTACT GAAGTCAGAG TGTATGAGAC
491 AGCCTAAGGA GAGAATNCAC ACAGGAGAAG AAAGAACTAA ACATTCACTG GCTGGCCAGA GGATGAGAAA
561 CCAAGAGAT TGGACTGTTT AGGAGCAACA GTGTTGNGAA AAGGGAGAAA NGGTTGAAAT T

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SEQ. ID NO:59

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1 GGNTTTANNC NCTGGAGCTC CAAAGCAGNG GTAACAACGC AGAGTACGCC CATTGCGTAG CGTGATACATA
71 AAGGGGTTGG AGCTGAAGGA GGAGATAAAG AAGAAGACAG CCAGAACCTT GTCCTCTGTC GGAGATCGCA
141 GGGATCTTGG GCCGTAGATA GGTATAAGCA AAGGGTGCAT AGTAGAAAGT CACTACAGTG AGGTGGGTGC
211 TGCAGGTCGA ATAGGCCTTC TTCCTCCCTT CTGCAGAGTG CATGTGGTAG ACAGCAAGGA GAATCCGGCC
281 ATAGGAACAT GCAATACAAA TGAAGGGAAA CACAAGAAAA ATGGTGGTGC TCAAAAACAC CGTGCACTCA
351 TAGACCCAGG TATCCGTGCA GGCTAGGGTC AACATAGCTG GAACATCACA GAAAAATGA TTGATGGCTC
421 TGGACTTGCA ATATGGGATA CGGAGTGCAT ATACCGTGTG AGCACAAGAG TTGATGGAGC CTATCATCCA

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491 AGATCCTGTT ATCATCAGTG CACACACTCT TTTTCTCATA CGGATGAGAT AGTGGAGAGG AAAGCAAATA
 561 GCCACATAAC GATCATAGGC CATTGATGTC AGGAGCAGCG CTTCTGCACC TGCTAAAGTC AGGAAGAAGA
 631 T

SEQ. ID NO: 60

1 TGTTANTCCN NTTNCTNCC ATTGGAGCTC CCAAGCAGTG GTAACAACGC AGAGTACGCC CTCCTTGT
 71 CTGAGAGTGT AGATGAAGGG GTTATAGGAG ATAAAGATCA GGGCAATATG TAGGACAAGG ACACAGACAC
 141 TGACAACAAA GTTGATTATC TCATTGACAG TGGTGTCTGT GCAGGCCAGC TTCAGCAGGG GTCTCACATC
 211 ACAGAAGAAG TGGGAGATGA CAAAGTCATC ACAAAGGGC AGGCCAAACA TAGATGTTAC TTGGACAATA
 281 GCCATGCCCA GGCCAATCCT CAGTGACCCA GATCCCAGTC AGACACAAGC CCTCTTACCT ATGAATACCG
 351 TAAGGGGTTG CAGAAGACCA CATAGCAATC ATATCCCATG GCTATGAGAA GAAAGCAGTT GTTGATGCCA
 421 AAAGTCACAT AGAAGAGCTG AGTGACACAG CTTGTCATGA CAATAAGCTA GTGAGGATTC AAGAGGCGAG
 491 AAAGCATATG GGGAGTAATG GCCACCATGT AGCAGGTCTC AGAGATAGAC AGCAATGCCT AGGAAAAAGT
 561 ACATGGGCCG TACTTCTGTC GTCTTGAGCG TACTGATGGT ACCCAGCTTT TGTTCCCTTT

SEQ. ID NO: 61

1 GTNANNCCNN TGTAGCTCCN AAGCNGAGCT AACAACNNAG AGAACAACGC AGAGTACGCC CCCGATGTAC
 71 TTGTTCTTAC TCTTGCTGG ATTTGAAAAC TTCCTCTGT CCGTGATGGC CTATGACCGG TTTGTGGCCA
 141 TCTGTCACCC CCTGCACTAC ATGGTCATTA TGAACCTCA CCTCTGTGGA CTGCTGGTTC TAGCATCCTG
 211 GACCATGAGT GCTCTGTATT CCTTGCTACA AATCTTAATG GTAGTACGGC TGTCCTTCTG CACAGCCTTA
 281 GAAATCCCCC ACTTTTTCTG TGAACCTAAT CAGGTCATCC AACTTGCTTG TTCTGATAGC TTTCTTAATC
 351 ACATGGTGAT ATATTTTACA GTTGCCTGTC TGGGTGGAGG TCCCCTCACT GGGATCCTTT ACTCTTACTC
 421 TAAGATAATT TCTTCCATAC ATGCAATCTC ATCAGCTCAG GGGAAGTACA AGGCATTTTC ACCTGTGCAT
 491 CTCACCTCTC AGTTGTCTCC TTATTTTATG GTGCAATCCT AGGGGTGTAC CTTAGTCTGC TGCCACCCCG
 561 AACTCACACT CAAGTGCAAC AGCCTCAGTG ATGTACACTG GGGCACCCCC AT

SEQ. ID NO: 62

1 GNNNNNNNAT TTNATGCCNT TNNTGATTCC CNTNNNNNNN NCAAGCAGNG GTAACAACGC AGAGTACGCC
 71 CCTATGTAT TTCTTCCTAA GATCCAAATA TTAAATAAAA AGACAGTCAT CCCACCACTA ACTAAAGTAG
 141 TGTTTCCAC ACTTCTCTAT TAAGAAGCAT GTGAGATACT TGTACAAAC ATAACATCCT GGTCCCACCC
 211 CAAAGCCACT CAATCAAATA TCCCAGGGAA GGGATCTAGG AATTCCGTAGG TTTAACGAGT GCCCCAAAT
 281 GATTATTACC GTTGGAGAA TCTAGGCAAC AATGAATTAA GGAAAGCTCT CTACCATTG GTACTGGTAC
 351 CAGGTTTGA GATCACAGGG AAGAGGGTAA GCATATCAGA CTAGCAGAGC TGCCAGAACT CGGGCTTTCA
 421 AAAGAGAGGT GCCACCTCT CCCATGTCCA TGTAAGTAGC AAACAACCT CTCTGTGAGAA CTCTGAGGAA
 491 CAAGGGGGCG TACTTCTGTC GTCTTGAGCG TACTGATGGT ACCCAGCTTT TGTCCTTTTA GTGAGGGTTA
 561 ATTGCGCGCT TGCGTAATC ATGGTCATAG CTGTTTCTG TGTGAAATG TTATCCGCTC ACAATTCT

SEQ. ID NO: 63

1 TGTAGCTCCA AAGCAGTGGT AACAACGCAG AGTACGCCCT CTTGGTTACG TAAGGGAATA GATGATGGGG
 71 TTCAGCATGG GGGTGACTAC AGTGATCATG ACAGTGGCCA CACGGTCCCA CTCTGCTCGC GTCGGGACGT
 141 GGCCTGGAAG TAGACTGCAA TGACTGTCCT ATAGAAAGAG GCTCACCACA NCCAGGTGGG AGCCACAGGT
 211 GGGNCACAAG TCCCGGAGCC TCCAGAGGC TTGAGGGCAG CTGGAGCAGC GGNAAGCTTG NTATGGNCCC
 281 ACAAGGAGGC GAGGATGAGC AGNAAGGGAG TGACCACCAC TTGCNCGGCC CTNGGTGAAG ATGAGCAGCT
 351 TGATGTGGT GGNTGTCAGA GCACGAGAGC CTTTAAGAGA GGCTTGGTGG GTCACAGAAG AAGTGGGNGC
 421 ACTTTGTGGG AAAGCACAGA AAGGACAAGC GAGCCATGAG CAGGATATAC AGGAGGGAGT TGTCCGTGGG
 491 ACACAGCCA TGCCATTCCA ACCAGGGCTG CGCACATNGC CGGGGACATT CTCGTGGGAT AAGGGAAGGG
 561 GTGCCGGATN GGCACGTATC AGTCATAGGC CTTGGNCGCC AGAAGACAGC TTTNAATTTA CCCCAGG

SEQ. ID NO: 64

1 GTTANNCCNT NTANCTNCAA NNGAGGTAAC AACGCAGAGT ACGCCCCCA TGTATTTGCT TCTTGTCCAA
 71 CCGTGCCTTT GTAGAGATCT GCTACACCAC CGTTGTGGTG CCCTTGATGC TTTCCAACAT TTTTGGGGCC
 141 CAGAAGCCCA TTCCATTGGC TGGATGTGGG GCCCAAATGT TCCTCTTTCT CACACTTGGT GGTGTGACT
 211 GTTTCCTCTT GCGGATCGTG GCCTATGACC GCTATGTGGC CATCTGCCAC CCTTTGCAT ACCCTCATC
 281 ATGACCTGCA CTCTGTGCGT GCAGATGCTG GCGGCGCTG TGGGCTGGC CCTCTTCTC TCCCTGCAGC
 351 TCACCGCCTT AATCTTCACC TTGCCCTTCT GCGGCTACCG CCAGGAAATT AACCATTCC TCTGCGATGT

421 ACCTCCGTCC TGC GCCTGGC CTGCGCTGCA TCCGTGTTCA CCAGGCTGCC TCTATGTCGT GAGCATCCTC
 491 GTGCTGACCG TCCCTTCTT GCTCATCTGC GTCTCCTACG TGTTTCATCAC CTGTGCCATC CTGAGCATCC
 561 GTTCTGCTGA GGGCCGGCAC CAGGCCTTTT CAACTGCTCT TCCGG

SEQ. ID NO:65

1 TGTAGCTCCN AAGNNGAGNT ANCAACGCAG AGTACGCCCG CGGAATCTAT AGATGAAAGG GTTTGGNGAG
 71 TCAGAAGAAG GAAGTACATG GGAGTCATAA CAGTGTAGGA CAATGATGGC AGCTTCTTGC CCTCAGGTGA
 141 ATTATTTGAT TTAGGCCCGGA AGTAGGTGAG GCTTAATGAT ATATAGAAAA GAGAGACAAC AAGGAGGTGT
 211 GAGGAACATG TAGAAAAGGC TTTATTCTTC CTTTATAGTG ATGGGATCTT GAGGATGGCA GCAGCAATGT
 281 GAGTATAGGA ACACAAGATC AGCAAGCGGG GGATCATGAC CACCAGAATG GTTCCGACGA TGGCGTAGAT
 351 CTCAAAGAGT GCTGTGTCTG CACAGACCAG CCTCAGCACA GGTGGGCTGT CACAGAAGAA GTGGTTTACC
 421 TTGTTGGTGC CACAGAATGG AAAACTGAAG AGCCATGTGG TCTGCACAGT AGCTACAGGA AAGCCTGGGA
 491 ACCAGGAGGT AGCAGCCAGT TTGGCACGAG TCCTTTGGTT CATGATGACT GGGTAAGTGC AAGGGACTGC
 561 AGATGGCCAC ATAGCCGGTC ATATGCCATT GGTAGCCCAG GANGAAGCT

SEQ. ID NO:66

1 GTTATNCCCTT GTTGCTCCCN AGCAGAGGTA ACAACGCAGA GTACGCCCTT ATTTCTCAGA TATANGATGA
 71 AGGGGTTTCA AAAAAGAATG AGCAAAGAAA ATCTGGGCCA GGCGGGCATC AAAAGAAATA GTCTTGTGCT
 141 CAACCAAGAA GTCTGCAATC ATTTTAGGGG TAGCAGAGAA GGCAACACAT ACGTCTATAA ATGACAGGTT
 211 GGCAAGAAGC AAATACATTG GGGGCGTACT TCTGTCGTCT TGAGCGTACT GATGGTACCC AGCTTTTGT
 281 CCCTTTAGTG AGGGTTAATT GCGCGCTTGG CGTAATCATG CCGGAGCATA AAGTGTAAAG CCTGGGGTGC CTAATGAGTG
 351 TCCGCTCACA ATTCCACACA ACATACGAGC CCGGAGCATA AAGTGTAAAG CCTGGGGTGC CTAATGAGTG
 421 AGCTAACTCA CATTAAATTG GTTGCGCTCA CTGCCCCGTT TCAGTCGGGA AACCTGTCGT GCCAGCTGCA
 491 TTAATGAATC GGCCAACGCG CCGGGGAGAG GCGGTTTGC TATTGGGCGC TCTTCCGCTT CTCGCTCACT
 561 GACTCGCTTG CGCTCGGTCG TTCGGCTTGC GGCGAGCGGT ATCAAGCTCA CTCAAAT

SEQ. ID NO:67

1 GGGTTTTACN CTGTGCNCCC CCAGCAGNGG TAACAACGCA GAGTACGCC TGTGTCGAA GAAATAAATG
 71 AATGGGTTTA AAATAGACGT GAAGATGGTG TAGAATACAG CAAGGACTTT GTCAACTGAG TAACTGCTGA
 141 AGGGCCACAC ATAGATGAAA ATACACGATC CAAAGAATAA AGTGACCACA GTGATGTGAG CAGTCAATGT
 211 GGAGTGGGCC TTCACCATGC TTACAGAGGA GCGATTCCCTA ACTGTAATAA GTATTACAGT GTAGGANACA
 281 ACCAANAGGA GAAAGGAAT CAGAGAAAGA AAGCCACCAT CTGCAACTAT TAGTAGGCTG ACAACATAAG
 351 TGTCTATGCA GGCTAACTTN GTNGCTAGAG GAAGGTACACA GAAAAAACT ATCTACCTTA TTAGGACCAC
 421 ANAATGGCAG ATTAACCGTG AATGCCAAT GGCTGGTGGT ATGGATGAAG CCCACAAACC AGGAAATGAG
 491 GACGAGCACA ACACATACAC AGNAGCTCAT GATTGANATG TAGTGNNGAG GTTNTCTNTN GCTCATANCC
 561 GTNTTNGCCA TNGNACTNG GANCACCATT TTACTTGACG TGNNGGAGNG AACATGAAAT N

SEQ. ID NO:68

1 GTTANNCCNN TTTAATNCNA TGGAGCTCCA AAGCAGTGGT AACAAACGCAG AGTACGCCCC CGATGTACTT
 71 GTTCCCTACTC TTTGCTGGAT TTGAAAATT CCTCTGTCC GTGATGGCCT ATGACCGGTT TGTGGCCATC
 141 TGTCACCCCC TGCACTACAT GGTCATTATG AACCCTCACC TCTGTGGACT GCTGGTTCTA GCATCCTGGA
 211 CCATGAGTGC TCTGTATTCC TTGCTACAAA TCTTAATGGT AGTACGGCTG TCTTCTGCAC AGCCTTAGAA
 281 ATCCCCCACT TTTTCTGNGA ACTTAATCAG GTCATCCAAC TTGCTTGTTC TGATAGCTTT CTTAATCACA
 351 TGGTGATATA TTTTACAGTT GCGCTGCTGG GTGGAGGTCC CCTCACTGGG ATCCTTTACT CTACTCTAA
 421 GATAATTTCT TCCATACATG CAATCTCAT AGCTTAGGGG AAGNACAAGG CATTTTCCAC CTGTGCATCT
 491 CACCTTTCAG TTGCTCCTTA TTTTATGNG CAATCTAGGG GTGACCTTAG TTTTGTCTGNC ACCCGCAACT
 561 CACACTTAAG TGCAACAACC TCAGTGATGT AACTGGGGT CACCCCATGC C

SEQ. ID NO:69

1 GNGNNNCAG NTTANNCCCTT GGACTCCAG TAGAGCTACN ANGANTNCGC CNAGCGCGCA NTTNNNCCAG
 71 GGTNNNTN TN GTATACCAA TGAATAGAAA ACAGACACCA CCTTGTCCT GCCTAGCAAG TAGCTGGAGC
 141 TGGGTCGCAA GTACACGAAA AGGGCTGTCC CAAACGCAG AGTCACCACC ATCAGATGCG AGGCACACGT
 211 GTTGCAAGCT TTCCATCGGC CCTCTGCTGA AGGGATCTTC AGGACCGCAG ACACATATGTA ACCATAGGAG
 281 ATAAGGAGTT GGAGGAACGA TGTTCTCCG ACGGTGACCA CCACGAGGAA ATTCACCACT TGAAGGAGGA
 351 AGGTGTCAGA GCAAGACAGA GCCAGGACTG GTGGGAGGTT GCAGAAGAAG TGTTGGGTCC

421 GCAAAAGTGA AGCCTAAATA TGGAGCTGGC CTGGATCAGG GAGCTCAGGA AGCCACCAAC ATATGCCCCA
 491 ACCACCATGC GTGTACAGAG GCCCTGGGTC ATGATAGTGG GGTANAGAAG GGGGCTGGAG ATGGCTTGCA
 561 TATCGGTCGT ATGCCATAGC AGTCANGAGG AGGCACTCAA GACAGACCCA TGCCGACNAA GAAAT

SEQ. ID NO:70

1 GNNNNNTTTTA CCCCTGNNGC ACANAGCAGT GGTNACAACG CNCGAGTACG CCCCCTATGT ATTTTTTTCCT
 71 ATTCTGGACA CGCTACTCCT GACCGTGATG GCCTATGACC GGTTTGTTGGC TGTCTGCCAC CCTCTGCACT
 141 ATATGATCAT CATGAACCCC CACCTCTGTG GCCTCCTGGT TTTTGTCAAC TGGCTCATTG GTGTCATGAC
 211 ATCCCTCCTC CATATTTCTC TGATGATGCA TCTAATCTTC TGTAAAGATT TTGAAATTCC ACATTTTTTTC
 281 TCGCAACTGA CGTACATCCT CCAGCTGGCC TGCTCTGATA CCTTCCTGAA CAGCACGTTG ATATACTTTA
 351 TGACGGGTGT GCTGGGCGTT TTTCCCTCC TTGGGATCAT TTTCTCTTAT TCACGAATTG CTTTCATCCAT
 421 AAGGAAGATG TCCTCATCTG GGGGAAAACA AATAGCACTT TCCACCTGTG GGTCTCACCT CTCCGTCGTT
 491 TCTTTATTTT ATGGGACAGG CATTGGGGTC CACTTCACTT CTGCGGTGAC TCACCCTTCC CAGAAAATCT
 561 CCGTGGCCTC GGTGATGTCA CTGNGGTCA CCCCATGTTG ACCCTTTCAT TTACACCCTT AGCAAG

SEQ. ID NO:71

1 GNNNNNNNNN GTTNATNCCN NTTTAAATGC CANTNGAGNT AACAAACGCAN GAGTACNCCN NNGNGTACGC
 71 CCAGGGTTCA ACCNNTGAAT AGAAAACAGA CACCACCTTG TCCCTGCCTA GCAAGTAGCT GGAGCTGGGT
 141 CGCAAGTACA CGAAAAGGGC TGTCCAAAC AGCAGAGTCA CCACCATCAG ATGCGAGGCA CACGTGTTGC
 211 AGGCTTTCCA TCGCCCTCTG CTGAAGGGAT CTTCAGGACC GCAGACACTA TGTAAACATA GGAGATAAGG
 281 AGTTGGAGGA ACGATGTTCC TCCGACGGTG ACCACCACGA GGAATTCAC CACTTGACTG AGGAAGGTGT
 351 CAGAGCAAGA CAGAGCCAGG ACTGGTGGGG AGGTTGCAAG AAGAAGTGGT TGATGATTGT TGGGTCCCCG
 421 AAAAGTGAAA GCCTAAATAT NGAGCTGGCC TGGATCAGGG GAGCTCAGGA AGCCACAACA TATGCCCCAA
 491 CCACCATGCG TGTACAGAGG CCCTGGGTCA TGATAGTGGG GGTNGAGAAG GGGGCTGGA GATGGCTGCA
 561 TATCGGTCGT TGCCATAGCA AGTCAGGAGG AGGCACTTCA GACAGACCCA TGCCNCNAAG AAAAAAACT
 631 GNC

SEQ. ID NO:72

1 GNNNNNNNNN NTTNNNNCN TNACTCCNGC AGTGGTAACA ANNANTACGC NCAGCGCGCA GTTAACCCCT
 71 ACTAANGGTA ANNTNAGCTG GAACACATCA NTACGNTCAN GNNNGCNCNA TGACCGGTTT GTGGNCATNT
 141 GTCACCCCTT GCACTACATG GGTCAATTATG AACCTCACC TCTGTGGACT GCTGGTTCTA GCATCCTGGA
 211 CCATGAGTGC TCTGTATTCC TTGCTACAAA TCTTAATGGT AGTACGGCTG TCCTTCTGCA CAGCCTTAGA
 281 AATCCCCCAC TTTTCTGTG AACTTAATCA GGCATCCAAC TTGCTTGTTT TGATAGCTTT CTTAATCACA
 351 TGGTGATATA TTTTACAGGT TGCCTGCTG GGTGGAGGTC CCCTGACTGG GATCCTTTAC TCTTACTCTA
 421 AAGATAATTT CTTNCATACA TGCAATCTCA TCAGCTCAAG GGGAAAGTCAA GGCATTTTTC ACCTGTGCAT
 491 CTACCCCTCA GTTGCTNCTT ATTTTATGGN GCAATCCTAG GGGTGACCTT AGTTCTGGTG GCACCCGCAA
 561 CTACACTCAA TGCACAAGCT CAGTGATGTA CACTGTGGCA CCCATGCTGA ACCN

SEQ. ID NO:73

1 GTNNNNNCCN TTGATTNCCA TTGGAGCTCC AAAGCAGTGG TAACAACGCA GAGTACGCCC CCTATGTATT
 71 TTTTCTTATT CTGGACACGC TACTCCTGAC CGGGATGGCC TATGACCGGG TTGNGGCTGG CTGCCACCTT
 141 CTGNANTATA TGATCATCAT GAACCCCCAC CTNTGTGGCC TCCNGGTTTT TGNCACCTGG CTCATTGGTG
 211 TNATGACATN CCTCCTCCAT ATTTCTCTGA TGATGCATCT AATCTTCTGT AAAGANTTTG AAANTNCACA
 281 TTTTTTTNTG CGAACTGACG TACATNCTCC AGCTGGCCTG CTCTGATACC TTCCTGAACA GCACGTTGAT
 351 ATACTTTATG ACGGGTGTGC TGGGCGTTTT TCCTCCTTG GGATCATTTT CTTCTTATTC ACGAATTGNT
 421 TTNATCCATA AGGAAGAATG TCCTCATNTG GGGGAAAACA AATAAGCACT TTTNCACCTG TGGGNCCTAA
 491 CCTCTTCCGN CGTTTCTTTA TTTTATGGGG ACAGGCATTT GGGGTCCAC TTTACTTTTT GNGGNGACTC
 561 ACCCCTTCCA GAAANTTTT CGTGGGCNTC NGGATGTAC ACTGGNGGCA CCCCATGTT GAACCTTTT

FIGURE 2

SEQ. ID NO: 111

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gggccntcg ngatatnctt naccctctga tgctgctcga ggggccggca gggatgatga 60
tatctgcaga attcgccctt ctgttaacga ggaatatata aaggggttac tgaggaataa 120
ataaatgggt tactgaggaa taaataaatg gggtactgag gaacaaatac ataggggtga 180
aagaactgta aaatagaaaa aggacctntt gctgctcctc aggatggcgg nacttagggg 240
ccatgtacat gacgatgnng ctgccnntna agagtccac tntcancng cctcagcccg 300
ncttttntct cacnnncnt nttntctnc cctctnnnc tctttntctc ctattcccc 360
ccctccnct cctccctttt gcntnaccat tgnccctnat ccctttaatt cnntcnntcn 420
tctccctct attccttcnn tnttgcnctt cantctctnc ctctttctcc ccnctttct 480
ctctctnct ctctctctng tcatcctngt tcnttctctt ncctanttcc ctctancctt 540
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nnctcttcn ctccgtctnc cnccttctct tcntnacgcc acccctcnnt cntnctctct 660
ntctctctc cactctctcc tctccctnnc cntcactntt ctccnctct acntcctatn 720
ctcncttct nncttnactt tgtaacgctc tctctctct ctctacgcac nttttatctc 780
ttatctcnnc catcnccctc nntctncaac nctattnact cttttctcnc atactntatn 840
ctcctntcnn cttanctnc ctcccttctn tnancnntc actgcn 886

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SEQ ID NO: 112

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gctgctcgag cgcgcgagcg tcggcagtg nagggnnatn tgccnnnntn gcnnttagat 60
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gtgagttgag ggtggcagca gaactaaggt acacccttag gattgcacca taaaataagg 180
agacaactga gaggtgagat gcacaggtgg aaaatgcctt gtacttcccc tgagctgatg 240
agattgcatg tatggaagaa attatcttag agtaagagta aaggatccca gtcaggggac 300
ctccaccag cagcgcaact gtaaaatata tcaccatgtg attaagaaag ctatcagaac 360
aagcaagtgt gatgacctga ttaagttcac agaaaaagt ggggatttct aaggctgtgc 420
agaaggacag ccgtactacc attagattt gtagcaagga atacagagca ctnatggtcc 480
aggatgccag aaccagcagt cacagagggg nggggtttca tantgncct gtagngtcag 540
cnnngacna gatggccnca aaccgntctt nggccctcac gnccttgga ggnngttttc 600
tantccacca cnnntnttct nannc 625

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SEQ ID NO: 113

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catgcnngag caggctcgag cgccggcagn gtgagggata tctgcagaat tcgcccttcc 60
tatgtacttt ttctgagcg tatacacaat cccatcatgt actggggaga agncagacca 120
tatcattnac aagctgnctt tngcagatgn actttgnttt ctcattaggc tgncagagt 180
acttctctc ggcagccatg gcttatgacc gctgtcttgc catctgctat cctttacact 240
acggagccat catgagtagc ctgctctcag cgcagctggc cctgggctcc tgggtgngtg 300
gtttcgcgcn cantgcagcg cccacagccc tcagnagcgg tcttgctctt ctgngncccc 360
cgtgccatta accactnctt tngcngcant gnccttgca ttgtcttgc ctgccacca 420
nacagcagna nancntgngn cnnttngatc gctgntncgc tctcngntct cactccttc 480
caccttncc ntgcattcc nntntcenn tcgncctct gncnntcnn tctctcttc 540
tnaacgcgtc ctccgannng nctnnatgt cgtctctntn ntgngcnng ncagcnnnnn 600
nnccannnn tngtgccgc gctcc 625

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SEQ ID NO: 114

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catagaagag accaaagaac ttgcccctcc cttgggcata cggatttttg ggctggaggt 180
agacagcnat gactgagctg tagaagaggg tgaccacagt gagatgggag gagcaggtcc 240
caaaggcctt tctccatgct gtggcagagt taactctcag cactgcctgg gcagtggctc 300
cataagagcg aaggatgagg ctgagaggca caaccacgaa gatgacactg gacacagcca 360
actggatttc attgnaggag gcatctccac aggagagtn gnatcagaga tgggancctc 420
acataaaaaa gtcactatc tgntgggtgg gacagaatgn ccatgtggag gntnnatgtn 480

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cgtntennac ctcttatttt tnttnccctt ttctttcgct cnntcccent tntccennct 540
cgccanttec atnncntct ntcnnttttt ttntntnacc ntntntcat ntctctctt 600
tattctcttt ctcttgntct tccctctctt ctctntttcc canctctccc g 651

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SEQ ID NO: 115

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ttcctccttg tggccatggc ctatgaccgc tatgtggcca tctgcttccc cctgcaactac 180
accgccatca tgagcccat gctctgtctc gccctgggtg cgctgacctg ggtgctgacc 240
accttccatg ccatgttaca cactttactc atggccagnt tgtgcttntg tncnnacna 300
ttgttgntnc cccactnnnc tntgtntna gtctnctctn cctnnactg ctctcctct 360
tntccnnga gtcctcnggn nncgtngtcg nttncngcnn tcaattgcan tncnnctc 420
atcctttctt tantntcca tntnttactc nattntctt tatcncnnt ntncctctc 480
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ttctctcnct tntctctcnc tnnnncccn nntctctctg ntctctgctc cntcttnacg 600
tctnnnctt tatttantnt ctncnctn tctcnnctc cancgngta ccngccctat 660
nnctctctc gannntgntc atggcatctn cacattngc cctactatnn ncgatctatn 720
ttcncgcat ntattncaca tccactgca ctctactcn ctctctancc nccgtacatc 780
gcnctacng ntgcnntcn nccgtctctn cgccnctat nntccactt tntctnggtc 840
ccccctctcg 850

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SEQ ID NO: 116

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gatgcatgct cgagcgcccg cagtgtgatg gatattctgca gaattcgccc ttccaatgta 60
cttttctctg aagaacctct ctgttttgga tctgtgctac atctcagta ctgtgcctaa 120
atccatccgt aactccctga ctgcagaag ctccatctct tatcttggt gtgtggctca 180
agcctatctt ttctctgctt ttgatctgct tgagctggcc ttcttactg tcatgtctta 240
tgaccgctat gttgccattt gccacccct ccaatacaga gccgtgatga catcaggagg 300
gtgctatcag atggcagta ccacctggct aagctgctt tctacgcag ccgtccacac 360
tggaacatg tttcgggagc acgtttgcag atccaatgtg atccaccagt tcttcctga 420
catccctcag gtgttgccc tggtttctg ngaggtttc tttgtagagc tttgaccng 480
ccctgagcct caatgcttg ntctgggatg ctttattccc atgatgatct ccnattttcc 540
anatctctn aanggggctc nagaatccct ttaggaccag antcnagta aaagccttn 600
cccnctgct tcccccaag 620

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SEQ ID NO: 117

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ttccaatgta tttgttctg ttatttgag aactggagag ctctcctct gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc cctgcacta caccgccatc atgagccca 180
tgctctgtct cgccctggg gcgctgtcct ggggtgtgac cacttccac gccatgttac 240
acactttact catggccagg ttgtgtttt gtgcagacaa tgtgatcccc cacttttct 300
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tatttatcat gggagggtc attcttgcat ccatctcta ctatccttg ggtcctatgc 420
aagaattgct tctccatcc tcaaggtccc ttcttctaag ggtatctgca aggccttctc 480
tacttggtgc tcccacctg tctgnggtgt cactggttct atggaaccgt tattggtctc 540
tacttatgct cntcagctaa tagttctact cttaaaggaca ctgcatggct atgatgtaca 600
ctgtggtgac ccccatgctg aacctct 628

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SEQ ID NO: 118

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gcaactggca tctactggg gagaagacag accatatcat ttacaagctg cttttgag 180
atgnacnntg tttctcant angcctaca gngnncatgt ttncgcnngc cntgacttat 240
gacgcgcntn cnnnntatc nnnntntct ntnacnctac ttctcatna tntgncntn 300

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nnttcnccn tggcnnetcn nntcneggnc ttncctntgn negtcntenc ccttnggcct 360
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tccctccctt ctctgnntgc nntcnncnnn catctnnntg ntctgatenc tntcttntnt 480
ccatcnngtn ctnttctctc gtntcttctn cncgcncctt gcatcaetgn gcattatatn 540
cncngtctca tnnctatctt cegtntctgt cnetttctct ctatgcnega cgtcntntntn 600
tactatgctc ntctcnnat tnnngcctgt tcnngnenc ccgnntctcc anntactctc 660
cangntctnc ctnttcctnt ncnctgtcta attcnntctt accgntctn gnctctctct 720
cgctnntccc nnttctctcc nctcncgnnn cnttcagct ntcnanttct antnngnnn 780
cnc

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SEQ ID NO: 119

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gccaagtta ctgtttagtt ttgtgtctgc gaacaacagc atctctttca cactctgtat 180
gatacaactg tactttctca ttgtctncat gngcacagaa tgcgtgcttc tggccgccat 240
ggcctatgac cgntatgtgg ncatctggcg cccactccac taccacaacca taantgagcc 300
atgggctcct gctcnnctt cgtntnnna tanngaaccn acagntagc gncanctccc 360
tgtngagaa tctacttcat cntnctgcct tannttntgt gggcccaatg tgcntaanca 420
cttngntctg nggacatttn ctccagnant tnaantctct tnetgnaca aganactgtt 480
cnttancttg annatnttn ggnacattnt tcttanggnn ttggnacgag cntntctanc 540
accngcactn cncantaant gctncngtgc tantcngtgc cattctgtg nctnccctt 600
tcatingctn nctcccncg aaagcnaant aagtngngt cttnactttc gccccccacn 660
ncatncant ggcc

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SEQ ID NO: 120

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ggccctctag atgcatgctc gagcggccgc cagtgtgatg gatatctgca gaattcgccc 60
ttcctatgta ttttttcctg ttatttggag acctggagag cctcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgtcttc cctgcaacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggt gcgctgtcct ggggtgctgac cacttccat gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgct tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtng 360
atatttatca tngagggct cattctgtc atccattcc tactcatcct tgggtcctat 420
gcgagaattg tctcctcctt cctcaaaggc ccctctctct aangggatc tgcaaggcct 480
tctctacttg gtggctcccc ccctgntgt ggtgtcactg ttcctattgg aaaccgntat 540
tgggactcta cttatgctca tcangetaat agttttactc ttangggaca ctgncaatgg 600
cctntgaagn taccctgggn gtggaccccc atnntngaac ccc

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SEQ ID NO: 121

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ggccctctag atgcatgctc gagcggccgc cagtgtgatg gatatctgca gaattcgccc 60
ttccaatgta ctttttcctg ttatttggag acctggagag cttcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgtcttc cctgcaacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggt gcgctgtcct ggggtgctgac cacttccat gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgct tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggctc attcttgcct cccattccta ctcatcctg ggtcctatgc 420
aagaattgnc tcttccatc tcaaggncct ttnttctaaa gggtagctgc aaggccttct 480
ctanttggtg ctcaccctt gtcttggtgn tggcactgnt tctaattgga accggaatt 540
gnancnctna cnttatgctc natcaactta aatagtttct nactttnaaa gggaccactn 600
ntcattggct tanggatngn ncnttggtt cntggaaatc ccnatcattc ttacnng 657

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SEQ ID NO: 122

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ataattccca	atatgctaga	tcatattagc	tcaggaatta	agctgatttc	ttatggggag	180
tgtctgacac	aactctatct	ctctggccta	tttgacagatc	tggacaacaa	ctttctcctg	240
gctgtgttgg	cccttgaccg	ctatgtggcc	atcagccatc	ctctccatta	tgccctaacc	300
atgaactccc	aacgctgtgt	cctgttgggt	gctgtgtcat	gggtgatcac	tattttacat	360
gccctagtgc	ataccctcct	agtgaccagg	ctttccttct	gtggtccaaa	tattatccct	420
cacttcttct	gtgatctggc	cccactcctg	aagctggcct	gctccagtac	ttgtgtcaat	480
gatctgggtg	tcaccttgtg	ggcaggaaca	ctgctgaatg	cgccctttgc	tgcattctta	540
tgncctactt	ttacattgca	ttggccatcc	tgagaattga	ttcccnagg	ggtatgcaaa	600
gggccttnt	ccagctcnc	nn				622

SEQ ID NO: 123

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gcttccccct	gcactacacc	gccatcatga	gccccatgct	ctgtctcgcc	ctgggtggcg	180
tgtcctgggt	gctgaccacc	ttccatgcca	tgttacacac	tttactcatg	gccaggttgt	240
gtttttgtg	agacaatgtg	atccccact	ttttctgtga	tatgtctgct	ctgctgaagc	300
tggccttctc	tgacactcga	gttaatgaat	gggtgatatt	tatcatggga	gggtcattc	360
ttgtcatccc	attcctactc	atccttgggt	cctatgcaag	aattgtctcc	tccatcctca	420
aggctccctc	ttctaagggt	atctngcaag	gccttctcta	cttgccgctc	cacctgcctg	480
tgggtgtcact	gttctatgga	accgttattg	gtctctactt	atgtcatca	gccaaatagt	540
tttactctaa	aaggacactt	gtcatggnnt	atgatgtacn	ctgtgngnac	ccccatgctn	600
aaccctntn						610

SEQ ID NO: 124

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cgcccttctt	tattcctgag	tgaatatatg	agggggttg	cactgctgtt	aagagtggac	120
aggaaaatgg	aaactagacg	aacgtgacaa	atccacgtgg	atccagaaaa	ataggaatca	180
ctgaatgcca	aagggcaggt	cacagaggag	gaagaccagc	actctgagca	ggatgggtcat	240
gtacagcctg	gtcaagggca	tcttccggga	tccacaaagg	atcctgacca	gcagaaccgg	300
gctggaccgg	cagagaacca	cacataaaaa	aatcagccat	gtgactgtga	tgaatctga	360
tgtttcacac	caaacagaat	caagcaccac	tagacaggaa	gccacagAAC	atccattcca	420
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gnttgcttnt	cgnnncccta	nctatgcctt	ngctcctgtn	nangettgc	nattgncct	600
cncccacgng	gcttaannnt	ctcnnngncc	atttanancg	tnatnntact	tccctgtcg	660

SEQ ID NO: 125

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tctctatgta	cttcttcctg	ttattttggag	acctggagag	cttcctcctt	gtggccatgg	120
ccatgaccg	ctatgtggcc	atctgcttcc	ccctgacta	caccgccatc	atgagcccca	180
tgtctgtct	cgccctgggt	gcgctgtcct	gggtgctgac	caccttccat	gccatgttac	240
acactttact	catggccagg	ttgtgttttt	gtgcagacaa	tgtgatcccc	cactttttct	300
gtgatatgtc	tgctctgctg	aagctggcct	tctctgacac	tcgagttaat	gaatgggtga	360
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tacttaatgc	tcataaagct	aatagttcta	ctctaaagga	cactgncatg	gctatgatgt	600
acactgtggt	gaccccnat	gctgacccat	tc			632

SEQ ID NO: 126

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tgtacttggt	cctggcagcc	atggcttatg	accgctgtct	tgccatctgc	tatcctttac	120
actacggagc	catcatgagt	agcctgctct	cagcgagct	ggccctgggc	tcctgggtgt	180
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tgnnntttta	ncaaaagctt	ggncnncgnc	ctgaaanact	gnngtngact	tcangnttta	600
aaactccttt	natntcactn	ttanggggaa	cnagggcggn	ac		642

SEQ ID NO: 127

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gcccttccca	tgtatttatt	ccttagcctg	ttggattccc	agctgcacag	ctggattgtg	120
ttacacaact	caccttcttc	aagaatgtgg	aaancataaa	ttttttttct	gtgacccatc	180
tcaacttctc	aaccttgcc	gttctgacag	catcatcaat	aacatattat	gtattttaga	240
tatccctata	tttggttttc	ttcccatnnc	agggatcctt	ttgncttacc	atanaattgt	300
cctccctcat	tccaagaatt	ccattgncag	acgggacgna	tnangccttc	tctacctgt	360
cntctnacc	gnnagtcgnt	tncttatctn	tnantnccc	tnngggcgnc	ncctgncct	420
cagcttngt	cancnttctc	cncacnnntt	cgctcgtgtt	ncctcgtct	gtctctctnc	480
tctctnctnc	ttctgctc	ccctccanng	tctncttttc	tcagcncct	tnngncnct	540
gccagcncn	nangntccnc	ccctctccct	cntgtctnct	cnctcctntt	cttctntctc	600
tnnctcatnn	nnncgcnctc	ncgtctccn	ccctntctn	tacgactccn	gncgtctctn	660
cgctacgac	ctccctgtnc	ncnccgg				688

SEQ ID NO: 128

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atatgctcac	tgacttcttc	tgaggacaga	agaccatata	atttggtggc	tgtgctgctc	180
agtttttttt	ctttgtcggc	atgggtctgt	ctgagtgcct	cctcctgact	gctatggcat	240
acgacggata	tgcagccatc	tccagccccc	ttctctaccc	cactatcatg	acccagggcc	300
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ccagnnccat	atttaggctt	cacttttgcg	gacccaacat	catcaaccac	ttcttctgct	420
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tnctccgtgg	tgntcaantg	tcgngaggaa	acatcgnttt	cctccaaccc	cttantctcc	540
cangggntac	catagngtct	gcgngtccct	gaagaatcct	tttngccaan	cgggccaatn	600
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SEQ ID NO: 129

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ntaggtcna	ccnntcgngc	tcccgttcca	ncanchnaac	ccnttcgttc	ctgnanactt	420
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cncctganct	gcnnttctt	ccangcngc	ncgcnance	cgntctntct	gnngaancct	540
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nncttnenct ctnaacctnt cnnatectca cctnngatat cctcncgntc tttegnentc 660
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SEQ ID NO: 130

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ccctaagatg ctgatgaaca tgcagactca gcacctagcc gtcttttaca agggatgcat 180
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gagccagtgt gtcattgtgg tggctgggtc ctgggtcatc gcttgtgcgt gtgctctttt 360
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SEQ ID NO: 131

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tcgggttgcg gaaggaataa atacatcggt ttgcggaagg aataaataca tcgggttgcg 180
gaaggaataa atcatcggt tgcggaagga ataaatacat cgggttgcg aaggaataa 240
tacatcggt tgctgaagga ataaatcatt ggttgcgta aggaataaat cattgggttg 300
cgtaaggaat aaatcatttg gttgcgtaag gaataaatca ttgngttgcg taaggaataa 360
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gaccnagctt gncttccttg cgtnaanttt cnttattcct cctntntntc ttctccccc 600
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SEQ ID NO: 132

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tcacacctaa gctcttggtc aacttctctg tctctgacaa gtccatctct tttgagggtc 180
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actactgtga cataccaccc cttctccacc tggcttgtgc caacacagcc acagcaagag 480
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ggactcccca cttntgcctc ccnn 624

SEQ ID NO: 133

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cagaagaggg tgaccacagt gagatgggag gagcagggtc naaaggcctt tctccatgct 180
gtggnagagn taattctcag cactgcctgg gcagtcggt ncataagagg caaggatgag 240
gctgagaggc acaaccacga agatgacact ggacacangc caactgtatc cattgttaga 300
ggnatctcca caggagagtn gaatcagaga tgggacnttc acattaanaa gttatttatn 360
tgctggcggg nacagatgcc caagcggnan ggngntatgg tntcggncna ttnttcgtc 420
canaccatt atctcangcc acatgtatnt cagcntttta ntncnntnt nagtntagtc 480
tngntgntnt ncnntattn cennctcttn tccntcann tatcattntc attccttncn 540
ncncanant atggnncc cgnacnct cngtnactcc cctnnngncg 590

SEQ ID NO: 134

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tgatctctct tgcttttccc cacacactgc aacctctgcc tccacattca agtgattctc 180
ctgcctcagc ctcttgagta gctggaatta cagatgtgag ccaccatgcc tggcctgtcc 240
agatgttttt gaaacaaccc ccaccagcac tggagggagt caagggaaga caagccaggc 300
atctgagctc ctctgtctct gcctttcctt ctactgtcc ccagggtaac ccgtcaccac 360
ccccatcacg aaccccttca tctacacatt acgtaacaag ggcgaattcc agcacactgg 420
cgcccggttac tagtgatcc gagctcggtta ccaagcttga tgcatagctt gagtattcta 480
acgntcacc taatatagctt ggcgtnatca tngncccnag cttgntttct gtgtgaaatt 540
tgntatccgc tcacaaattc cacacaacat acgagccnga agcaataagn nntaaagcct 600
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SEQ ID NO: 135

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cagcagtgcc caaagcacgc gccatcctac tggggagaag tcagaccata tcatttacia 180
gctgtctttt gcagatgtac tttgttttct cattaggctg cacagagtac ttctccttgg 240
cagccatggc ttatgaccgc tgtcttgcca tctgctatcc ttacactac ggagccatca 300
tgatgagctc gctctcagcg cagctggccc tgggctcctg ggtggtgtgg ttctgtggcc 360
attgcagtgc ccacagccct catcagtggc ctgtccttct gtggttcccg tgccatcaaa 420
cacttcttct gtgacattgc accctggant gccctggcct gcaccaacac cacaggcagn 480
aagagcttgt ggcctttgng aatcgctgn tggggctanc cttnngtcat gccctnatca 540
ccntttntcn nctatgnngt acantcatta agcnccaatc nctcatggga tccccctttg 600
cnagtggccc ggcngncaaa ngnectnctc cccgtncen 639

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SEQ ID NO: 136

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tccatcccca aaatgctggc caacattcat acccagagtc agatcatctc gtattctggg 180
tgtctngcac agctatattt cctccttatg tttgngggcc ntgacaactg cctgctggct 240
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agtcccccagc tctgtgcact antgctgcnc gtgtgctgng tgcnanccan ttgtctgcct 360
gctgcacatn ctgttncnc cccnccngng nctctttnnn ccgnaccnc cctacaantc 420
cntatcannt tengetnccc tttcttctcc cccnnttct tncnccttc ctcnnccta 480
ctttcttctc tenccntnct canatnatca gtccnacctc nccttctttt ctctactnan 540
tnctctcnct cccnctcacc ngntngtcta gtctgcccgc gcccctcgc tatcnctncc 600
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SEQ ID NO: 137

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gcccaaagca ctggccatcc cactggggag aagtcagacc atatcattta caagctgtct 180
tttgcatagc tactttgttt tctcattagg ctgcacagag tacttctctc tggcagccat 240
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cctgctctca gcgcagctgg ccctgggctc ctggncgtgn ggcttngtgn cnttgcnngn 360
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nacacttgta cctcncgntc tgccctnnnc tgccttctaa tccctnngtt gtantnctn 480
gccttntctc cccttcgctn gttnatcttn anntnctgc ntctntgnc ctctccttcg 540
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ntgtcncccg antangntac ntntcacnnt ntntcnctn ctctcctaac tcttncgg 658

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SEQ ID NO: 138

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cagtgcctaa agcactggcc atcctactgg ggagaagtca gaccatatca tttaacaagt 180
gtcttttgca gatgtacttt gttttctcat taggctgcac agagtacttc ctcctggcag 240
ccatggctta tgaccgctgt cttgccatct gctatccttt aactacgga gccatcatga 300
gtagcctgct ctcagcgcag ctggccctgg gctcctgggt gngtggnntc gtggccantg 360
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nngnttncnn gnetcggcnc cccctttgac ntantncntt gntgngcgct tatncntgcg 540
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nnngtcnncc

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SEQ ID NO: 139

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aagcactggc catcctactg gggagaagtca agaccatatc atttacaagc tgccttttgc 180
agatgtactt tgttttctca ttaggctgca cagagtactt cctcttgga gccatggctt 240
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ctnagcgcag ctgncctggg ctccctgggtg ngtggttcng ngccattcag cgcacacagn 360
cttcatcagt ggncttgtn tctgngccc cgcncatcn aaccantttc tctgngana 420
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ntggcncncc tgnctcgnt ngtnnccng ntancngnc tnnacgtcct tcnncact 540
ttntctctat gttntcaacn tcnngncta ttcgctcang atanccactc ttnccantnt 600
cggannnta nnttttcnn accntctttc cntnc

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SEQ ID NO: 140

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cagcagtgcc caaagcactg ggccatccta ctggggagaa gtcagaccat atcatttaca 180
agctgtcttt tgcagatgta ctttgttttc tcattaggtc gcacagagta cttcctcctg 240
gcagccatgg cttatgaccg ctgtcttgcc atctgctatc ctttacacta cggagccatc 300
atgagttagc tgcctcagc gcaagctggc ctgggctcct ggggtgtgtg tttcggnggc 360
cattgcagng cccacagcnc tnatcagtgg gctgtccttt ctgtgggccc ccnggccat 420
tcaaccaacn tttcttttg nggatattgg caaccctng gnatttgncc cctnggccct 480
ngcacncaa ccancaccag ggtcngnna caantttgn cgggcccctt tntgaaatt 540
ggcctnggtg ngggnntaat tcnctttggn tttnaatgcc cttccaatna accttttgn 600
cnttctatg gngnncct tnnattcnag caccacanc ttangggaac ccncctttt 660
gtcaagtng nccgtnann naaaagcct ntccnnntg cccccccg 709

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SEQ ID NO: 141

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ccttccatg tatttttttc taagcaacct ctccctcctg gagatttggg ataccacagc 120
agcagtgcct aaagcactgg ccactctact ggggagaagt cagaccatat catttacaag 180
ctgtcttttg cagatgtact ttgttttctc attaggctgc acagagtact tcctcctggc 240
agccatggct tatgatcgt gtcttgccat ctgctatcct ttacactacg gagccatcat 300
gagtgcctg ctctcagcgc agctggccct gggctcctgg gtctgtggtt tcgtggccat 360
tgaagtgncc acanngcctc atcagntggc cntgtccttc tgcnncccc cgtnncattn 420
nncacttctt tcgtgacatt gccannctnn tnttgccctn gtccttnnc natcatccat 480

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ggcngttngn gctgttgcc ctttcgctca cncngtctgc gccattctc nctgtnncaa 540
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cctcgatctc ctttcangnc tccgctncac tgctenctna acgtccnttt ctccctnnt 660
nntcnntnnc g 671

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SEQ ID NO: 142

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gatcatctcg tattctgggt gtcttgacata gctatatctc ctcttatgt tngnggcct 240
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gncnatttc ntttcccn 739

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SEQ ID NO: 143

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caccacagac aggtgggagc cacaagtaga gaaggccttg cagataccct tagaagaagg 240
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ggacagcgcc accagngcga gacagagcat ggggtcatg atggcgngt agtgcnnggn 540
gangcagatg nccacantag tgnatnagn ccatggtcac angggaggn gctttcaggn 600
ctttnaataa c 611

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SEQ ID NO: 144

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cccctccctt gggcatacgg attttgggc tggaggtaga cagcaatgac tgagctgtag 180
aagagggtga ccacagtga atgggaggag caggteccaa aggcctttct ccatgctgtg 240
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agaggcacia ccacngaaga tgacactgta cacagccaac tgtattttat tgnaggnggn 360
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tacntccct cntccctnt nttttcttct cncctnctc ttcntttnc cntntccnt 540
gtncnctnt atctcccta ntntcttnt tntnctntt tngnnccct cctctntctt 600
tncntccctc tcnantat cncctgncc cncnntnc c 641

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SEQ ID NO: 145

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gagatttggt ataccacagc agcagtggcc aaagcactgg ccactctact ggggagaagt 180
cagaccatat catttacaag ctgtcttttg cagatgtact ttgtttctc attaggctgc 240
acagagtact tcctcctggc agccatggct tatgaccgct gtcttgccat cctgctatcc 300
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ccctttgntc tctacnctct tncgnantca ctnnnatntc tntcaacng cteectcnnn 600
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nntnctcac cnnntacatg gttccttntn ntccatctcg tcnntctctc cnnataacgn 780
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SEQ ID NO: 146

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caatctgccg accactccgc tatgagaccc tgatgaatgg ccatgtctgt tcccaactag 180
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tnccanngnn tnntngctca ntccctntnc tentencaat cntnnngcn ctentgntnn 600
gtanactgcc nttaattnga ccnctttccc naenncac 639

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SEQ ID NO: 147

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tacctggcaa tctgccgacc actccgctat gagaccctga tgaatggcca tgtctgttcc 180
caactagtgc tggcctcctg gctagctgga ttcctctggg tcctttgccc cactgtcctc 240
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cccttgctca ggctttcttg tggggacacc cacctgctga aactggnggc tttcatgctc 360
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gtcactgtct caggncctc nnagntgctg ngcgaaggaa agegcntttc acttgcgcct 480
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tcccagctat antccaaagt nctnaaaaca ngancctcgg nangannct nntattctac 600
ccttctctgt aacctncc 618

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SEQ ID NO: 148

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SEQ ID NO: 149

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cagagtgggc ccaccaggat gaacatgcag gctgcaaaga tgaccacctg gttgagccag 360
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SEQ ID NO: 150

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SEQ ID NO: 151

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SEQ ID NO: 152

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gaccttctgt ctgaaagana gaccatctcc ttcaatcatt gctccactca gatgtttcta 180
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<211> 613
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 3, 8, 11, 17, 28-29, 34, 40, 48, 67, 71, 613
<223> N can be any nucleotide

<400> 1
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 aaatganccg nttaaggaga ggagtgaaga cagtaaaaaa acacagagat aaatttatca 120
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 catatagcaa tgtatctatc ataggccatg gcaacaagaa gcaccatctc actaccccca 600
 aaaacatgca agn 613

<210> 2
<211> 578
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 3, 4, 6, 8
<223> N can be any nucleotide

<400> 2
 ggnntntnac acggactcca agcagtggta acaacgcaga gtacgcccgt tcctgagtga 60
 gtagatgaag gggttcagca tgggattgat gacagtgttg aaaattccaa cagctttatc 120
 cttgtctgaa agcttggttg aaccagtcg catatagtta aagatacctg aaccatagaa 180
 tatggcaacc acagtgaggt gggagccaca tgtggagaag gctttcttcc tgccctctac 240
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 tgagggggccc ggcagatggg caggaatcgg tcataggg 578

<210> 3
 <211> 588
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 4, 5, 13, 16, 27, 576, 578, 588
 <223> N can be any nucleotide

<400> 3
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 cgaagcgtgt agattagggg gttcagtagg ggagtatga cagtgtagggt caccgagatc 120
 agctgggtcat gttctctggt gttctctgac ttgggcttga ggtaggcaat ggaggcacag 180
 ctgtagtggg caatgaccac agtgaggtgg gatgcacagg tggcaaaagc cttcttccgg 240
 ccctcaactg aagtaatctt gaggattgta gagataatga gaacataaga aatgaaaacc 300
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 gtggtgtcaa tgcaggagag cttcatcaca gggcggatgt cacagaagaa gtggggcacc 420
 ttttctagca cagaagggta acctgaatac agatgtcact tgcgttattg ctacaatcag 480
 cccaatgctg caaggccccc aggacaagtt ggatacgcag cctcttggtc ataataacca 540
 tgtatctcaa gggggttgca agatggccac atagcngntc atattccn 588

<210> 4
 <211> 583
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 3, 7, 13, 437, 485, 488, 506, 521, 524, 545, 558
 <223> N can be any nucleotide

<400> 4
 gtngttntta acnccattgg agctccaaag cagtggtaac aacgcagagt acgcccccaa 60
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 caaaatctat tgttagttcc ttgactcatg atacttccat ttctttcttt gggtgtgctc 180
 tgcaagcctt ctttttcatg gacttggtgaa ctacggaggt agccatcctt acagtgtatg 240
 cctgtgaccg ctatatggcc atctgccggc ctttacatta tgagggtcatc ataaaccaag 300
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 gtaattttcc acaactncta agcctcttag accccaaagt aattaccatt gagattggag 480
 tcatnggntt ttgggtacaag tcttgngata atcctctttg ntgnaattac tctctcctac 540
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<210> 5
 <211> 584
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2, 5, 8-9, 11, 14, 17, 550, 557-559, 561, 576, 582
 <223> N can be any nucleotide

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 gccctcaggt gaattatttg atttagggccg gaagtaggtg aggccttaatg atatatagaa 180
 aagagagaca acaaggaggt gtgaggaaca thtagaaaag gctttattct tccctttagc 240
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ggggatcatg accaccagaa tggttccgac gatggcgtag atctcaaaca gtgctgtgtc	360
tgcacagacc agcctcagca caggtggggt gtcacagaag aagtgggttca ccttggttgg	420
gccacagaat ggaaaactga agagccatgt ggtctgcaca gtagctacag gaaagcctgg	480
gaaccaggag gcagcagcca gtttggcacg agtcctttgg ttcattgatga ctgggtagtg	540
caagggactn gcagatnnnc ncattcgggc atatgncatg gnag	584

<210> 6

<211> 572

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2

<223> N can be any nucleotide

<400> 6

cnttggagct ccaaagcagt ggtaacaacg cagagtacgc ccgctccgca gagaatagat	60
gaaaggggtc agggtcgggg gcacgactgt gtagaacgca gacaggaaaa catccagaac	120
ggggggagaa tttgaaattg gcttcacata ggcaatgctg ccagatatca taaagagtgt	180
tacaaccaca agatgtggaa tgcaggtaga aaatgttttt gatctaccct ccttagaagg	240
aatcctcatg atgacagaaa aaatgtacat gtaggagaga gtaattacaa caaaggagat	300
tatcacaa ga cttgtaccaa aaaccatgac tccaatctca atggtaatta ctttggggtc	360
taagaggctt agtagtttgt ggaatattac agaaaaattg acgtattcta ttgcgccac	420
agaatggtaa tgagaatgtt gctatcacat gcatgaatcc acagatcacc ccactgagcc	480
acgacatggc catcatcctc agacagacac cttggtttat gatgacctca taatgtaaag	540
gccggcagga tggccatata gcggtcatag ga	572

<210> 7

<211> 549

<212> DNA

<213> Homo Sapien

<400> 7

gcagtggtaa caacgcagag taccgcccc tatgtacttt ttcttgggaa acttgtctgt	60
gtttgacatg ggtttctcct cagtgaactg tcccaaatg ctgctctacc ttatggggct	120
gggcccgaactc atctcctaca aagactgtgt ctgccagctt ttcttcttcc atttcctcgg	180
gagcattgag tgcttcttgt ttacggtgat ggcctatgac cgcttactg ccactctgta	240
tcctctgcga tacacagtca tcatgaaccc aaggatctgt gtggccctgg ctgtgggcac	300
atggctgtta ggggtgcatc attccagtat cttgacctcc ctcaccttca ccttgccaca	360
ctgtggtccc aatgaagtgg atcacttctt ctgtgacatt ccagcactgt tgcccttggc	420
ctgtgctgac acatccttag cccagagggt gagcttcacc aacgttggcc tcatatctct	480
ggctgcttct tgctaaatct tttatcctac actagaatca caaatatcta tcttaagcat	540
tcgtacaac	549

<210> 8

<211> 548

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 537, 542

<223> N can be any nucleotide

<400> 8

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tttgtgttac ttccaccacc attccaaaaa tgcgtatgaa catccagaca cagaacaaag	120
tcatcaccta catagcctgc ctcatgcaga tgtatttttt catactcttt gctggatttg	180
aaaacttctt cctgtccgtg atggcctatg accggtttgt ggccatctgt cacccttgc	240
actacatggt cattatgaac cctcacctct gtggactgct ggttctggca tcctggacca	300

tgagtgtctt	gtattccttg	ctacaaatct	taatggtagt	acgactgtcc	ttctgcacag	360
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atagctttct	taatcacatg	gtgatataat	ttacagtttg	cgctgtggg	tgaggtccc	480
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gntcaggg						548

<210> 9
 <211> 583
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 8, 13, 14, 16, 25, 232, 271, 305, 438, 488, 497, 500, 505, 512, 524, 544, 558, 578
 <223> N can be any nucleotide

<400> 9	
gggttttnac	ccnntnggag
aggctataaa	tgaaggggtt
ttgggttgat	cccttgagat
taaaataaga	aaactacaat
ttggaagatt	tgatcttaaa
catantggga	cagctaacat
ttttcaccac	aggcaatctt
ttgagaccac	acagtggnaa
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ggtntagtga	agaggttntc
	agaatggcca
	cataccgntc
	aaa
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	120
	180
	240
	300
	360
	420
	480
	540
	583

<210> 10
 <211> 569
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 7, 28, 174, 232, 237, 314, 341, 445, 447, 449, 470, 494, 497, 503, 510, 515, 527, 553, 554, 569
 <223> N can be any nucleotide

<400> 10	
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agagcccttc	cgagagaga
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tcgtggtaat	tctnagnccc
ccaccatcct	agnnaaagtc
	ctccttctn
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	120
	180
	240
	300
	360
	420
	480
	540
	569

<210> 11
 <211> 582
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 3-4, 12, 14, 504, 513, 522
 <223> N can be any nucleotide

<400> 11
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 gtacttggttc ttgagaaact tgtcttttctt agatttttgt tacatctctg tcacaattcc 120
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<210> 12
 <211> 579
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 3, 384, 528, 572, 578
 <223> N can be any nucleotide

<400> 12
 ggnnttgacc acggagctcc aagcagtggt aacaacgcag agtacgcctt cttgtcctcg 60
 tgccgataca tgatggggtt caacatggga gtcataacag tgtaggacaa tgatagcagc 120
 ttcttgccct cagggtgaatt atttgattta ggccggaagt aggtgaggct taatgatata 180
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<210> 13
 <211> 577
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-4, 7-10
 <223> N can be any nucleotide

<400> 13
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 gctgctgtgg aacctaaaag gacctgacaa aacaatcaca ttcctgggtt gtgtcatcca 180
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 tgatcgctat gctgcagttt gcaaacctct ccactatacc gccgtaatga accctcagct 300
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 tagccaagggt ggcataagga tcaagtcagt ccagcct 577

<210> 14
 <211> 577
 <212> DNA
 <213> Homo Sapien

<220>

<221> variation

<222> 3-4, 6, 8, 252, 375, 474, 506, 515, 532, 541, 545-546, 556, 562, 573

<223> N can be any nucleotide

<400> 14

ggnntntnac	tccatggact	ccaagcagtg	gtaacaacgc	agagtacgcc	catacatgat	60
gggtttcagt	aggggagtga	tgacagtgtg	ggtcaccgag	atcagctggg	catgtttctt	120
ggtgtttctt	gacttgggct	tgaggtaggc	aatggaggca	cagctgtagt	ggacaatgac	180
cacagtgagg	tgggatgcac	aggtggcaaa	agccttcttc	cggccctcaa	ctgaagcaat	240
cttgaggatt	gnagagataa	tgagaacata	agaaatgaaa	accagaccca	taggtacaac	300
aagcaccagc	acactgataa	tcaaagtcag	gatttcattg	acagtgggtg	caatgcagga	360
gagcttcatc	acagnccgga	tgacacagaa	gaagtggggc	acctttctag	cacagaaggg	420
taacctgaat	acagatgtca	cttgcgttat	tgctacaatc	agcccaatgc	tgcnngcccc	480
caggacaagt	tggatagcga	gccttntcgt	tctantaacc	atgtatctca	angggcttgc	540
ngatnccac	atactngcat	anaccattgc	tgngagc			577

<210> 15

<211> 583

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 5, 7, 13, 427, 485, 488, 532, 559, 569, 574, 583

<223> N can be any nucleotide

<400> 15

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cctttgttga	gcagtttgga	ctgagcctct	gacatacgaa	tgtagagaaa	gatggaactg	180
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tcagcagctg	tagggggcct	gagaacagtg	gcaagaatgc	aggcatagga	aactgaggtc	300
agagccagtg	agcccagtaa	caccaacgta	gagagcatga	aagccaccag	tttcagcagg	360
tgggtgtccc	cacaagaaag	cctgagcaag	ggccaactgt	cacgaaagaa	gtgggtcaata	420
ccattgnggc	cacagaaagg	catggctggc	catgaggaca	gtggggcaaa	ggaccagag	480
gaatncanct	agccaggagg	ccacactagt	ttgtgaacag	acatggccat	tnattagggt	540
ctcatagcgg	agttgtcgnc	agatttgcnt	ggtnacgatt	can		583

<210> 16

<211> 577

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3-4, 12, 14, 549

<223> N can be any nucleotide

<400> 16

ggnnttttac	cncnattgga	ctccaaagca	gtggtaacaa	cgcagagtac	gccccctatg	60
tattttattct	tgctcacctc	tccttagttg	atatctgttt	taccaccagt	attgtccccc	120
agctgctgtg	gaacctaaaa	ggacctgaca	aaacaatcac	attcctgggt	tgtgtcatcc	180
agctctacat	ctccctggca	ttgggctcca	ctgagtgtgt	cctcctgggt	gtaatggctt	240
ttgatcgctg	tgctgcagtt	tgcaaacctc	tccactatac	cgccgtaatg	aacctcagc	300
tgtgccaggc	tctggcaggg	gttgctgtgc	tgagtggagt	gggaaacact	cttatccagg	360
gcactgtcac	cctctggctt	ccccgctgtg	gacaccgatt	gctccaacat	ttcttcgtga	420
ggtaccctcc	atgattaagc	ttgcatgtgt	ggacatccat	gataatgagg	ttcagctctt	480

tggtgcttca ctggtcttgc tctcttggcc cttagtgtca atactgctgc ctatggacat 540
 atagccaang tggcataaag gatcaagtca gtccagg 577

<210> 17
 <211> 621
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-5, 8, 13, 618
 <223> N can be any nucleotide

<400> 17
 gnnnntntt cantccattg ggccctctag atgcatgtc gagcgccgc cagtgtgatg 60
 gatatctgca gaattcgccc ttattccgga gggatacat gaagggattg gtaactagac 120
 gtaaaactga agccaagaac agaatttctc ttagaaaaga gaattgaaac taaagagaaa 180
 gaactagcaa agaaggaaat attgaatata caagagagag gagacagatg atggaacaag 240
 actctgaaag aggtggaagg gattgaatac aatcaaaagt atggtgactg ctagtccaa 300
 gatggtggcg taggggcaag ctggcttgc ttacccccct ggcagaaaac caaaaacaaa 360
 tagcaccaag attatcacta gcaatatccc agaactcaca tataaggatg agacagttcc 420
 cagggcccag agaagatcag aagcacaagt gggagaagtc agctttggat gctactttgt 480
 tctaagggag acaagttggg aggatgattg cagatgtata ttcaatgtta taaaacagcc 540
 cataaaaaca agattggaaa atgttgaaat ttgcaaccag gagcaaatac tgggaaaggg 600
 gaattccagc cacttgcneg c 621

<210> 18
 <211> 615
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-5, 8, 10, 14, 21, 583
 <223> N can be any nucleotide

<400> 18
 gnnnnttnan tcantgcctt ngggccctct agatgcatgc tcgagcgcc gccagtgtga 60
 tggatatctg cagaattcgc ccttggtgag caaggtgtaa atgaaaggg ttgcgcagga 120
 gtaaatgaag ggattacgca ggagtaaag aagggtattg gcaggagtaa atgaaggat 180
 tacgcaggag taaatgaagg gattacgcag gagtaaag agggattacg caggagtaa 240
 tgaagggatt acgcaggag aaatgaagg attacgcagg agtaaagaa gggattacgc 300
 aggagtaaag gaaggatta cgcaggagta aatgaaggga ttacgcagga gtaaatgaag 360
 ggattacgca ggagcaata cataggaagg gcaaatcca gcacactggc ggccgttact 420
 agtggatccg agctcggtag caagcttgat gcatagcttg agtattctaa cgcgtcacct 480
 aaatagcttg gcgtaatcat ggtcatagct gtttcctgtg tgaaattgtt atccgctcac 540
 aattccacac aacatacgag cccggaagca taaagtgtaa agnctgggg gcctaatagag 600
 tgacttactc catta 615

<210> 19
 <211> 696
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-3, 5, 7, 287, 300, 309, 313, 328, 331, 343, 345, 347, 360, 366,
 386, 388, 391, 394, 401, 407, 416, 420, 428, 432, 434, 437, 441,
 443, 448, 450, 452, 457-458, 463, 476, 484-485, 493, 503, 506, 514,
 518, 520, 524, 528, 540, 541, 548, 550, 553-554, 557, 561-562,

566-568, 571-572, 575, 582, 584-585, 587-588, 603, 607, 614,
620,
623, 627, 629, 641, 648, 652, 661-662, 665-666, 668, 672, 675, 678,
684, 695

<223> N can be any nucleotide

<400> 19

gnnantnatt	ccatccattg	tcccttcaga	tgcattgctg	agcggccgcc	agtgtgatgg	60
atatctgcag	aattcgccct	tcttggtttt	tgtgctgata	gatcatggga	ttcagcatgg	120
gggtgaccac	agtgtacatc	actgaggctg	ttgcacttga	gtgtgagttg	cgggtggcag	180
cagaactaag	gtacaccctt	aggattgcac	cataaaataa	ggagacaact	gagaggtgag	240
atgcacaggt	ggaagatgcc	ttgtacttcc	cctgagctga	tgagatngca	tgtatggaan	300
gaaattatnt	tanaagtaag	agtaaagnat	nccagtcagg	ggnancnttc	acccatcagn	360
tgcaanttgt	aaaaattata	ttcaancnat	ntgnatttaa	ngaaaaancct	tatcangtan	420
acactgcnaa	gntntgnatt	nanccctnng	anttaanntt	tcnacaagaa	aataangtgc	480
gttnnaatct	ttntaagtcc	ctntcnccat	taangtcnan	tcntccnta	tcccttttctn	540
nattttgnan	tcnngantac	nntctnnngc	nntcnatttc	tntnntnnt	gacctactaa	600
ccnattnagt	tacnacaagn	ccnttcnant	ctctataatt	nctgcangt	tntccctctt	660
nncanntncc	cntttntntc	cctnttcccc	atctnc			696

<210> 20

<211> 615

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 495, 545, 582, 600

<223> N can be any nucleotide

<400> 20

ccattggccc	tctagatgca	tgtctgagcg	gccgccagtg	tgatggatat	ctgcagaatt	60
cgcccttcct	atgtattttc	tcttactggg	ctttcctggg	tctcaaactc	ttcagctctc	120
tctctttatg	ctttttctgg	tgatgtacat	cctcacagtt	agtggtaatg	tggtctatctt	180
gatgttggtg	agcacctccc	atcagttgca	tacccccatg	tacttctttc	tgagcaacct	240
ctccttctctg	gagatttggg	ataccacagc	agcagtgccc	aaagcactgg	ccatcctact	300
ggagagaagt	cagaccatat	catttacaag	ctgtcttttg	cagatgtact	ttgttttctc	360
attaggctgc	acagagtact	tcttcttggc	agccatggct	tatgaccgct	gtcttgccat	420
ctgctatcct	ttacactacg	gagccatcat	gagtagcctg	ctctcagcgc	aactggcctt	480
gggcttctgg	gtggntgggt	tcgggggcaa	tgacagtgccc	acaggccttc	aatcaagtgg	540
gctgntcctt	ctggtggccc	ccggtgccaa	tcaaccactt	tntttttggg	acaattgcan	600
ccctggaatt	ggccc					615

<210> 21

<211> 745

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-3, 8, 21, 23, 26, 33, 43, 116, 201, 212, 222, 239, 252, 279, 282,
288, 292-293, 308, 320, 325, 328-330, 333-334, 339-341, 344, 354, 360, 365,
372, 377, 382-383, 388, 390, 394, 397, 402, 415, 418, 422, 424-425, 427, 431,
436, 441, 445, 450, 451, 457, 466, 493, 495, 498, 501, 508-509, 513, 515,
517-518, 520-523, 525, 528-529, 535, 538, 540-542, 544-546, 548-550, 553,
555, 565, 584, 586, 592-593, 607-608, 615, 617, 619, 621, 634, 636-637, 644-
645, 651, 656, 662, 671, 685, 693, 697, 699, 710, 714, 735, 737, 740, 745
<223> N can be any nucleotide

<400> 21

gnncttantt caateccacc nancentgcc gangcatgct cgngcggccg ccagtgtgat	60
ggatatctgc agaattcgcc ctctctatgt atttactctt actgggcttt cctggntctc	120
aaactcttca gctctctctc tttatgcttt ttctggatgt gtacatcctc acagttagt	180
gtaatgtggc tatcttgatg ntggtagca cntcccatca gntgcatacc cccatgttnt	240
tctttctgag cnacctctcc ttcctggaga ttgtgtatnc cncaagcngc anngcccaaa	300
gctttgcnc tcttattgcn cagangcnnn ccnntacann nacnctcctg tttntcgctn	360
ccttncctct tcttctctc anntactnctn tctnctntag tntctttctt ctctntctct	420
cntnnncct ntaatnttcc ncctnttctn nttctnttt tccctnctct gtttcacccc	480
tacctcttat centnctnct nacttcannc tcngncnntn nnnncnctt aaatntangn	540
nnannntnnn atntnctctt ctcentttat atcgctctt ctctnctctc cnntctctc	600
tcctcannca tatchantnt nttctactct cgtncnntat ctannctct nttctngtcc	660
tcttctctct ntcatttcta tattncttct canacantnt tcgcatcgtn gcancatctc	720
ctcccatctc ctgtnctnctn ttccn	745

<210> 22

<211> 614

<212> DNA

<213> Homo Sapien

<220>

<221> 2-4, 9, 19, 23, 47, 613

<222> (3)...(3)

<223> N can be any nucleotide

<400> 22

gnnnntaant cattccccnc tcnatgcatg ctcgagcggc cgccagngtg atggatatct	60
gcagaattcg cccttgtttc ggaggcagta gatgaatggg ttgatggaat ctgagacagt	120
gctctagaat ctgtgtttca tacaggatga gatataaatg aaacaaatgc taaataatga	180
cacaaggtac cttgccgaga gaggaatcat ccacctggaa gggtaggctg tttgtgaata	240
atgtagggtg ggagagaagg ctttactaag gagatgggct taaagaatgt gaacgatgtg	300
ctcacagagg ccacagaaga gaaattatag ccaggagaac aacctgaaag acaaaggaca	360
cggtagcatg agcgcatgta acacaatgta ctgaggaat ggctggcatc ctgagatatg	420
gagtgggaata cagtacaggg ctttgtaaac tcagcttggg gtcagatcac agaaagcctt	480
gacaaggaac tgaaaatggg ttctgaaggc cagaagccca ttcaagattc ccaaagggaa	540
aaacacaaat cagcttggtt tcaggacgta attcttggca gttgctagaa ttacatcaga	600
aaggaggttc acnt	614

<210> 23

<211> 621

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-4, 6, 8, 12-13, 16, 507, 561, 583, 592

<223> N can be any nucleotide

<400> 23

gnnnntnanc anncantggg ccctctagat gcatgctcga gcggccgcca gtgtgatgga	60
tatctgcaga attcgccctt cctatgtatt tcctcttact gggctttcct gggtctcaaa	120
ctcttcagct ctctctcttt atgctttttc tggtagtgta catccccaca gttagtggta	180
atgtggctat cttgatgttg gtgagcacct cccatcagtt gcataccccc atgtacttct	240
ttctgagcaa cctctccttc ctggagattt ggtataccac agcagcagtg cccaaagcac	300
tggccatcct actggggaga agtcagacca tatcatttac aagctgtctt ttgcagatgt	360
actttgttat ctcataggc tgcacagagt acttcctcct ggcagccatg gcttatgacc	420
gctgtcttgc catctgctat cctttacact acggagccat catgagtagc ctgctctcag	480
cgcagctggc cctgggctcc tgggtgnggg ggttcgtggc cattgcaagt gccacaagc	540
cctaatacgt ggcctgtcc ntctgggggc ccccgggcca ttnaccactt tntctggga	600
caattgcacc cctggaattg g	621

<210> 24

<211> 612
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-3, 8, 16, 20, 26, 557
 <223> N can be any nucleotide

<400> 24
 tnnttaantc attcctnttgn cccctcnagat gcatgctcga gcggccgcca gtgtgatgga 60
 tatctgcaga attcgccctt tccttggttac tgagggagta gattagggga ttgatggaat 120
 ctgagacagt gctctagaat ctgtgtttca tacaggatga gatataaatg aaacaaatgc 180
 taaataatga cacaaggtac cttgccgaga gaggaatcat ccacctggaa gggtaggctg 240
 tttgtgaata atgtaggggtg ggagagaagg ctttactaag gagatgggct taaagaatgt 300
 gaacgatgtg ctcacagagg ccacagaaga gaaattatag ccaggagaac aacctgaaag 360
 acaaaggaca cgggtggcata agcgcattgta acacaatgta ctcaggaaat ggctggcatc 420
 ctgagatatg gagtggaata cagtacaggg ctttgtaaac tcagcttgga gtcagatcac 480
 agaaagcctt gacaaggaac tgaaaatggg ttctgaaggc cagaagccat tcaagattcc 540
 caaagggaaa aacacanatc acttgttttc aggacgtatt cttgggcagt tgctagaatt 600
 acatcagaaa gg 612

<210> 25
 <211> 632
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-5, 9, 614
 <223> N can be any nucleotide

<400> 25
 gnnnnnttant ccatgccctt ctagatgcat gctcgagcgg ccgccagtgt gatggatattc 60
 tgcagaattc gcccttggtt cgcagcctat aaatgaaggg gttgatggaa tctgagacag 120
 tgctctagaa tctgtgtttc atacaggatg agatataaat gaaacaaatg ctaaataatg 180
 acacaaggta ccttgccgag agaggaatca tccacctgga agggtaggct gtttgtgaat 240
 aatgtaggggt gggagagagg gctttactaa ggagatgggc ttaaagaatg tgaacgatgt 300
 gctcacagag gccacagaag agaaattata gccaggagaa caacctgaaa gacaaaggac 360
 accggtggca taagcacatg taacacaatg tactcaggaa atggctggca tcctgaggta 420
 tggagtggaa tacagtaccg gggctttgta aactcagctt ggagtcagat ccagaaagcc 480
 cttgacaagg aactgaaaat tgggttcttg aaggccagaa gccattcaag gattcccaa 540
 aggggaaaaa cacaaatcaa gcttgttttc agggaccgtt aattctgggg ccaggttgct 600
 tgaattacct tcangaaagg gaggttcaca ct 632

<210> 26
 <211> 628
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-3, 419, 423, 426, 437, 439, 453, 460, 463, 469, 478, 489, 492,
 536, 539, 579, 583, 586, 594, 598, 616, 623, 627
 <223> N can be any nucleotide

<400> 26
 gnncttattc atccccctct agatgcatgc tcgagcggcc gccagtgtga tggatatctg 60
 cagaattcgc cctttctttg ttctcagag tgtagattag ggggttgatg ggggttgatg 120
 aatctgagac agtgccttag aatctgtgtt tcatacagga tgagatataa atgaaacaaa 180
 tgctaaataa tgacacaagg taccttgccg agagaggaat catccacctg gaagggtagg 240

ctgtttgtga ataatgtagg gtgggagaga aggctttact aaggagatgg gcttaaagaa	300
tgtgaacgat gtgctcacag aggccacaga agagaaatta tagccaggag aacaacctga	360
aagacaaagg acacgggtggc ataagcgcac gtaacacaat gtactcagga aatggctgnc	420
atnctnagat atggagngng aataccagta canggctttt tanactcanc ttggagtnc	480
gaatcacana angccttgca aggaactgaa aatgggttct gaaaggccag aagccttna	540
agattcccaa agggaaaaaa cacaaatcaa gcttttttna agnacngtaa ttcntggngc	600
cagttgctta gaattnccat canaaang	628

<210> 27
 <211> 803
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 3-4, 19, 168, 190, 202, 245-246, 250, 260, 266, 280, 281, 284, 286, 289, 301, 303, 305, 313, 332-333, 348, 355, 357, 360, 365-366, 370, 372, 376, 379, 384, 387-390, 394-396, 400, 406-407, 411-412, 416-418, 421, 423, 430, 439-440, 442-443, 446, 448, 462-463, 468-469, 480, 482-483, 490, 493, 498, 506-508, 518-519, 523, 532, 534, 536, 539, 547, 549, 556, 559, 573-575, 580-581, 587, 590, 595-596, 600-601, 603, 612, 614, 618, 623, 629, 633, 640, 643, 646, 655-656, 658, 666, 682, 689, 696, 704, 708-709, 718, 721, 732, 738-739, 743, 746, 751, 759, 764-765, 771, 775, 782-783, 788-789, 791-792, 795, 801
 <223> N can be any nucleotide

<400> 27	
ggnttaagcc ttccccctnc gatgctgctc gagcggccgc cagtgtgatg gatattctgca	60
gaattcgccc ttcccatgta tttcctctta ctgggctttc ctggttctca aactcttcag	120
ctctctctct ttatgctttt tctgggtgatg tacatctca cagttagnng taatggggct	180
atcttgatgn ttggtagcac cncctatcag ttgcataccc ccattgactt ctttctgagc	240
aaccnntccn tcttgagag tttgggatac cacacgcaan nagnngccna aggcacttgg	300
nctnctaca ggnggagaag gcttgaccat annattttac catgcctngc cttangncan	360
accnntctn tncctntnt tccnctnnn ggtnnntcan ccgcannctt nnatcnntg	420
nanctcatn gaatatgggn tngtntntc ttgagagcct cnngatcna ttttttccan	480
cnctaaagn ggngcttntc tctctnnnat ctacttntt ggntctcttt tntntnctna	540
cccgtnntc cctatntgt gtctcttct acnnctgcn nttatntan atcanntctn	600
ncttgcctc cntntacnac atnatcatn tcnctcccn ctntcnctct ctatnctna	660
ccatcnctct cttctcatc anctcttnt cattgnttgt tcanttannc actctcctc	720
ncatcttcta tncactannt ttntntttt nctctctant tctnnttcca ntgtncactc	780
cnntctnnnc nntncccta ncg	803

<210> 28
 <211> 620
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 3, 4, 7, 9, 10, 11, 24, 563
 <223> N can be any nucleotide

<400> 28	
gtnttnnann ncattgcccc tctngatgca tgctcgagcg gccgccagtg tgatggatat	60
ctgcagaatt cgcccttctc atgtacttcc tcttaccggg ctttctctgt tctcaaactc	120
ttcagctctc tctctttatg ctttttctgg tgatgtacat cctcacgggt agtggtaatg	180
tggtctattt gatgttgggt agcacctccc atcagttgca tcccccatg tacttcttct	240
tgagcaacct ctcttctctg gagatttgggt ataccacagc agcagtgcc aaagcactgg	300
ccatcctact ggggagaagt cagaccatat catttacaag ctgtcttttg cagatgtact	360
ttgttttctc attaggctgc acagagtact tctctctggc agccatggct tatgaccgct	420
gtcttgccat ctgctatctc ttacactacg gagccatcat gagtagcctg ctctcagcgc	480
agctggccct gggcttcttg gtgggtgggt ttccggggcca ttgcaagtgc ccacagccct	540

tatcaagtgg cctgtccttc tngggccccc gggcccatca accacttttt tctggggaca 600
attgcaccct ggaatggccc 620

<210> 29
<211> 620
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 3-5, 7-9, 15, 567, 574, 585, 596, 606, 611-612, 616, 618-619
<223> N can be any nucleotide

<400> 29
gtnnntnnnt ccatnccatt gggccctcta gatgcatgct cgagcggccg ccagtgtgat 60
ggatatctgc agaattcgcc ctttcattggt tccggaaaca gtaaattatg gggttcagtc 120
atggtaacag gaggaggctg agtgtatggg catggatggg ggctgtgaat gtggcgggag 180
ctcatggatg tgctcttctg agtgcttcac gtttctgagt gaaataagaa gcaaggatcat 240
caccgagagg gaggagacag gctcgggtga gtttagtgga tatgaatcca agagagacca 300
ttcaacttag ttgtctatct tttttttctc cagttagatg cacttgcagc aatgtatagc 360
tggaagtact gatcataaga tccattttat ggcagaagac attatttttc tgagccttct 420
gctgtcagtt tctaaataag caggccagcc gggctgtgca cctaaatgct tgtctgggag 480
gagcaggctg agaagtcttg cagtctgcag gacaccgag gaatcgtatt gtgggaaccg 540
tccccgagaa ccacacgagc cgtgctnctc agtnctgact ggaanaatga aattgnaagc 600
caagtngttc nnggancnnt 620

<210> 30
<211> 616
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 2-4, 7, 9-10, 580
<223> N can be any nucleotide

<400> 30
gnnnntnnnn ccatgagcc ctctagatgc atgctcgagc ggccgcccagt gtgatggata 60
tctgcagaat tcgcccttcc tatgtatttc tcttcctaac gattggaatg cctgggatta 120
ggcagatgat tttctttttc ccccatatcc ctctattatt taggtgattg agtttaaatc 180
cctttatcta cacccttcgg aacaagggcg aattccagca cactggcggc cgttactagt 240
ggatccgagc tcggtaccaa gcttgatgca tagcttgagt attctaacgc gtcacctaaa 300
tagcttgccg taatcatggt catagctggt tcctgtgtga aattgttatc cgctcacaat 360
tccacacaac atacgagccg gaagcataaa gtgtaaagcc tgggggtgcct aatgagttag 420
ctaactcaca ttaattgcgt tgcgctcact gccgcttctc cagtcgggaa acctgtcgtg 480
ccagctgcat taatgaatcg gccaacgcgc ggggagaggc ggtttgcgta ttgggcgctc 540
ttccgcttct tcgctcactg actcgtggg cttcggctcgn tcggctgcgg cgagcgggat 600
cagctcactc aaaagg 616

<210> 31
<211> 612
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 2-9, 13, 507, 554, 585, 598, 600, 609
<223> N can be any nucleotide

<400> 31
gnnnnnnnnt cangccattg ggccctctag atgcatgctc gagcggccgc cagtgtgatg 60
gatatctgca gaattcgccc ttcctatgta tttctcttca ctttctccga catcactcac 120

agccacccca	ccctcagcct	ctccctcctc	ccatgtattt	tctcttcaat	ctctccttct	180
ttgatatcct	gaactttctg	tagctcttta	ttttctcttc	caatcccttc	atatacacgt	240
ttcgtaacaa	gggcgaattc	cagcacactg	gcggccgtta	ctagtggatc	cgagctcggt	300
accaagcttg	atgcatagct	tgagtattct	aacgcgtcac	ctaaatagct	tggcgtaatc	360
atgggtcatag	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	acaacatacg	420
agccggaagc	ataaagtgtg	aagcctgggg	tgccaatga	gtgagctaac	tcacattaat	480
tgcggtgcgt	cactggccgc	tttccangtc	gggaaacctg	tcggccagct	gcattaaatg	540
aatcggccaa	cgcncgggga	gaggcggttt	gcgtattggg	cgctntttcg	ttcttcgntn	600
actgatcgnt	gg					612

<210> 32

<211> 616

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-9, 15, 521, 596

<223> N can be any nucleotide

<400> 32

gnnnnnnnnt	tcatnccatt	gggccctcta	gatgcatgct	cgagcgggcg	ccagtgtgat	60
ggatatctgc	agaattcgcc	cttggtgctt	agagtgtaaa	taaaaggggt	aacattgggt	120
tagaggtgaa	gagtaaatac	ataggaaggg	cgaattccag	cacactggcg	gccgttacta	180
gtggatccga	gctcggtacc	aagcttgatg	catagcttga	gtattctaac	gcgtcaccta	240
aatagcttgg	cgtaatcatg	gtcatagctg	tttctgtgt	gaaattgtta	tccgctcaca	300
attccacaca	acatacgagc	cggaagcata	aagtgtaaag	cctgggggtgc	ctaattgagt	360
agctaactca	cattaattgc	gttgcgctca	ctgcccgctt	tccagtcggg	aaacctgtcg	420
tgccagctgc	attaatgaat	cggccaacgc	gcggggagag	gcggtttgcg	tattgggcgc	480
tcttcgcgtt	cctcgctcac	tgactcgctg	cgctcggtcg	ntcggtcgcg	gcgagcggtg	540
tcaagctcac	tcaaaggcgg	taatacggtt	atccacagaa	tcagggggat	acgcangaaa	600
gaacatgtga	gcaaat					616

<210> 33

<211> 621

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 4, 6, 8, 19, 27, 31, 464, 526, 554, 578, 598, 600, 615

<223> N can be any nucleotide

<400> 33

gntntnanc	atgccccenc	cgatgcntgc	ncgagcggcc	gccagtgtga	tggatatctg	60
cagaattcgc	ccttggtgcg	gagcgaatat	atgaaggggt	taagggaaga	gaaaatacat	120
aggaagggcg	aattccagca	cactggcggc	cgttactagt	ggatccgagc	tcggtaccaa	180
gcttgatgca	tagcttgagt	attctaacgc	gtcacctaaa	tagcttggcg	taatcatggt	240
catagctggt	tcctgtgtga	aattgttata	cgctcacaat	tccacacaac	atacgagccg	300
gaagcataaa	gtgtaaagcc	tggggtgcct	aatgagttag	ctaactcaca	ttaattgcgt	360
tgcgctcact	gcccgctttc	cagtcgggaa	acctgtcggtg	ccagctgcat	taatgaatcg	420
gccaacgcgc	cggggagagg	cggtttgcgt	attgggcgct	cttncgcttc	ctcgctcact	480
gactcgcttg	cgctcggtcc	gttcggctgc	ggcgagcggt	atcaantcac	tcaaaaggcg	540
ggaatacggg	ttncacaga	aatcaggggg	ataacgcngg	aaagaacatg	tgagccanan	600
ggcagcaaaa	gggcnaggaa	t				621

<210> 34

<211> 614

<212> DNA

<213> Homo Sapien

<220>
 <221> variation
 <222> 2-9, 13-14, 593
 <223> N can be any nucleotide

<400> 34
 gnnnnnnnt cannccattg ggccctctag atgcatgctc gagcgggccgc cagtgtgatg 60
 gatattctgca gaattcgccc ttgttccgaa ggctatagat gaagggggtt taggttttta 120
 ggaacacagg ctaaggggga agagaaaata catgggaagg gcgaattcca gcacactggc 180
 ggccgttact agtggatccg agctcggtag caagcttgat gcatagcttg agtattctaa 240
 cgcgtcacct aaatagcttg gcgtaatcat ggcatagct gtttcctgtg tgaaattgtt 300
 atccgctcac aattccacac aacatacgag ccggaagcat aaagtgtaaa gcctgggggtg 360
 cctaattgagt gagctaactc acattaattg cgttgcgctc actgcccgtt tccagtcgg 420
 gaaacctgtc gtgccagctg cattaatgaa tcggccaacg cgcggggaga ggcggtttgc 480
 gtattgggag ctcttcgctc tcctcgctca ctgactcgct gcgctcggtc gtcgggtgag 540
 gcgagcggta tcagctcact caaaggcggg aatacgggta tccacagaat cangggataa 600
 cgcaggaaaa gaca 614

<210> 35
 <211> 614
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 3-4, 7, 9, 23, 599, 611
 <223> N can be any nucleotide

<400> 35
 ggnnttnant cattgccccg ctngatgcat gctcgagcgg ccgccagtgt gatggatatc 60
 tgcagaattc gcccttccga tgtattttct tctacgttaa ggtattttta attgttacta 120
 atgcataagg gcaacacatt ctgtaatgct gacaagatga aagagccaaa agtaattaat 180
 gatgctgtta cctcacaat atgtatgtgt ggatgtatat atatctatc aatatatgta 240
 actatacata tgtctgtttc taattgaaaa caccaggtaa ttatcatctg tagaaaccct 300
 agtgtctcag ataagttggc tagttttttg tttcacataa aggaacaaac atttatagat 360
 ttatatgtat attaaaaatg gtaaaaaattg gctgggtgca gtgggttcag cctataatac 420
 cagcactttg ggaagccgag gtgggaggat tacttgaggt aaggagccca gcctgaccaa 480
 caagggtgaa ccccatccct actaaaaata caagaattag cccggggatg gtgggtggcca 540
 cctgtaatcc cagctacttg ggagactgaa gccaggaaaa tcacttgacc caggaagcng 600
 aggttgagg ngag 614

<210> 36
 <211> 611
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 1, 3-5, 10, 18-20, 22, 26, 605
 <223> N can be any nucleotide

<400> 36
 ngnnnttgan tcaattcnnn gncgangcat gctcgagcgg ccgccagtgt gatggatatc 60
 tgcagaattc gcccttccga tgtattttct tctagccaac ctcccactca ttgatctgtc 120
 tctgtcttca gtcatagcc ccaagatgat tactgacttt ttcagccagc gcaaagtcat 180
 ctctttcaag ggctgccttg ttcagatatt tctccttcac ttctttgggtg ggagtggatg 240
 ggtgatcctc atagccatgg gctttgacag atatatagca atatgcaaac cctacacta 300
 cactacaatt atgtgtggca acgcatgtgt cggcattatg gctgtcgcag ggggaattgg 360
 ctttctccat tcgggtgagc agttggcctt tgccgtgcac ttacccttct gtgggtccaa 420
 tgaggtcgat agtttttatt gtgaccttcc tagggtaacc aaacttgcct gtacagatac 480
 ctacaggcta gatattatgg tcattgctaa cagtgggtgt ctactgtgt ggtcttttgt 540

cttctaataca tctcatatac tatcatccta atgaccatcc agcattgccc tttagataag 600
tcgtncaaag g 611

<210> 37
<211> 616
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 2-4, 6, 8, 12-14, 17, 19-20, 442, 595, 599
<223> N can be any nucleotide

<400> 37
gnnnntnanc cnnncncnn ctagatgcat gctcgagcgg ccgccagtgt gatggatatac 60
tgcagaattc gcccttccca tgtatttgct tctcagcaac ttgtccttct ctgacctctg 120
cttctcttcc gtgaccattc ccaagttgtt acagaacatg cagaaccagg acccatccat 180
ccctatgcg gactgcctga cccaaatgta cttcttctctg ttatttggag acctggagaa 240
cttctcctt gtggccatgg cctatgaccg ctatgtggcc atctgcttcc cctgcacta 300
caccgccatc atgagcccca tgctctgtct cgccctgggt gcgctgtcct ggggtgctgac 360
caccttccat gccatgttac acactttact catggccagg ttgtgttttt gtgcagacaa 420
tgtgatcccc cactttttct gngatatgtc tgctctgtg aagcaggcct tctctgacac 480
tcgagttaat gaatgggtga tatttatcat gggagggctc attcttgtca tccattcct 540
actcattctt gggtcctatg caagaattgt ctctcatcc tcaaggctcc tttntaang 600
gtatctgcaa ggcct 616

<210> 38
<211> 615
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 1, 3-6, 9, 11, 14, 16, 20, 21, 23, 540, 566
<223> N can be any nucleotide

<400> 38
ngnnnnntna ntcnangcnn ngngccctct agatgcatgc tcgagcggcc gccagtgtga 60
tggatatctg cagaattcgc ccttccaatg tatttacttc tcagccagct ctcccttatg 120
gacctgatgt acatctccac caccgtcccc aagatggcgt acaacttcct gtccggccag 180
aaaggcatct ctttctggg atgtggtgtg caaagcttct tcttctgac catggcgtgt 240
tctgaaggct tactcctgac ctccatggcc tacgaccgtt atttggccat ctgccactct 300
ctctattatc ctatccgcat gagtaaaatg atgtgtgtga agatgattgg aggctcttgg 360
acactggggg ccatcaactc cttggcacac acagtctttg cccttcata tccctactgc 420
aggctaggg ctattgacca tttcttctgc gatgtcccag ccattgtgt tcttgctgta 480
cagatacttg ggtctatgaa tatatggttt ttgtaaggac aaagcctctt tcttcttttn 540
cctttcattg gcatacttc ttctgngggc cgagtcctaa ttgctggcta tataatgcac 600
tcaaaggagg ggagg 615

<210> 39
<211> 615
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 4-8, 12-13, 17-18, 22-23, 26-28, 469, 591, 596
<223> N can be any nucleotide

<400> 39
tagnnnnntt anntcanngc cnnatgnggc tcagatgcat gctcgagcgg ccgccagtgt 60

gatggatata	tgcagaattc	gcccttccaa	tgtattttct	tctcagcagg	agagatat	120
atcctcactg	ccatgtccta	tgaccgctat	gtagccatct	gctgtcccct	gaactacgag	180
gctgcacaga	gtacttccct	ctggcagcca	tggcttatga	ccgctgtctt	gccatctgct	240
atcctttaca	ctacggagcc	atcatgagta	gcctgtcttc	agcgcagctg	gccctgggct	300
cctgggtctg	tggtttcgtg	gccattgcag	tggccacagc	cctcatcagt	ggcctgtcct	360
tctgtggccc	ccgtgccatc	aaccacttct	tctgtgacat	tgcaccctgg	attgccctgg	420
cctgcaccaa	cacacaggca	gtagagcttg	tggcctttgt	gattgctgnt	gtggttatcc	480
tgagttcatg	cctcatcacc	cttgtctcct	atgtgtacat	catcagcacc	atccttagga	540
tcccctctgc	agtggccgga	gcaaagcctt	ctcccgtgct	cctcgcatct	naacngngtg	600
ctcatttggt	atggg					615

<210> 40

<211> 586

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 14, 21, 23, 479, 498, 534, 584

<223> N can be any nucleotide

<400> 40

catgctcgag	cggncgccag	ngngatggat	atctgcagaa	ttcgcccttc	ctatgtattt	60
gcttctcagc	aggagagata	tttatcctca	ctgccatgtc	ctatgaccgc	tatgtagcca	120
tctgctgtcc	cctgaactac	gaggtgattc	atgtgcccat	tagagcttga	gaagcactgc	180
ttggaagccc	cttctgccat	caatgaggct	gcacagagta	cttcctcctg	gcagccatgg	240
cttatgaccg	ctgccttgcc	atctgctatc	ctttacacta	cggagccatc	atgagtagcc	300
tgctctcagc	gcagctggcc	ctgggctcct	gggtctgtgg	tttcgtggcc	attgcagtgc	360
ccacagccct	catcagtggc	ctgtccttct	gtggcccccg	tgccatcaac	cacttcttct	420
gtgacattgc	accctggatt	gccctggcct	gcaccaacac	acaggcagta	gaagcttgng	480
gcctttgtga	attgctgntg	tgggtatccc	gagttcatgc	ctcatcacc	ttgncttcta	540
tgtgtacatc	atcaggcacc	attctcagga	tcccttctgc	aagngg		586

<210> 41

<211> 857

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 5-12, 16-18, 22, 27, 32, 42, 60, 99, 159, 171, 202, 212, 240, 242, 251, 306, 330, 371, 568, 669, 750, 802, 840, 856

<223> N can be any nucleotide

<400> 41

atggnnnnnn	nntttnnnaa	anttttnccc	antttggggc	gnccccccct	tctttaaggn	60
aatgggccc	ttgggccctt	cccgggaaggc	ccgggggnc	ccggccccaa	aggtttgggt	120
tgggaaatgg	ggggaattta	aattcctttg	ggccaaggna	aaaattttcc	ngccccctt	180
tttttcccct	tttggttttt	anccggggga	angggggggt	tgattaatta	atcgggaagn	240
tnggggggaa	nttttttaaa	aaaaaccttg	ggggaagggt	ccaacccaac	aaggttgggt	300
ttccanggga	ccgttgggac	caggcttttn	gaatcaagaa	tcccaaagg	cattcttttg	360
gattaaggaa	nggtgccggg	accggtgaaa	gggaaaaaac	tggtggaccc	cataccaaaa	420
tgagaaccac	ggtgagatgc	cgaggagcac	gtggagaaag	gctttgcttc	cggccactgg	480
cagaggggat	cctgaggatg	gtgcttgatg	atgtacacat	agggagacaa	gggtgatgag	540
gcatgaactc	aggataacca	caacagcnat	cacaaaggcc	acaaagctct	actgcctgtg	600
tgttgggtgc	aggccagggc	aatccagggg	tgcaatgtca	caagaaagaa	agtggttgat	660
ggcacggng	ggccacagaa	ggacaggcca	cttgatgaag	ggcttggtgg	cactgcaatg	720
gccacgaaac	caccagaccc	aggaaccan	ggccaagctt	gcgcctgaag	agcaaggcta	780
ctcatgaatg	gcttccgtag	tngtaaagga	tagcaagatg	gcaaaggcaa	gccggtcatn	840
aagccatggc	ttgccng					857

<210> 42

<211> 620
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-4, 8-10, 43, 611, 613
 <223> N can be any nucleotide

<400> 42
 gnnnttannn cattgcgccc tctagatgca tgctcgagcg gcncgccagt gtgatggata 60
 tctgcagaat tcgcccttgt tgcgcaagga gtagatgaac ggattcaggg caagggagtg 120
 ctgaggagat agacgggtat aactgggca caagtccatg agtaatcaag gcctgttatt 180
 taaaaaaaaa aaaaaaaaaa cttgaacaat atagaatccc attaccaga gatagactgg 240
 atggtgaatt aaactttctg gtgaatttct tccagatat ctctctatgc atatgtatac 300
 acaagcaatt tttggaagaa aagatacttt ataaggataa gcctgaaaac tgcaacgaat 360
 gcaatgtgga gaatgaaggc aagatgtggc gaagaagggc accacaatct ggtggctgag 420
 agagtgaac tgtcactaca gctaaaagga gagctggaga agctgggtgag gacagtaaga 480
 gatgaatctg gtttaagaca cgctgagtct caaatgccat ggctccccta ggttgccctc 540
 tcagatgtaa atcttaagct caaagcaggt ggatgagaaa tcacatttca tagtccctgc 600
 acagacggct ntnttgagct 620

<210> 43
 <211> 608
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-5, 10, 22-24, 27, 592
 <223> N can be any nucleotide

<400> 43
 gnnntttaan tcattgcccc gnnngangca tgctcgagcg gccgccagt tgatggatat 60
 ctgcagaatt cgcccttccc atgtatttgc ttctcagcaa cttgtccttc tctgacctct 120
 gcttctcttc cgtgaccatt cccaagttgt tacagaacat gcagaaccag gacctcca 180
 tcccctatgc ggactgcctg acccaaatgt acttcttctt gttatttggga gacctggaga 240
 gcttctctct tgtggccatg gcctatgacc gctatgtggc catctgcttc cccctgcact 300
 acaccgccat catgagcccc atgctctgtc tcgccctggg ggcgctgtcc tgggtgctga 360
 ccacctcca tgccatgtta cacactttac tcatggccag gttgtgtttt tgtgcagaca 420
 atgtgatccc ccacttttct tgtgatatgt ctgctctgct gaagctggcc ttctctgaca 480
 ctcgagttaa tgaatgggtg atatttatca tgggagggct cattcttgca tccattccta 540
 ctcatccttg ggtcctatgc aagaaatgct cctcatcctc aaggcccttc tntaagggtg 600
 tctgcaag 608

<210> 44
 <211> 608
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-5, 7, 9, 12, 20, 24, 26, 29, 31-32, 480, 530, 557, 579
 <223> N can be any nucleotide

<400> 44
 gnnntnant cntgccctgn ccncngcnc nngcgccgcg gcggatggat atctgcagaa 60
 ttgcccttg ttactaagag tatagatgaa cggattcagg gcaagggagt gctgaggaga 120
 tagacgggta tacactgggc acaagtccat gagtaatcaa ggcctgttat ttaaaaaaaa 180
 aaaaaaagct tgaacaatat agaatcccat taccagaga tagactggat ggtgaattaa 240
 actttctggt gaatttcttt ccagatatct ctctatgcat gtgtatacac aagcaatttt 300

tggaagaaaa	gatactttat	aaggataagc	ctgaaaactg	caacgaatgc	aatgtggaga	360
atgaaggcaa	gatgtggcga	agaagggcac	cacaatctgg	tggtctgagag	agtgcaactg	420
tcactacagc	taaaaggaga	gctggagaag	ctgggtgagga	cagtaagaga	tgaatctggg	480
ttaagacacg	ctgagtcctca	gatgccatgg	cttccctagg	ttgcctcttn	cagatgtaaa	540
tcttaagctc	aaagcangtg	gatgagaaat	acacatttna	tagtcacctg	cacagacggt	600
tttttgat						608

<210> 45

<211> 602

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 14, 16, 19, 21, 23-24, 27, 38, 40, 50, 52, 520, 551

<223> N can be any nucleotide

<400> 45

catgccccgt	ccncnagnt	ncnngcncgg	cgcccgcnan	ggatatctgn	anaattcgcc	60
cttctctatgt	atttacttct	ccaactttct	cttcccatct	ctatcattag	aaccattca	120
tatacacct	acgaaacaag	ggcgaattcc	agcacactgg	cgcccggtac	tagtggatcc	180
gagctcggta	ccaagcttga	tgcatagctt	gagtattcta	acgcgtcacc	taaatagctt	240
ggcgtaatca	tggtcatagc	tgtttctctgt	gtgaaattgt	tatccgctca	caattccaca	300
caacatacga	gccggaagca	taaagtgtaa	agcctggggg	gcctaattgag	tgagctaact	360
cacattaatt	gcgttgcgct	cactgcccgc	tttccagtcg	ggaaacctgt	cgtgccagct	420
gcattaatga	atcgccaac	gcgcggggag	aggcggtttg	cgtattgggc	gctcttccgc	480
ttctcgctca	ctgactcgct	gcgctcggtc	gttcggctgn	ggcgagcggt	atcagctcac	540
tcaaaggcgg	naatacgggt	atccacaaga	atcaggggga	taacgcaaga	aaagacatgt	600
ga						602

<210> 46

<211> 620

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-4, 6, 10

<223> N can be any nucleotide

<400> 46

gnnntnattn	attgcattgg	gccctctaga	tgcatgctcg	agcgcccgcc	agtgtgatgg	60
atatctgcag	aattcgccct	tagtgagtag	atgaaagggt	tcagcatggg	ggtcaccaca	120
gtgtacatca	tagccatgac	agtgtccttt	agagtagaac	tattagctga	tgagcataag	180
tagagaccaa	taacgggttc	atagaacagt	gacaccacag	atagggtggga	gccacaagta	240
gagaaggcct	tgagacaccc	cttagaagaa	gggaccttga	ggatggagga	gacaattctt	300
gcataggacc	caaggatgag	taggaatggg	atgacaagaa	tgagccctcc	catgataaac	360
atcacccatt	cattaactcg	agtgtcagag	aaggccagct	tcagcagagc	agacatatca	420
cagaaaagg	gggggatcac	attgtctgca	caaaaacaca	acctggccat	gagtaaagt	480
tgtaacatgg	catggaagg	ggtcagcacc	caggacagcg	ccaccagggc	gagacagagc	540
atggggctca	tgagggcggt	gtagtgcagg	gggaagcaga	tgccacata	gcggtcatag	600
gccatggcca	caaggaggaa					620

<210> 47

<211> 607

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 572, 578, 594

<223> N can be any nucleotide

<400> 47

cnatgggccc	tctagatgca	tgctcgagcg	gccgccagtg	tgatggatat	ctgcagaatt	60
cgcccttcca	atgtatttgc	ttctcagcaa	cttgctcttc	tctgacctct	gcttctcttc	120
cgtgaccatt	cccaagtgtg	tacagaacat	gcagaaccag	gacccatcca	tcccctatgc	180
ggactgcctg	acccaaatgt	acttcttcct	gttatttggg	gacctggaga	gcttctctct	240
tgtggccatg	gcctatgacc	gctatgtggc	catctgcttc	cccctgcaact	acaccgccat	300
catgagcccc	atgctctgtc	tcgccctggg	ggcgctgtcc	tgggtgctga	ccaccttcca	360
tgccatgtta	cacactttac	tcatggccag	gttgtgtttt	tgtgcagaca	atgtgatccc	420
ccacttttct	tgtgatttgt	ctgctctgct	gaagctggcc	ttccctgaca	ctcgagttaa	480
tgaatgggtg	atatttatca	tgggagggct	cattcttgtc	atcccatcc	tactcaatcc	540
ttgggtctat	gcaagaaatt	gtcttcttca	tnctcaangg	ccctttcttc	taanggtatc	600
ttgcaag						607

<210> 48

<211> 613

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-4, 7, 9, 257, 266, 295, 313, 322, 331, 334, 338, 340, 345, 348, 356, 358, 365, 378, 397, 398, 402, 410, 447, 480, 536-537, 557, 563, 576, 580, 584-586, 606, 610-612

<223> N can be any nucleotide

<400> 48

annnccntng	gagctccaaa	gcagtggtaa	caacgcagag	tacgccccct	atgtacttac	60
ttttgttaa	gagctccaaa	gcagtggtaa	caacgcagag	tacgccccct	atgtacttac	120
cttcaaaa	ccttggtcac	tcactcttct	tcagctctct	ttgtggattc	ttcctcattt	180
atttgacctc	ttgctgggtg	accctttcat	atacactctc	cgtaacaaag	aggcggtact	240
tctgtcgtct	tgagcgnact	gatgggnacc	agcttttgtt	cccttttagt	agggntaatt	300
gcgcgcttgg	cgnaatcatg	gncatagctg	ntnctgngn	gaaantgnta	tttcgntnac	360
aattncacac	aacatacnag	ccgggagcat	aaaggggnna	gncctggggg	gcctaataag	420
ggagcttact	cacaataaatt	ggggtgngcc	cactggcccc	ttttcaggcg	ggaaaacctn	480
gcggggccag	ctggaataaaa	tgaatcgggc	cacgcgcggg	ggaggagggc	gggttnngga	540
attgggcgct	tttccntttt	ctnggttaatt	ggactnggtn	ggcnnngtcc	gttcggttgg	600
ggggancggn	nnt					613

<210> 49

<211> 593

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 177, 298, 506, 515, 578, 582

<223> N can be any nucleotide

<400> 49

aacgcagagt	accgcccact	acgtaatctg	tacatgaaag	ggtttaaaag	agactgggaa	60
gagaggaatt	ggcaagatca	agcagaggca	actccttcta	gtccttctag	taccgcaagg	120
ggcagataaa	tggaaatggg	aacacctaga	ggaaagtata	cttgccaaaa	gcaaatncat	180
aggggggagt	acattatcgg	gttgaaaaaa	gtattccatg	cagataaaaa	ccaaaagcaa	240
atacatcggg	ggcgctactt	tgctgtcttt	gagcgctact	atggtagcca	gcttttgnct	300
ctttagttag	gggttaattg	gcgcttggcg	taatcatggg	catagctggg	ttctgtgtga	360
aattgtttat	ccgctcacia	ttcacacaac	atacagagcc	gggagcataa	agtgtaaagc	420
ctgggggtgc	taatgagtgg	agcttactta	cattaaattg	cggtgcgctc	actggccgct	480
tttccaagtc	gggaaacctg	tcgtgncagc	ttcantaatg	aatcggccaa	cgccgcgggg	540
agaggcgggt	tgctgtattg	gcgctcttcc	gcttcttngt	tnactgactt	cgg	593

<210> 50
 <211> 624
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-4, 11, 16, 20, 22
 <223> N can be any nucleotide

<400> 50
 gnnntttaac nccggngctn cnagcagtgg aacaacgcag agtacgcccc cgatgtactt 60
 tctttttcag tctcaagtct tctctttctc caaagatttt gtctttttcta ctacctgagc 120
 taccaaatcc cttgtcatca atttcaataa ctgtattctc ttcattcattt caacttcaaa 180
 cgtgtcatct cagaacaagc ttcatgttac ttccaatttt atccttcttg tttgctgatt 240
 ccaagaattc cagtcccatc taggcccgcga atgcattgtt cctgccaccc tttcatatc 300
 ctcaattccc ttgtatcatc actttccttt tatatagcac agattccatg attcataaca 360
 ataattatgt ttttttttgc atgtgctctt aatttccttt cttgctccta ttatcttcta 420
 tcatactttt ctggaaacac taattctggt gaaatatact ctttgtggac tttgcaactta 480
 tgctcagtca gctgaagatg atggctagac aaatactcac aatcatgctg actggcccaa 540
 tttatagtca tgaccaccga ttacaaaccc cttcatttat tctccgcaac aggggcgtct 600
 tctgcgcttg agcgtccggt gggg 624

<210> 51
 <211> 584
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 584
 <223> N can be any nucleotide

<400> 51
 gcagtggtaa caacgcagag tacgcccgtt acggaggctg taaataaagg ggttgaggaa 60
 gtaaagtact tcacagtact ggagcacaca gcatgtgaat ttcagccaaa ggacaaatgc 120
 ctccaaaaaa agttaattca cagtgcagca gggcgaggca cttgtcttat tcgctgggtc 180
 tcacattgac cctgaaagga cttttttttg ttaatcccat tttcacagat gggaaaggga 240
 ctctgtatgg ttgtcacttt tatccaaagt ctcatagcca gtaagaagct gccctcaaag 300
 tccctaccct gtcttccatt cgactattct gaggttcaga cccagaaacc ccatacctct 360
 gccttatatt ttaatgaaaa gtatgtctcc aggtttatgt ggagaataac caagacctca 420
 gaaacattta gtgaaaatca gagctagaag gaatctgttt ttttgcgagt tcagagaaac 480
 tgacttggat aagacatcaa agttgtcttg tgcagcaaat tctcctccgg cacatagtag 540
 gcactctgat aaattcaaaa aggcttctaa gaagaggcag aagn 584

<210> 52
 <211> 613
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 6, 10-12, 16-17, 20, 553, 594, 607, 613
 <223> N can be any nucleotide

<400> 52
 gtgaanccan nntaannccn attggagctc caagcagtgg taacaacgca gagtacgccc 60
 ccgatgtagt ttcttcttcc cttccttccc tcttctctc cttcttctct ttctctctct 120
 ctccctctcc ctctccctct cctctctctc ctcttcttcc ttctctctcc tctctctccc 180
 cccaatccgt tcatgacttc ttcttcttcc tcttcttctt ctttcttctt ttcttctttt 240

tctctaagca	ggatcctggg	ctgttcaaac	cagagagctg	taagtctttt	ctttcccat	300
tactgttaga	tccgttgaat	cggctccaga	aaccaaaca	gttaaccctt	gcatttacac	360
gtttcgtaac	ggcggtactt	ctgtcgtctt	gagcgtaactg	atggtagcca	gctttgttc	420
ccttttagtga	gggttaattg	cgcgcttggc	gtaatcatgg	tcatactgt	ttcctgtggg	480
aaattgttat	cgcctcaca	ttccacacaa	catacgagcc	gggagcataa	aagtgtaaag	540
cctgggggtgc	ctnatgagt	agctaactca	cattaattgc	gttgcgctta	ctgnccgttt	600
tcagtcngga	aan					613

<210> 53

<211> 611

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 4-5, 7-9, 14-15, 601

<223> N can be any nucleotide

<400> 53

tnannnnnt	taanncccat	tgagctcca	aagcagtgg	aacaacgcag	agtacgcccc	60
cgatgtactt	gcttcttctt	ctttggagt	gctgaatgct	tcctcctggc	taccatggca	120
tatgaccgct	atgtggccat	ctgcagtccc	ttgcactacc	cagtcacat	gaaccaagg	180
actcgtgcca	aactggctgc	tgctcctgg	ttccaggct	ttcctgtagc	tactgtgcag	240
accacatggc	tcttcagttt	tccattctgt	ggcaccaaca	aggtgaacca	cttcttctgt	300
gacagccac	ctgtgctgag	gctggctgt	gcagacacag	cactgtttga	gatctacgcc	360
atcgtcgga	ccattctgg	ggcatgac	ccctgcttg	tgatcttgt	ttcctatact	420
cgcattgctg	ctgccatcct	caagatcca	tcagctaaag	ggaagaataa	agcctttct	480
acatgttct	cacacctcct	tggtggctct	ctttctata	tatcattaag	cctcacctac	540
ttccggccta	aatcaaataa	ttcacctgag	ggcacgaagc	tgctatcatt	gcctacactg	600
ntatgactcc	a					611

<210> 54

<211> 606

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 4, 483, 509-510, 606

<223> N can be any nucleotide

<400> 54

gtntttccat	ggactcccaa	gcagtggtaa	caacgcagag	tacgccccct	atgtacttac	60
ttcttggctg	cttatcattt	atagatatca	tttattcttc	atccatttcc	cacagatcga	120
tttcagactt	gttctttggg	aataattcca	tatccttccc	atcttgcttg	gccagctct	180
ttacagagcg	cctttttgg	gggtcagagg	tctttcttct	gttgggtgat	gcctatgacc	240
ttgcattact	tggttatcat	gagacaatgg	gtgtgtgttt	tgctgctgg	agtgtcctgg	300
gttggaggat	ttctgcactc	agtatttcaa	cttagtgtaa	tttatgggct	cccattctgt	360
gacctcaatg	tcattgatca	ttttttctgt	gatatgcacc	ctttattgaa	actgggtctgt	420
accgataccc	atgttattgg	cctcttagtg	gtggcaatgg	aggactaggt	tgactattg	480
ggnattctgt	cttactcatc	tcttatggnn	catctgcact	ctctaaagaa	ccttagtcag	540
aaagggaggt	gaaaagccct	ctcaacctgc	agttccacat	aactgggggg	tggtttcttc	600
tttgtn						606

<210> 55

<211> 630

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 4-5, 8-9, 12, 16, 19, 295, 298, 321, 472, 481, 573, 617

<223> N can be any nucleotide

<400> 55

ttannccnnt tnaatncnt tggagctcca aagcagtggg aacaacgcag agtacgcccc	60
caatgtactt gctttcttct ttttggggct gctgagtgtt gcctcctggc caccatggca	120
tatgaccgct acgtggccat ctgtgacccc ttgcactacc cagtcatcat gggccacata	180
tcctgtgccc agctggcaag ctgcctcttg gttctcaggg ttttcagtgg ccaactgtgca	240
aaccacatgg attttcagtt tccctttttg tggccccaac aggggtgaacc acttnttntg	300
tgacagccct cctgttattg naactggctgt tgctgacacc tctgtgtttt gaactggagg	360
ctcttgacag ccactgccta attcattctc tttcctttct tgctgacccct gggatccctat	420
ttcgcattct ctctactatc ttttaaggatg ccgtcagctg aggggaaaca tnagcattct	480
ncacctgttc cgcccacctc ttgggtggct ctctcttcta tagcactggc aatccttaac	540
gtatttttccg accccaattc aagtgccttt ttntgagaag caaagaaact ggttgctact	600
tttttttcac aagggngnac ttccaatgtt	630

<210> 56

<211> 631

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 4, 8-10, 493, 582

<223> N can be any nucleotide

<400> 56

gngntttnnn ccatggagct ccaaagcagt ggtaacaacg cagagtacgc ccccatgta	60
ctttcttctt ctttggagtg gctgaatgct tcctcctggc taccatggca tatgaccgct	120
atgtggccat ctgcagtccc ttgcactacc cagtcatcat gaaccaaagg actcgtgcca	180
aactggctgc tacctccttg ttcccaggct ttctgtagc tactgtgcag accacatggc	240
tcttcagttt tccattctgt ggcaccaaca aggtgaacca cttcttctgt gacagccac	300
ctgtgctgag gctggctgtg gcagacacag cactcttga gatctacgc atcgtcggaa	360
ccattctggt ggtcatgac ccctgcttgc tgatcttgtg ttctatact cacattgctg	420
ctgccatcct caaggtcca tcagctaaag ggaagaataa agccttttct acatgttct	480
cacacctcct tgntgtctct cttttctata tatcattaag cctcacctac ttccggccta	540
aatcaaataa ttcactgag ggcaagaagc tgctatcatt gncctacact gttatgactc	600
catgttgaac ccataattt attcattcag c	631

<210> 57

<211> 637

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 5-6, 76, 82, 92, 106, 122, 125, 142-143, 190, 214, 223, 244, 247, 259, 283, 290, 320, 402, 416, 455, 470, 529, 558, 561, 607, 618, 620, 630

<223> N can be any nucleotide

<400> 57

ttatnnccat tggagctcca aagcagtggg aacaaccgca gagtacgccc cccatgtatt	60
ttctttttct tggggnagct gnatgcttcc tntgggtac catggnatat gaccggctat	120
gnggncatct gcagtccctt gnntcccgag tcattatgaa ccaaaggaca cgggccaac	180
tggtggtgn ttctgggtc ccaagcttct ctgnagctac tngcaagac cacaatggct	240
cttnagnttt ccattctgng gcaccaacaa ggtgaaccac ttntttctgn gacagccggc	300
tgtgctgaaa gctggctgng tgcaagacac agcactgttt gagatctacg ccatcgctgg	360
aaccattctg gtgtcaatg aaccctgct tgctgatctt gngttcctat actcgnattg	420
gtgtgctat ccctcaagaa ccatcaagc taaangggaa gcaataaagn ctttctcta	480
cgtgtcctt aacacctccc ttggtggcct ctcttttcta atataatct ctaagcctca	540
acctacttct tgggcctnaa ntcaaataaa ttcttctgga gaggaagaa ggtggtattc	600

atttatncta cactggtn gn gactccatgn tggaact

637

<210> 58

<211> 621

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 6, 9, 16, 19, 507, 597, 611

<223> N can be any nucleotide

<400> 58

gtnatnccnt ttaatnccnt tggagctcca agcagtggtgta acaacgcaga gtacgcccgt	60
tcctcagaca gtatatgaat gggttaaaaa tgggccagag cagatgcagg aagatcaaat	120
aggaggctac tgcaagtagag tcaaatctag ggctgatggt ttcttgggat gcatagtaat	180
aggtagatag agaaagtctt taggaggttag aatggacagg acttcacaat gcattaaatg	240
tagggagaaa aaaaatgatt cctgggttct tagcttgagc tagtagggat agtggttagaa	300
tttactgata tggaaaactg gaggaataag agtttggaag agaaagatgg caagttaaat	360
acctgtggga aatataatca cagacactaa ataggcagct gtgtgggtgg caaaggagag	420
ccatgggcta ggaacataca gtgggattcc ctggcatgtc attggttact gaagtcagag	480
tgatagagac agcctaagga gagaatncac acaggagaag aaagaactaa acattcagtg	540
gctggccaga ggatgagaaa cccaagagat tggactgttt aggagcaaca gtgttngaa	600
aaggagagaaa nggttgaaat t	621

<210> 59

<211> 631

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 8, 9, 11, 29

<223> N can be any nucleotide

<400> 59

ggntttannc nctggagctc caaagcagng gtaacaacgc agagtacgcc cattgcgtag	60
cgtgtacata aaggggttgg agctgaagga ggagataaag aagaagacag ccagaacctt	120
gtcctctgtc ggagatcgca gggatcttgg gccgtagata ggtataagca aaggggtgcat	180
agtagaaagt cactacagtg aggtgggtgc tgcaggtcga ataggccttc ttccctccct	240
ctgcagagtg catgtggttag acagcaagga gaatccggcc ataggaacat gcaatacaaa	300
tgaagggaaa cacaagaaaa atggtggtgc tcaaaaacac cgtgcactca tagaccagag	360
tatccgtgca ggctagggtc aacatagctg gaacatcaca gaaaaaatga ttgatggctc	420
tggacttgca atatgggata cggagtgcac ataccgtgtg agcacaagag ttgatggagc	480
ctatcatcca agatcctgtt atcatcagtg cacacactct tttcttcata cggatgagat	540
agtggagagg aaagcaata gccacataac gatcataggc cattgatgtc aggagcagcg	600
cttctgcacc tgctaaagtc aggaagaaga t	631

<210> 60

<211> 620

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 6, 10-11, 15, 18

<223> N can be any nucleotide

<400> 60

tggtantccn ntttctncc attggagctc ccaagcagtg gtaacaacgc agagtacgcc	60
ctccttgttt ctgagagtgt agatgaaggg gttataggag ataaagatca gggcaatatg	120

taggacaagg	acacagacac	tgacaacaaa	gttgattatc	tcattgacag	tggtgtctgt	180
gcaggccagc	ttcagcaggg	gtctcacatc	acagaagaag	tgggagatga	caaagtcate	240
acaaaagggc	aggccaaaca	tagatgttac	ttggacaata	gccatgccca	ggccaatcct	300
cagtgaacca	gatcccagtc	agacacaagc	cctcttacct	atgaataccg	taaggggttg	360
cagaagacca	catagcaatc	atatcccatg	gctatgagaa	gaaagcagtt	gttgatgcca	420
aaagtcacat	agaagagctg	agtgacacag	ccttgcatga	caataagcta	gtgaggattc	480
aagaggcgag	aaagcatatg	gggagtaatg	gccaccatgt	agcaggcttc	agagatagac	540
agcaatgctt	aggaaaaagt	acatggggccg	tactttctgtc	gtcttgagcg	tactgatggg	600
accagcttt	tgttcccttt					620

<210> 61

<211> 612

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 3, 5-6, 9-10, 20, 25, 37-38

<223> N can be any nucleotide

<400> 61

gtnannccnn	tgtagctccn	aagcngagct	aacaacnnag	agaacaacgc	agagtacgcc	60
cccgatgtac	ttgttcctac	tctttgctgg	atttgaaaac	ttcctcctgt	ccgtgatggc	120
ctatgaccgg	tttgtggcca	tctgtcacc	cctgcactac	atggtcatta	tgaaccctca	180
cctctgtgga	ctgctgggtc	tagcatcctg	gaccatgagt	gctctgtatt	ccttgctaca	240
aatcttaatg	gtagtacggc	tgctcttctg	cacagcctta	gaaatcccc	actttttctg	300
tgaacttaat	caggtcatcc	aacttgcttg	ttctgatagc	tttcttaatc	acatgggtgat	360
atattttaca	gttgcgctgc	tgggtggagg	ttccctcact	gggatccttt	actcttactc	420
taagataatt	tcttccatac	atgcaatctc	atcagctcag	gggaagtaca	aggcattttc	480
acctgtgcat	ctcacctctc	agttgtctcc	ttattttatg	gtgcaatcct	aggggtgtac	540
cttagtctgc	tgccacccgc	aactcacact	caagtgcac	agcctcagtg	atgtacactg	600
gggcaccccc	at					612

<210> 62

<211> 628

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-8, 13, 19, 22, 32, 35-41, 49

<223> N can be any nucleotide

<400> 62

gnnnnnnnat	tnatgcctt	tnttgattcc	cntnnnnnn	ncaagcagng	gtaacaacgc	60
agagtacgcc	ccctatgtat	ttcttcctaa	gatccaaata	ttaaaataaa	agacagtcac	120
cccaccacta	actaaagtag	tgtttcccac	acttctctat	taagaagcat	gtgagatact	180
tggtacaaac	ataacatcct	ggccccaccc	caaagccact	caatcaaata	ctccagggaa	240
gggatctagg	aattcgtagg	tttaacgagt	gccccaaaat	gattattacc	tggtggagaa	300
tctaggcaac	aatgaattaa	ggaaagctct	ctaccatttg	gtactggtag	cagggttgag	360
gatcacaggg	aagagggtaa	gcatatcaga	ctagcagagc	tgccagaact	cgggctttca	420
aaagagaggt	gccaccctct	cccatgtcca	tgtaagtagc	aaacaaccct	ctcatgtaca	480
ctctgaggaa	caagggggcg	tactttctgtc	gtcttgagcg	tactgatggg	accagcttt	540
tgctccctta	gtgaggggta	attgcgcgct	tggcgtaatc	atggtcatag	ctgtttcctg	600
tgtgaaattg	ttatccgctc	acaattct				628

<210> 63

<211> 627

<212> DNA

<213> Homo Sapien

<220>
 <221> variation
 <222> 191, 214, 263, 271, 277, 303, 325, 333, 363, 418, 528, 570, 596, 614
 <223> N can be any nucleotide

<400> 63
 tgtagctcca aagcagtggt aacaacgcag agtacgccct cttgggttacg taagggaata 60
 gatgatggg ttcagcatgg gggtgactac agtgtacatg acagtggcca cacggtccca 120
 ctctgctcgc gtcgggacgt ggcctggaag tagactgcaa tgactgtcct atagaaagag 180
 gtcaccaca nccaggtggg agccacaggt gggncacaag tcccggagcc tcccagaggc 240
 ttgagggcag ctggagcacg ggnaagcttg ntatggnncc acaaggaggc gaggatgagc 300
 agnaagggag tgaccaccac ttgcngcgcc ctnggtgaag atgagcagct tggatgtggt 360
 ggntgtcaga gcacgagagc ctttaagaga ggcttggtgg gtcacagaag aagtgggngc 420
 actttgtggg aaagcacaga aaggacaagc gagccatgag caggatatac aggagggagt 480
 tgtccgtggg acaccagcca tgccattcca accagggctg cgcacatngc cggggacatt 540
 ctggtgggat aaggggaagg gtgccggaatn ggcacgtatc agtcataggc cttggncgcc 600
 agaagacagc tttnaattta ccccagg 627

<210> 64
 <211> 605
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 5-6, 9, 11, 14, 17, 21-22
 <223> N can be any nucleotide

<400> 64
 gttannccnt ntanctncaa nngaggtaac aacgcagagt acgccccca tgtatttgct 60
 tcttgtccaa cctgtccttt gtagagatct gctacaccac cgttgtggtg cccttgatgc 120
 tttccaacat ttttggggcc cagaagccca ttccattggc tggatgtggg gcccaaatgt 180
 tcctctttct cacacttggt ggtgctgact gtttctctt ggcgatcgtg gcctatgacc 240
 gctatgtggc catctgccac cctttgcact acccctcatc atgacctgca gtctgtgcgt 300
 gcagatgctg ggcggcgtg tgggcctggc cctcttctc tccctgcagc tcaccgcctt 360
 aatcttcacc ttgcccttct gcggctaccg ccaggaaatt aaccacttcc tctgcgatgt 420
 acctccgtcc tgcgcctggc ctgcgctgca tccgtgttca ccaggctgcc tctatgtcgt 480
 gagcatcctc gtgctgaccg tccccttctt gctcatctgc gtctcctacg tgttcacac 540
 ctgtgccatc ctgagcatcc gttctgctga gggccggcac caggcctttt caactgctct 600
 tccgg 605

<210> 65
 <211> 609
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 10, 14-15, 19, 22, 67, 603
 <223> N can be any nucleotide

<400> 65
 tgtagctccn aagnngagnt ancaacgcag agtacgcccg cggaatctat agatgaaagg 60
 gtttgngag tcagaagaag gaagtacatg ggagtcataa cagtgtagga caatgatggc 120
 agcttcttgc cctcaggtga attatttgat ttaggccgga agtaggtgag gcttaatgat 180
 atatagaaaa gagagacaac aaggaggtgt gaggaacatg tagaaaaggc tttattcttc 240
 ccttttagctg atgggatctt gaggatggca gcagcaatgt gagtatagga acacaagatc 300
 agcaagcggg ggatcatgac caccagaatg gttccgacga tggcgtagat ctcaaagagt 360
 gctgtgtctg cacagaccag cctcagcaca ggtgggctgt cacagaagaa gtgggtcacc 420
 ttgttggtgc cacagaatgg aaaactgaag agccatgttg tctgcacagt agctacagga 480
 aagcctggga accaggaggt agcagccagt ttggcacgag tcctttgggt catgatgact 540

gggtaagtgc aagggactgc agatggccac atagccggtc atatgccatt ggtagcccag 600
gangaagct 609

<210> 66
<211> 617
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 6, 20
<223> N can be any nucleotide

<400> 66
gttatncctt gttgctcccn agcagaggta acaacgcaga gtacgcccct atttctcaga 60
tatangatga agggggttcag aaaaagaatg agcaaagaaa atctggggcca ggcgggcatc 120
aaaagaaata gtcttggtgct caaccagaaa gtctgcaatc attttagggg tagcagaaga 180
ggcaacacat acgtctataa atgacagggt ggcaagaagc aaatacattg ggggcgtact 240
tctgtcgtct tgagcgtact gatggtaccc agcttttgtt cccttttagtg agggttaatt 300
gcgcgcttgg cgtaatcatg gtcatactgt tttcctgtgt gaaattgtta tccgctcaca 360
attccacaca acatacgagc cgggagcata aagtgtaaag cctgggggtgc ctaatgagt 420
agctaactca cattaattgc gttgcgctca ctgcccgtt tcagtcggga aacctgtcgt 480
gccagctgca ttaatgaatc ggccaacgcg ccggggagag gcggtttgcg tattgggcgc 540
tcttcgctt ctcgctcact gactcgcttg cgctcggtcg ttcggcttgc ggcgagcggt 600
atcaagctca ctcaaat 617

<210> 67
<211> 621
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 10, 17, 28, 277, 286, 370, 373, 422, 513, 527, 536, 545, 548, 550, 558,
563, 566, 572, 574, 579, 583, 603-604, 609, 621
<223> N can be any nucleotide

<400> 67
gggttttacn ctgtgcnccc ccagcagngg taacaacgca gagtacgccc ttgttgcgaa 60
gaaataaatg aatgggttta aaatagacgt gaagatggtg tagaatacag caaggacttt 120
gtcaactgag taactgctga agggccacac atagatgaaa atacacgatc caaagaataa 180
agtgaccaca gtgatgtgag cagtcaatgt ggagtgggcc ttcaccatgc ttacagagga 240
gcgattccta actgtaataa gtattacagt gtagganaca accaanagga gaaaggaact 300
cagagaaaga aagccaccat ctgcaactat tagtaggctg acaacataag tgtctatgca 360
ggctaacttn gtngctagag gaaggtcaca gaaaaaaact atctacctta ttaggaccac 420
anaatggcag attaaccgtg aatgccaaact ggctggtggt atggatgaag cccacaaacc 480
aggaaatgag gacgagcaca acacatacac agnagctcat gattganatg tagtgnggag 540
gtttncntn gctcatancc gtnttngcca tngnaactng gancaccatt ttacttgcag 600
tgnnggagng aacatgaaat n 621

<210> 68
<211> 611
<212> DNA
<213> Homo Sapien

<220>
<221> variation
<222> 5-6, 9-10, 17, 19, 298, 464, 519, 549
<223> N can be any nucleotide

<400> 68
 gttannccnn tttaatncna tggagctcca aagcagtggg aacaacgcag agtacgcccc 60
 cgatgtactt gttcctactc tttgctggat ttgaaaactt cctcctgtcc gtgatggcct 120
 atgaccgggtt tgtggccatc tgtcaccccc tgcactacat ggtcattatg aacctcacc 180
 tctgtggact gctggttcta gcatcctgga ccatgagtgc tctgtattcc ttgtacaaa 240
 tcttaatggt agtacggctg tcttctgcac agccttagaa atccccact ttttctgnga 300
 acttaatcag gtcacccaac ttgcttggtc tgatagcttt cttaatcaca tgggtgatata 360
 ttttacagtt gcgctgctgg gtggagggtcc cctcactggg atcctttact cttactctaa 420
 gataatttct tccatacatg caatctcatc agcttagggg aagnacaagg cattttccac 480
 ctgtgcatct cacccttcag ttgctcctta ttttatggng caatctaggg gtgaccttag 540
 tttgtctgnc acccgcaact cacacttaag tgcaacaacc tcagtgatgt acactgggggt 600
 caccatgc c 611

<210> 69

<211> 625

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2, 4-6, 11, 15-16, 40, 42, 45, 47, 52, 61, 64-66, 74-75, 77, 80, 586, 618

<223> N can be any nucleotide

<400> 69
 gngnnncgag nttannccctt ggactcccag tagagctacn angantncgc cnagcgcgca 60
 nttnnnccag ggtntntntn gtatcaccaa tgaatagaaa acagacacca ccttgtccct 120
 gcctagcaag tagctggagc tgggtcgcaa gtacacgaaa agggctgtcc caaacagcag 180
 agtcaccacc atcagatgcg aggcacacgt gttgcaggct ttccatcggc cctctgtgta 240
 agggatcttc aggaccgcag aactatgta accataggag ataaggagtt ggaggaacga 300
 tgttctccg acggtgacca ccacgaggaa attcaccact tgactgagga aggtgtcaga 360
 gcaagacaga gccaggactg gtgggagggt gcagaagaag tgggtgatga tgttgggtcc 420
 gcaaaagtga agcctaaata tggagctggc ctggatcagg gagctcagga agccaccaac 480
 atatgcccc accaccatgc gtgtacagag gccctgggtc atgatagtgg ggtanagaag 540
 ggggctggag atggcttgca tatcggctcg atgccatagc agtcangagg aggcactcaa 600
 gacagaccca tgccgacnaa gaaat 625

<210> 70

<211> 626

<212> DNA

<213> Homo Sapien

<220>

<221> variation

<222> 2-5, 17-18, 24, 34, 42, 584

<223> N can be any nucleotide

<400> 70
 gnnnntttta cccctgnngc acanagcagt ggtnacaaac cncgagtacg cccctatgt 60
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 tgtctgccac cctctgcact atatgatcat catgaacccc cactctgtg gcctcctggg 180
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 ccagctggcc tgccttgata ccttcttgaa cagcacgttg atatacttta tgacgggtgt 360
 gctgggctgt tttccctcc ttgggatcat tttctcttat tcacgaattg cttcatccat 420
 aaggaagatg tcctcatctg ggggaaaaca aatagcactt tccacctgtg ggtctcacct 480
 ctccgtcggt tctttatatt atgggacagg cattggggtc cacttcactt ctgcggtgac 540
 tcacccttcc cagaaaatct ccgtggcctc ggtgatgtca ctgnggtcac ccccatggtg 600
 accctttcat ttacaccctt agcaag 626

<210> 71

<211> 633
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-10, 4, 7, 10-11, 33, 35, 39, 50, 57, 60, 61-62, 65, 84-85, 441, 615, 617, 632
 <223> N can be any nucleotide

<400> 71
 gnnnnnnnnn gtnnatnccn nttttaatgc cantngagnt aacaacgcan gagtacnccn 60
 nngngtacgc ccagggttca accnntgaat agaaaacaga caccaccttg tccctgccta 120
 gcaagtagct ggagctgggt cgcaagtaca cgaaaagggc tgtcccaaac agcagagtca 180
 ccaccatcag atgcgaggca cacgtgttg aggctttcca tcgccctctg ctgaagggat 240
 cttcaggacc gcagacacta tgtaaccata ggagataagg agttggagga acgatgttcc 300
 tccgacggtg accaccacga ggaaattcac cacttgactg aggaagggtg cagagcaaga 360
 cagagccagg actggtgggg aggttgcaag aagaagtggg tgatgattgt tgggtcccgc 420
 aaaagtgaag gcctaaatat ngagctggcc tggatcaggg gagctcagga agccacaaca 480
 tatgccccaa ccaccatgcg tgtacagagg ccctgggtca tgatagtggg ggtngagaag 540
 ggggcctgga gatggctgca tatcggtcgt tgccatagca agtcaggagg aggcacttca 600
 gacagaccca tgccncnaag aaaaaaact gnc 633

<210> 72
 <211> 614
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 2-11, 14-17, 19-20, 22, 28, 42-43, 45, 51, 76, 82-83, 85, 101, 106, 110, 112-114, 117, 119, 135, 139, 434, 507, 520, 614
 <223> N can be any nucleotide

<400> 72
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 gttaaccctc actaanggta anntnagctg gaacacatca ntacgntcan gnnngcncna 120
 tgaccggttt gtggnatnt gtcacccctt gcactacatg ggtcattatg aaccctcacc 180
 tctgtggact gctggttcta gcacccctga ccatgagtg tctgtattcc ttgctacaaa 240
 tcttaatggt agtacggctg tccttctgca cagccttaga aatccccac tttttctgtg 300
 aacttaatca ggcattcaac ttgcttgttc tgatagcttt cttaatcaca tggatgata 360
 ttttacaggt tgcgtgctg ggtggaggtc ccctgactgg gatcctttac tcttactcta 420
 aagataattt cttncataca tgcaatctca tcagctcaag gggaagtcaa ggcatttttc 480
 acctgtgcat ctacccctca gttgctnctt attttatggg gcaatcctag ggggtgacct 540
 agttctggtg gcacccgcaa ctacactcaa tgcacaagct cagtgatgta cactgtggca 600
 cccatgctga accn 614

<210> 73
 <211> 630
 <212> DNA
 <213> Homo Sapien

<220>
 <221> variation
 <222> 3-6, 8-10, 17, 124, 144, 146, 173, 184, 193, 212, 220, 266, 274, 276, 288, 306, 419, 423, 448, 474, 485, 500, 552, 555, 576, 588, 591, 606
 <223> N can be any nucleotide

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 cctatgtatt ttttctatt ctggacacgc tactcctgac cgggatggcc tatgaccggg 120

ttgnggctgg	ctgccaccct	ctgnantata	tgatcatcat	gaacccccac	ctntgtggcc	180
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tgatgcacct	aatcttctgt	aaagantttg	aaantncaca	ttttttntg	cgaactgacg	300
tacatnctcc	agctggcctg	ctctgatacc	ttcctgaaca	gcacgttgat	atactttatg	360
acgggtgtgc	tgggcgtttt	tccctccttg	ggatcatttt	cttcttattc	acgaattgnt	420
ttnatccata	aggaagaatg	tcctcatntg	ggggaaaaca	aataagcact	tttncacctg	480
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<210> 74

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<213> Unknown: Synthetic construct

<220>

<221> variation

<222> 3,12

<223> N can be any nucleotide

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<223> y = t/u or c

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ccnatgtayt tntccta

18

<210> 75

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<222> 3, 12

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<221> variation

<222> 9

<223> y = t/u or c

<400> 75

ccnatgtayt tntcctc

18

<210> 76

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<212> DNA

<213> Unknown: Synthetic construct

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<222> 3, 12

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<221> variation

<222> 9

<223> y = t/u or c

<400> 76

ccnatgtayt tntcctg

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<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 77
ccnatgtayt tntctcctt

18

<210> 78
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<222> 3, 12
<223> N can be any nucleotide

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<222> 9
<223> y = t/u or c

<400> 78
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18

<210> 79
<211> 18
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<213> Unknown: Synthetic construct

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<222> 3, 12
<223> N can be any nucleotide

<221> variation
<222> 9
<223> y = t/u or c

<400> 79
ccnatgtayt tntctcttc

18

<210> 80
<211> 18
<212> DNA
<213> Unknown: Synthetic construct

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<223> N can be any nucleotide

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<222> 9

<223> y = t/u or c

<400> 80

ccnatgtayt tncctcttg

18

<210> 81

<211> 18

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<220>

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<223> N can be any nucleotide

<221> variation

<222> 9

<223> y = t/u or c

<400> 81

ccnatgtayt tncctcttt

18

<210> 82

<211> 18

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<223> N can be any nucleotide

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<222> 9

<223> y = t/u or c

<400> 82

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18

<210> 83

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<221> variation

<222> 9

<223> y = t/u or c

<400> 83

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18

<210> 84
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<400> 84
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18

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18

<210> 86
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<221> variation
<222> 9
<223> y = t/u or c

<400> 86
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18

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<222> 9
<223> y = t/u or c

<400> 87
ccnatgtayt tnccttttc 18

<210> 88
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<400> 88
ccnatgtayt tnccttttg 18

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<222> 9
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<400> 89
ccnatgtayt tnccttttt 18

<210> 90
<211> 18
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<223> y = t/u or c

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18

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<223> y = t/u or c

<400> 92

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<210> 106
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<212> DNA
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<222> 4, 7, 10, 13, 20, 23, 26
<223> N can be any nucleotide

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<222> 1, 2, 8, 12, 15
<223> y = t or c

<220>
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<222> 11, 29
<223> r = a or g

<400> 106
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31

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<222> 1
<223> y = t or c

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<222> 3, 14, 20, 26
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<222> 8
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<210> 108
<211> 32
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<220>
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<222> 6, 18, 30
<223> r = a or g

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<222> 11
<223> k = t or g

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<222> 17
<223> w = t or a

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<222> 26
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<210> 109
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 <222> 5, 16
 <223> s = g or c

<400> 109
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32

<210> 110
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 <213> Unknown: Synthetic construct

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 <222> 4, 7, 10, 16, 22
 <223> N can be any nucleotide

<220>
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 <222> 1, 9, 13, 19, 25
 <223> r = a or g

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 <223> k = t or g

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 <222> 12
 <223> w = t or a

<220>
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 <222> 11
 <223> s = g or c

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27

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 7, 11, 16, 18, 21, 209, 231, 258, 259, 266, 267, 269, 282, 287, 289,
 301, 308, 314, 315, 316, 319, 321, 325, 329, 337, 338, 339, 346, 368, 383,
 385, 393, 398, 412, 413, 416, 417, 420, 439, 440, 442, 447, 453, 459, 474,
 479, 484, 488, 499, 508, 513, 521, 526, 536, 541, 549, 559, 574, 579, 587,
 590, 596, 597, 601, 602, 610, 618, 622, 633, 635, 648, 649, 650, 652, 654,

661, 666, 688, 690, 692, 698, 705, 713, 720, 724, 726, 731, 732, 736, 771,
788, 790, 795, 801, 802, 807, 811, 817, 829, 836, 840, 846, 849, 850, 855,
859, 870, 872, 874, 877, 878, 886

<223> n = any nucleotide

<400> 111

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tatctgcaga attcgccctt ctgttacgca ggaatatata aaggggttac tgaggataa 120
ataaatgggt tactgaggaa taaataaatg gggtactgag gaacaaatac atagggttga 180
aagaactgta aaatagaaaa aggacctntt gctgctctc aggatggcgg nacttagggg 240
ccatgtacat gacgatgnng ctgccnntna agagtccac tntcancng cctcagccc 300
ncttttntct cacnnncnt nttntctnc cctctnnnc tcttntcttc ctattcccc 360
ccctccnct cctccctttt gentnaccat tgnccctnat ccctttaatt cnntcnntcn 420
tctccctct attccttcnn tntcgnctt cantctctnc ctctttctcc ccnctttct 480
ctctctnct ctctctctng tcctctctng tcttctctt nctanttc ctctancctt 540
ntcttatnct tctctatnct cctctcatct cacntctct cctctctnct tacttntct 600
nctcttccn ctccgtctc cctctctct tctnaccgc acccctcnnt cntnctctct 660
ntctnctct cactctctcc tctccctnct tctcactnt ctcnctctct acntcctatn 720
ctcncttct nctttnactt tctcagctc tctctctct ctctacgac ntttatctc 780
ttatctcnct catcnccctc nttctnctc nctattnact ctttctctc atactntatn 840
ctctntcnnt cttnatnct cctctctctn tnanccntc actgcn 886

```

<210> 112

<211> 625

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 13, 31, 36-37, 40, 45-48, 50, 53-54, 61, 63, 67-68, 70, 473, 512,
523, 526, 535, 542-543, 545, 549, 558, 566, 571, 582, 589, 593-594, 603, 612-
614, 616, 621, 623-624

<223> n = any nucleotide

<400> 112

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gctgctcgag cgncgcagcg tcggcagtg nagggnnatn tgccnnnntn gcnnttagat 60
nanaggnntn agtatggggg tgaccacagt ggtacataac tgaggctgtt gcacttgagt 120
gtgagttgag ggtggcagca gaactaaggt acaccctag gattgcacca taaaataagg 180
agacaactga gaggtgagat gcacaggtgg aaaatgcctt gtacttcccc tgagctgatg 240
agattgcatg tatggaagaa attatcttag agtaagagta aaggatccca gtcaggggac 300
ctccaccag cagcgcaact gtaaaatata tcaccatgtg attaagaaag ctatcagaac 360
aagcaagttg gatgacctga ttaagttcac agaaaaagt ggggatttct aaggctgtgc 420
agaaggacag ccgtactacc attaagattt gtagcaagga atacagagca ctnatggtcc 480
aggatgccag aaccagcagt cacagagggt gngggtttca tantgncct gtagnctcag 540
cnncngacna gatggccnca aaccgntct nggcctcac gncctggna ggnngtttct 600
tantccacca cnnntnttct nannc 625

```

<210> 113

<211> 625

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 6-7, 30, 113, 128, 137, 142, 150, 157, 174, 297, 310, 313, 335, 354,
356, 377, 382, 385, 389, 393, 421, 429, 431, 433, 435, 438, 440, 442-443,
446, 455, 457, 465, 467, 477, 488, 491, 501-502, 504, 508-509, 515, 522, 525-
526, 529-530, 542, 557-559, 561, 564, 565, 568, 577, 579-581, 584, 587-589,
591, 596-603, 607-610, 612-613

<223> n = any nucleotide

<400> 113

```
catgcnnagag caggctcgag cgccggcagn gtgagggata tctgcagaat tcgcccttcc 60
tatgtacttt ttcctgagcg tatacacaat cccatcatgt actggggaga agncagacca 120
tatcattnac aagctgnctt tngcagatgn actttgnttt ctcattaggc tgcncagagt 180
acttcctcct ggcagccatg gcttatgacc gctgtcttgc catctgctat cctttacact 240
acggagccat catgagtagc ctgctctcag cgcagctggc cctgggctcc tgggtgngtg 300
gtttcgcgcn cantgcagcg cccacagccc tcagnagcgg tcttgcctct ctgngncccc 360
cgtgccatta accactnctt tngcngcant gcnccctgca ttgtcttgct ctgcccacca 420
nacagcagna nancntgngn cnnttngatc gctgntnecg tctcngntct cactccnttc 480
caccttttnc ntcgattcc nntntccnnc tcgcnctcct gncnntcnn tctcctcttc 540
tnaacgcgct ctcggannng nctnnatgnt cgtctcntnn ntgngcnng ncagcnnnnn 600
nnccannnn tnngtgcgcc gctcc 625
```

<210> 114

<211> 651

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 2, 12-13, 20, 23, 188, 375, 399, 402, 416, 443, 460, 472, 474-475, 480, 484, 487-488, 502, 505, 522-523, 529, 532, 537-538, 546, 553, 555, 557, 561, 564-565, 573, 575, 577, 581, 583, 586, 591, 594, 617, 634, 636, 643

<223> n = any nucleotide

<400> 114

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gnttaagccc tnnccctctn gangcatgct cgagcggccg ccagtgtgat ggatatctgc 60
agaattcgcc cttgttccgc aaacaataga tgaaaggatt aagtgaagga gtgcccaccg 120
catagaagag accaaagaac ttgcccctcc cttgggcata cggatttttg ggctggaggt 180
agacagcnat gactgagctg tagaagaggg tgaccacagt gagatgggag gacaggtcc 240
caaaggcctt tctccatgct gtggcagagt taatcctcag cactgcctgg gcagtggctc 300
cataagaggc aaggatgagg ctgagaggca caaccacgaa gatgacactg gacacagcca 360
actggatttc attgnaggag gcattctccac aggagagtnc gnatcagaga tgggancctc 420
acataaaaaa gtcattctatc tgntgggtggg gacagaatgn ccatgtggag gntnnatgtn 480
cgtntcnac ctcttatttt tnttncctt ttctttcgct cnntcccnt tntccnct 540
cgccanttcc atnncntct ntcnntttt ttntntnacc ntntntcat ntentctct 600
tattctctt ctcttgntc tcccttctct ctentnttc canctctcc g 651
```

<210> 115

<211> 850

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 3, 15, 279, 288, 292, 295, 296, 299, 307, 309, 317-319, 322, 326-327, 329, 335, 340, 343, 345-346, 354, 362, 367-368, 377, 380-382, 386, 391, 394, 396, 399-400, 410, 412, 415-416, 418, 433, 436, 442, 444, 451, 455, 466, 468-469, 471, 474, 482, 488, 490, 500, 505, 514, 516, 522, 530, 537, 548, 550, 552, 559, 562-565, 569, 570, 571-573, 576, 581, 592, 597, 603, 605-606, 608, 617, 619, 624, 627, 630, 635-636, 643, 647, 653, 661-663, 667, 673-675, 678, 690, 697-698, 709-711, 720, 724, 727, 731, 736, 746, 760, 768, 771, 783-784, 789, 791, 794, 796, 797, 800-801, 808, 810, 816, 818, 821-822, 832, 836

<223> n = any nucleotide

<400> 115

```
ggntctcggt acaanacttg gccctctaga tgcattgctg agcggccgcc agtgtgatgg 60
```

```

atatctgcag aattcgccct tccaatgtat ttattcctgt tatttggaga cctggagagc 120
ttcctccttg tggccatggc ctatgaccgc tatgtggcca tctgcttccc cctgcactac 180
accgccatca tgagcccat gctctgtctc gccctgggtg cgctgacctg ggtgctgacc 240
accttccatg ccatgttaca cactttactc atggccagnt tgtgcttntg tncennacna 300
ttgttgntnc cccactnnnc tntgtntna gtctnctctn ccntnnactg ctctcctct 360
tntccnnga gtccctcngn nncgtngtcg nttncngcnn tcaattgcan tncnncntc 420
atcctttctt tantntcca tntnttcaat nattnctctt tatccnncnt ntcnccctcc 480
anctcctnnc tagcttactn tttctgtctc tccngngctc anccctttcn ccataatntc 540
ttctctnncn tntctctcnc tnnnncccn nnntctcgt ntctctgtct cntcttnacg 600
tcntnnncnt tatttantnt ctncnccnctn tctcngctc cancgcncta ccngccctat 660
nnctcctcc ganntgntc atggcatctn cacattnngc cctactatnn ncgatctatn 720
ttcncgncat ntattncaca tccacntgca ctctactcnc ctctctance nccgtacatc 780
gennctacng ntgnncntcn nccgctcctn cggcncnat nctccactt tntctnngtc 840
ccccctccg
850

```

<210> 116

<211> 620

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 451, 479, 501, 533, 542, 550, 553, 561, 572, 582, 585, 600, 604-605

<223> n = any nucleotide

<400> 116

```

gatgcatgct cgagcgcccg cagtgtgatg gatatctgca gaattcgccc ttccaatgta 60
ctttttcctg aagaacctct ctgttttgga tctgtgctac atctcagtca ctgtgcctaa 120
atccatccgt aactccctga ctgcgagaag ctccatctct tatcttggct gtgtggctca 180
agcctatattt ttctctgcct ttgcatctgc tgagctggcc ttccttactg tcatgtctta 240
tgaccgctat gttgccattt gccacccct ccaatacaga gccgtgatga catcaggagg 300
gtgctatcag atggcagtc caccctggct aagctgcttt tctacgcag ccgtccacac 360
tggcaacatg tttcgggagc acgtttgcag atccaatgtg atccaccagt tcttcctgta 420
catccctcag gtgttggccc tggtttctct ngagggtttt tttgtagagc tttgaccnng 480
ccctgagcct caatgcttgg ntctgggatg ctttattccc atgatgatct ccnattttcc 540
anatctctn aanggggctc nagaatccct tnaggaccag antcnagcta aaagcctttt 600
cccnctgct tccccccag
620

```

<210> 117

<211> 628

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 5, 9, 403, 505, 552

<223> n = any nucleotide

<400> 117

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tggcnctcng atgcatgctc gagcggccgc cagtgtgatg gatatctgca gaattcgccc 60
ttccaatgta tttgttctct ttatttggag acctggagag ctctcctctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc ccctgacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggt gcgctgtcct ggggtgtgac caccttcac gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgtc tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggctc attcttgcac cccattccta ctnatccttg ggtcctatgc 420
aagaattgtc tctccatcc tcaaggtccc ttcttctaag ggtatctgca aggccttctc 480
tacttgtggc tcccaccctg tctgnggtgt cactggttct atggaaccgt tattggtctc 540
tacttatgct cntcagctaa tagttctact ctaaaggaca ctgcatggct atgatgtaca 600

```


ctgtggtgac ccccatgctg aaccctt

628

<210> 118

<211> 783

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 17, 25, 184, 187-188, 199, 202, 206, 212, 214-215, 223, 227-228, 232, 248, 250, 252-253, 255-256, 261-264, 266, 268, 271, 273, 276, 278, 284, 289, 292, 295-296, 298, 300-302, 306, 310, 315-316, 320-322, 325, 329, 333, 337, 340-341, 346, 349, 355, 369, 371, 373-374, 379-380, 383-384, 387-388, 391, 402, 407, 409, 417, 419-420, 436-437, 441-442, 445, 447-448, 450, 456-458, 461, 469, 472, 477-479, 486-487, 490, 493, 503, 510, 512, 517, 530, 540, 542, 544, 552-553, 565, 572, 587, 595, 597-598, 600, 611, 614, 617-618, 622-623, 625, 634-636, 639, 644-645, 646, 652-653, 663, 665, 668, 673-674, 679, 681, 683, 695-696, 699, 706, 710, 712, 716, 725-726, 731-732, 741, 745, 748-750, 763, 771, 774, 776, 772, 774-775, 777-778, 780, 782

<223> n = any nucleotide

<400> 118

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 ttgttccctga gcaacctctc ctccctggag atttggtata ccacagcagc agtgcccaaa 120
 gcactggcca tcctactggg gagaagacag accatatcat ttacaagctg ccttttgcag 180
 atgnacnntg ttttctcant angccntaca gngnncatgt ttncgcnngc cntgacttat 240
 gacgcgcntn cnnccntatc nnnntntnct ntnacnncac ttentcatna tntgnncntn 300
 nnttcnccn tggcnctcn nntcnccgnc ttncctntgn ncgtentcnc ccttnggcct 360
 gcatctctnc ntnntccnnc cncnccnct ntcttctctt cntacctntt ttctgtntnn 420
 tccctccct ctctgnntgc nntcnncnnc catctnnntg ntctgatcnc tntctnnnt 480
 ccactnngtn ctntctctc gntctctctn cncgcncct gcatcactgn gcattatatn 540
 cncngtctca tnnctatctt ccgtncctgt cnccttctct ctatgcncga cgtentntn 600
 tactatcgtc ntentcnnat tnnngcctgt tccnnngcnc ccgncntcc anntactctc 660
 cangntctc ctntccnt ntncctgtcta attcncntnt accgntctn gnetentctt 720
 cgtenntccc nnttctctc nctcncgncn cnttccagct ntnanttct antnngnncn 780
 cnc 783

<210> 119

<211> 674

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 1, 2, 114, 207, 212, 253, 261, 294, 316-317, 325, 327-329, 333-334, 340, 345, 352, 355, 364, 382, 384, 393-394, 397, 414, 418, 424, 426, 431, 440, 447, 449, 452, 455, 462, 467, 474, 482, 486, 492-493, 496, 500, 503, 509, 516, 519-520, 525, 532, 534, 539, 544, 550, 552, 555, 559, 564, 566, 573, 576, 586, 591, 594, 598, 605, 608, 610-611, 618, 626, 629, 635, 638, 644, 660-661, 666, 669

<223> n = any nucleotide

<400> 119

nntagatgca tgctcgagcg gcccgccagt gtgatggata tctgcagaat tcgcccttcc 60
 tatgtatttc ttccctggcca acctgtcctt cttggagacc tggatcatct ctgngactgt 120
 gcccaagtta ctgtttagtt tttggtctgc gaacaacagc atctctttca cactctgtat 180
 gatacaactg tacttcttca ttgctcncat gngcacagaa tgcgtgcttc tggccgccat 240
 ggccatgac cgntatgtgg ncatctggcg cccactccac tacccaacca taantgagcc 300
 atgggctcct gctccnncct cgctntnnna tanngaaccn acagngtagc gncanctccc 360

```

tgtncgagaa tctacttcat cntnctgcct tannttntgt gggcccaatg tgcntaanca 420
cttngntctg nggacatttn ctccagnant tnaantctct tncctgnaca aganactgtt 480
cnttancttg annatnttcn ggnacattnt tcctanggnn ttggnacgag cntntctanc 540
accngcactn cncantaant gctncngtgc tantcngtgc cattcntgtg nctncccntt 600
tcatngcntn ncctccncng aaagcnaant aagtngngnt cttnactttc gcccccaacn 660
ncatcncant ggcc 674

```

<210> 120

<211> 643

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 359, 373, 439, 463, 506, 537, 564, 584, 594, 604, 610, 620, 633-634, 636

<223> n = any nucleotide

<400> 120

```

ggccctctag atgcatgctc gagcggccgc cagtgtgatg gatatctgca gaattcgccc 60
ttcctatgta ttttttctctg ttatttggag acctggagag cctcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc cctgcaacta caccgccatc atgagcccca 180
tgctctgtct cgccctggtg gcgctgtcct ggggtgctgac caccttccat gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgct tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtng 360
atatttatca tgnagaggct cattcttgct atccattcc tactcatcct tgggtcctat 420
gcgagaattg tctcctcctt cctcaaaggc cccttcttct aangggatc tgcaaggcct 480
tctctacttg gtggctcccc cctgncctgt ggtgtcactg ttcctattgg aaaccgntat 540
tgggactcta cttatgctca tcangctaag agttttactc ttangggaca ctgncaatgg 600
cctntgaagn tacccttggg gtggaccccc atnntngaac ccc 643

```

<210> 121

<211> 657

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 429, 447, 453, 484, 510, 519, 542, 544, 546, 549, 552, 561, 581, 587, 600-601, 613, 618, 620-621, 623, 632, 643, 655-656

<223> n = any nucleotide

<400> 121

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ggccctctag atgcatgctc gagcggccgc cagtgtgatg gatatctgca gaattcgccc 60
ttccaatgta ctttttctctg ttatttggag acctggagag cttcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc cctgcaacta caccgccatc atgagcccca 180
tgctctgtct cgccctggtg gcgctgtcct ggggtgctgac caccttccat gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgct tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggtc attcttgcat ccatttccta ctcacccctg ggtcctatgc 420
aagaattgnc tccttccatc tcaaggncct ttnttctaaa gggatatctgc aaggccttct 480
ctanttggtg ctccaccct gtcttggtgg tggcactgnt tctaattggga accggttaatt 540
gnancnctna cnttatgctc natcaactta aatagtttct nactttnaaa gggaccactn 600
ntcattggct tanggatngn ncnttggttt cntggaaatc ccnatcatc ttacnng 657

```

<210> 122

<211> 622

<212> DNA
<213> Homo sapiens

<220>
<221> variation
<222> 9, 536, 543, 587, 609, 616, 619, 621-622
<223> n = any nucleotide

<400> 122
atgaccctna gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc 60
cttccaatgt atttgttccg gtccaacctg tcctttttgg atattggctt tatctctaca 120
ataattccca atatgctaga tcatattagc tcaggaatta agctgatttc ttatggggag 180
tgtctgacac aactctatct ctctggccta tttgcagatc tggacaacaa ctttctcctg 240
gctgtgttgg cccttgaccg ctatgtggcc atcagccatc ctctccatta tggccctaacc 300
atgaactccc aacgctgtgt cctgttggtg gctgtgtcat gggatgatcac tattttacat 360
gccctagtgc ataccctcct agtgaccagg ctttccttct gtgggtccaaa tattatccct 420
cacttcttct gtgatctggc cccactcctg aagctggcct gctccagtac ttgtgtcaat 480
gatctgggtg tcatccttgt ggcaggaaca ctgctgaatg cgccctttgc tgcattctta 540
tgnccctact ttacattgca ttggccatcc tgagaattga ttccccnagg ggtatgcaaa 600
gggcccctnt ccagctcnc nn 622

<210> 123
<211> 610
<212> DNA
<213> Homo sapiens

<220>
<221> variation
<222> 4, 445, 568-569, 580, 587, 600, 607, 610
<223> n = any nucleotide

<400> 123
gcgncgcagt gtgatggata tctgcagaat tcgcccctcc aatgtatttg tttctgttat 60
ttggagacct ggagagcttc ctcttgttgg ccatggccta tgaccgctat tgggccatct 120
gttccccct gacttacacc gccatcatga gccccatgct ctgtctcgcc ctgggtggcgc 180
tgtcctgggt gctgaccacc ttccatgcca tgttacacac tttactcatg gccagggtgt 240
gtttttgtgc agacaatgtg atccccact tttctgtga tatgtctgct ctgctgaagc 300
tggccttctc tgacactcga gttaatgaat gggatgatt tatcatggga gggctcattc 360
ttgtcatccc attcctactc atccttgggt cctatgcaag aattgtctcc tccatcctca 420
aggctccctt ttctaagggt atctngcaag gccttctcta cttgcggctc cacctgcctg 480
tgggtgtcact gttctatgga accgttattg gtctctactt atgctcatca gccaataagt 540
tttactctaa aaggacactt gtcattggnnt atgatgtacn ctgtgngnac ccccatgctn 600
aaccctntn 610

<210> 124
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> variation
<222> 469, 477, 482, 484, 493, 500, 509, 524, 527, 530, 536, 542, 549,
553-555, 561, 571, 580, 581, 583, 591, 597, 602, 609, 617-619, 624-625, 627,
636, 638, 642, 645-646

<223> n = any nucleotide

<400> 124
ccttgggccc tctagatgca tgctcgagcg gccgccagtg tgatggatat ctgcagaatt 60

```

cgcccttctt tattcctgag tgaatatatg aggggggttg cactgctgtt aagagtggac 120
aggaaaatgg aaactagacg aacgtgacaa atccacgtgg atccagaaaa ataggaatca 180
ctgaatgcc aagggcaggt cacagaggag gaagaccagc actctgagca ggatgggtcat 240
gtacagcctg gtcaaggga tcttccggga tccacaaagg atcctgacca gcagaaccgg 300
gctggaccgg cagagaacca cacataaaaa aatcagccat gtgactgtga tgaaatctga 360
tgtttcacac caaacagaat caagcaccac tagacaggaa gccacagaac atccattcca 420
ggatgctctg cagcaggagc agggcccaga gcaggacaca cgactgctna ccaggtnntt 480
tngngtggct gcnagctctn cttaggatng tccccaaagg ttgncnngn cggtnntt 540
gnttgcttnt cgnnncccta nctatgcctt ngctcctgt nngcttgac nattggncct 600
cnccacgng gcttaannnt ctcnngncgc atttanancg tnatnntact tccctgtcgc 660

```

<210> 125
 <211> 632
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 2, 488, 505, 507, 586, 618
 <223> n = any nucleotide

```

<400> 125
gnccctctag atgcatgctc gagcgggccgc cagtgtgatg gatatctgca gaattcgccc 60
ttcctatgta cttcttctctg ttatttggag acctggagag cttcctcctt gtggccatgg 120
cctatgaccg ctatgtggcc atctgcttcc ccctgcacta caccgccatc atgagcccca 180
tgctctgtct cgccctgggt gcgctgtcct ggggtgtgac caccttccat gccatgttac 240
acactttact catggccagg ttgtgttttt gtgcagacaa tgtgatcccc cactttttct 300
gtgatatgtc tgctctgctg aagctggcct tctctgacac tcgagttaat gaatgggtga 360
tatttatcat gggagggtc attcttgtca tcccattcct actcctcctt gggtcctatg 420
caagaattgt ctctccatc ctcaaggctc cttcttctaa gggatctctg aaggccttct 480
ctacttgnng ctcccacctg tcttngngg cactgttcta tgggaaccgg tattggtctc 540
tacttaatgc tcatcaagct aatagttcta ctctaaagga cactgncatg gctatgatgt 600
acactgtggt gaccccnat gctgacccat tc 632

```

<210> 126
 <211> 642
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 331, 422, 435, 441, 462, 467-468, 471, 479, 500, 502, 513, 521, 537,
 543-545, 549, 551, 563, 565-566, 569, 577, 582-583, 586, 594, 596, 611, 614,
 620, 624, 631, 639-640

<223> n = any nucleotide

```

<400> 126
tctagatgca tgctcgagcg gccgcagtgt gatggatata tgcagaattc gcccttccaa 60
tgtacttgtt cctggcagcc atggcttatg accgctgtct tgccatctgc taccctttac 120
actacggagc catcatgagt agcctgtctc cagcgcagct ggccctgggc tcctgggtgt 180
gtgggttcgt ggccattgca gtgccacag ccctcatcag tggcctgtcc ttctgtggcc 240
cccgtgccat caaccactc ttctgtgaca ttgcaccctg gattgccctg gcctgcacca 300
acacacaggc agtagagctt gtggcctttg ngattgctgg tgtggttatc ctgagttcat 360
gcctcatcac ctttgtctcc tatgtggaca tcatcagcac catccttcag gatccccctt 420
gncagtggcc ggagnaaaag ncttttccac gtgctcctcg cntctcnncg nggtgctcna 480
tttggtatgg gtccacaagn tnttcttca cgnccgatt ntccattcaa aagatgncct 540
tgnnttttna ncaaaagctt ggnncnncgnc ctgaaanact gnnngtngact tcangnttta 600
aaactccttt natntcactn ttanggaac naggggcggn ac 642

```

<210> 127
 <211> 688
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 1, 4, 54, 154, 269, 284, 294, 327, 339, 342, 344, 360, 362, 366, 372-373, 379, 382, 390, 393, 395, 397, 402, 408, 410-411, 417, 425, 428, 433, 435, 442, 446-448, 456, 461, 468, 473, 476, 479, 485, 487, 489, 508-509, 514-515, 526, 532-533, 535, 537, 539, 547, 550-551, 553, 555, 559, 572, 578, 582, 587, 595, 597, 602-603, 609-613, 617, 619, 621, 630, 634, 636, 640, 650, 652, 660, 679, 681, 683-684
 <223> n = any nucleotide

<400> 127
 ntgngccctc tagatgcatg ctcgagcggc cgccagtgtg atggatatct gcangaattc 60
 gcccttccca tgtatttatt ccttagcctg ttggattccc agctgcacag ctggattgtg 120
 ttacacaact caccttcttc aagaatgtgg aaanctataa ttttttttct gtgacccatc 180
 tcaacttctc aaccttgccct gttctgacag catcatcaat aacatattat gtattttaga 240
 tateccctata tttggttttc tccccattnc agggatcctt ttgncttacc atanaattgt 300
 cctcctccat tccaagaatt ccattgncag acgggacgna tnangccttc tctacctgtg 360
 cntctnaccg gnnagtcgnt tntttatctn tgnantnccc tngggcgncn nccctgncct 420
 cagcnttngt cancnttctc cncacnnntt cgtcgtgtgt ncccagtnct gtncctnctnc 480
 tctctnctnc tttctgcctc cctccannng tctnncttctc tcagcnccct tnnngcnent 540
 gccagncncn nangntccnc cctctccctc cntgtctnct cnetcctntt cttentntcc 600
 tnnctcatnn nnncgncncn ncgctctccn cccntntctn tacgactccn gncgtctctn 660
 cgcctacgac ctcctgtgnc ncnncggg 688

<210> 128
 <211> 619
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 10, 46, 60, 322, 365-366, 464, 472, 475, 482, 493, 498, 498, 504, 517, 535, 543, 547, 556, 564, 584, 590, 600, 602, 610
 <223> n = any nucleotide

<400> 128
 gcgtgctgcn agcggggcgg cagagtgagc ggatatctgc agaatncgcc cttccgatgn 60
 atttctttct aagcaactta tctttcattg acatctgcta ctcttctgct gtggctccca 120
 atatgctcac tgactttctc tgggagcaga agaccatata atttgtgggc tgtgctgctc 180
 agtttttttt ctttgtcggc atgggtctgt ctgagtgcct cctcctgact gctatggcat 240
 acgaccgata tgcagccatc tccagccccc ttctctaccc cactatcatg acccagggcc 300
 tctgtacacg catgggtggtt gnggcatatg ttggtggtt cctgagctcc ctgatccagg 360
 ccagnnccat atttaggctt cacttttgcg gacccaacat catcaaccac ttcttctgcy 420
 acctccacca gtcctggctc tgtcttgctc tgacaccttc cttnagtcaa gncgncgaat 480
 ntccccgtgg tgntcacntg tcgngaggaa acatcgnttt cctccaaccc cttantctcc 540
 cangggntac catagngtct gcgngtcctt gaagaatcct ttngccaan cgggcgaatn 600
 gnaagccctn ccaccgcc 619

<210> 129
 <211> 697
 <212> DNA
 <213> Homo sapiens

<220>

<221> variation

<222> 17, 223, 238, 260, 304, 310, 315, 317, 322, 325, 327, 329, 341, 345-347, 350, 351, 356, 361, 369, 373-374, 378, 386, 391, 394, 396, 403, 414, 416, 426, 447-448, 456, 459, 461-462, 469, 473, 475, 477, 482, 488, 493-495, 504, 508, 511, 515, 518, 523, 527, 532-533, 537, 543, 548, 555, 558, 561, 570-571, 578, 580, 587-588, 592, 598-599, 601-602, 606, 608, 613, 619, 622-623, 634-635, 645, 648, 656, 658, 661, 665, 674-675, 682, 685, 687, 694-695

<223> n = any nucleotide

<400> 129

```

gcgggcgcagt gtgatgntat ctgacgaatt cgcccttccg atgtatttat ttctaagcaa 60
cttatctttc attgacatct gctactcttc tgctgtggct cccaatatgc tcaactgactt 120
cttctgggag cagaagacca tatcatttgt gggctgtgct gctcagtttt ttttctttgt 180
cggcattgggt ctgtctgagt gcctcctcct gactgctatg gcntacgacc gatatgcngc 240
catctccagc ccccttctcn accccactat catgaccagc ggcctctgta cacgcattgga 300
ggtngegcen tatgntngtt gnetnctng agctcctga nccannnctn ntcacntatt 360
ntaggetcna ccnntcngc tcccgntcca ncancnaacc ccttcgttc ctgnanactt 420
ctccancacg ttcctggctt ttctgcnnct gcctcncgnc nnccttatnc ttnangntca 480
cncctganct gcnntttctt ccangcngc ncgcncancc cgtctctnct gngaancct 540
ttncatnct gctcnatnct nctctcatn ntctctantn ctctcnnct cncgctcnn 600
nncctnctnct ctnaacctnt cnnatcctca cctnngatat cctcncgntc ttctcncntc 660
nttctnctgtc cganntcctc anacnctcc ctanncg 697

```

<210> 130

<211> 625

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 473, 502, 524, 547, 550, 567, 572, 590, 596, 614-615, 619, 623

<223> n = any nucleotide

<400> 130

```

ctctagatgc atgctcgagc ggccgcccagt gtgatggata tctgcagaat tcgcccttcc 60
tatgtattta ttccttagcc acttgccct cactgacatc tccttttcat ctgtcactgt 120
ccctaagatg ctgatgaaca tgcagactca gcacctagcc gtcttttaca agggatgcat 180
ttcacagaca tattttttca tattttttgc tgacttagac agtttcttta tcaacttcaat 240
ggcatataac aggtatgtgg ccactcgaca tcctctacat tatgccacca tcatgactca 300
gagccagtgt gtcattgtgg tggctgggtc ctgggtcatc gcttggtcgt gtgctctttt 360
gcgtaccctc ctcttgcccc agctttcctt ctgtgctgac cacatcatcc ctcaactactt 420
ctgtgacctt ggtgccctgc tcaagtggc ctgctcagac acctccctca atnagtttagc 480
aatctttaca ggagcattga cnggcattat gcttccattc ctgngcatcc tgggttctta 540
tgggcanatn tgggggtcac cattctncag anttcttta ccagggcatn tgcaangcct 600
tggccacttg tggnnccnc tcncg 625

```

<210> 131

<211> 657

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 344, 419, 443, 464, 486, 521, 524, 535, 537-538, 545, 552, 564, 567, 572, 584, 586, 588, 601, 604, 608-609, 611-612, 616, 618, 620, 622, 626, 629-630, 633, 638-639, 643, 645, 655

<223> n = any nucleotide

<400> 131

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ttggcctcta gatgcatgct cgagcgccgc cagtgtgatg gatatctgca gaattcgccc 60
ttgatacatg attgggttgc ggaaggaata aatcatcggg ttgcggaagg aataaataca 120
tcgggttgcg gaaggaataa atacatcggg ttgcggaagg aataaataca tcgggttgcg 180
gaaggaataa atcatcgggt tgcggaagga ataaatacat cgggttgcg aaggaataaa 240
tacatcgggt tgcgtaagga ataaatcatt ggggttgcgta aggaataaat cattgggttg 300
cgtaaggaat aaatcattgg gttgcgtaag gaataaatca ttgngttgcg taaggaataa 360
atctttgtgc tgggtaccgat ctatcatggg gttacgaaag ggaagaaata cattggaang 420
ggcgaattcc agcacactgc cgnccgctac tagtgggatc cganctcggg accaagcttt 480
gatgcntagc ttgagtattt taacgcccgc aacctaaaat ngcnttggcc ttacncnntg 540
gaccnagctt gncctccttg cgtnaanttt cnttatctct cctntntntc ttctccccc 600
ncanaatnnt nccccngntn ancacncann ttntatannc ctngngctcc cctantc 657

```

<210> 132

<211> 624

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 7, 27, 34, 39, 481, 484, 489, 493, 502, 520, 566, 614, 623-624

<223> n = any nucleotide

<400> 132

```

tggccncta gatgcatgct cgagcgnccg cagngtgang gatatctgca gaattcgccc 60
ttcctatgta tttattcctt aatgtcctct cgcttcttga tatttggtac tcttctgtgg 120
tcacacctaa gctcttggtc aacttccttg tctctgacaa gtccatctct tttgagggct 180
gtgtggtcca gctcgcttc tttgtagtgc atgtgacagc tgagagcttc ctgctggcct 240
ccatggccta tgaccgcttc ctatccatct gtcaaccctt ccattatggg tctatcatga 300
ccagggggac ctgtctccag ctggtagctg tgtcctatgc atttgggtgga gccaaactccg 360
ctatccagac tggaaatgtc tttgccctgc ctttctgtgg gcccaaccag ctaacacact 420
actactgtga cataccaccc cttctccacc tggcttgtgc caacacagcc acagcaagag 480
ngnccctcna tgncttttct gntctggcac cctctggcn gctgcaggca ttctcacctc 540
taccggcttg ggcttggggg ccaatnggga ggatgcgcct caagaacagg gagggagaaa 600
ggactcccca cttntgcctc ccnn 624

```

<210> 133

<211> 590

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 161, 185, 190, 221, 278, 303, 320, 337, 348, 360, 371, 387-388, 390, 393, 395, 402, 407, 409, 413-414, 423, 437, 449, 455, 459, 461, 464, 466-467, 468, 471, 475, 482, 484, 487, 489, 491, 493-495, 499, 500, 503-504, 510, 515, 519-520, 528, 538, 540, 541, 543, 546, 548, 555-556, 558, 563, 566, 568, 572, 575, 584-586, 588

<223> n = any nucleotide

<400> 133

```

ggagttgata tgaacgggtt aagtgaagga gtgcccactg catagaagag accaaagaac 60
ttgcccctcc cttgggcata cggatttttg ggctggaggt agacagcaat gactgagctg 120
cagaagaggg tgaccacagt gagatgggag gagcagggtc naaaggcctt tctccatgct 180
gtggnagagn taattctcag cactgcctgg gcagtggct ncataagagg caaggatgag 240
gctgagaggc acaaccacga agatgacact ggacacangc caactgtatc cattgtagga 300
ggnatctcca caggagagtn gaatcagaga tgggacnttc acattaanaa gttatttatn 360
tgctggcggg nacagatgcc caagcggnan ggngntatgg tnctggncna ttnttctgctc 420

```

canacccatt atctcangcc acatgtatnt cagcncnttna ntcncnntnt nagtntagtc 480
 tngntgntnt ncnnnattnn cncntctttn tccntcann tatcatntc attccttncn 540
 ncncanantt atggncncnc cgnacncnct cngtnactcc cctnnngncg 590

<210> 134
 <211> 655
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 2-3, 5-11, 17485, 506, 512, 514, 518, 525, 543, 578, 590-592, 602, 609,
 612, 616, 637, 646

<223> n = any nucleotide

<400> 134
 gnntnnnnnn ntgttancct cgtccctcta gatgcatgct cgagcgcccg ccagtgtgat 60
 ggatatctgc agaattcgcc ctccgatgt atttatttct acacagacac agtgacaatc 120
 tgatctctct tgcttttccc cacacactgc aacctctgcc tccacattca agtgattctc 180
 ctgcctcagc ctcttgagta gctggaatta cagatgtgag ccaccatgcc tggcctgtcc 240
 agatgttttt gaaacaaccc ccaccagcac tggagggagt caagggaaga caagccaggc 300
 atctgagctc ctctgtctct gcctttcctt ctcactgtcc ccagggtaac ccgtcaccac 360
 ccccatcacg aacccttca tctacacatt acgtaacaag ggcgaattcc agcacactgg 420
 cgcccggttac tagtggatcc gagctcggtta ccaagcttga tgcatagctt gagtattcta 480
 acgntcacc taaatagctt ggcgtnatca tngncccnag cttgntttct gtgtgaaatt 540
 tgntatccgc tcacaaattc cacacaacat acgagccnga agcaataagn nntaaagcct 600
 gnggtgccna angagngagc taactcacia ttaattncgt tggctnactt gcccc 655

<210> 135
 <211> 639
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> 4, 449, 480, 499, 510, 519, 524-525, 536, 543, 547, 550-551, 557-
 558, 564, 574, 581, 602, 615, 518, 621, 623, 627, 636, 639
 <223> n = any nucleotide

<400> 135
 ttnggccttc tagatgcatg ctcgagcggc cgccagtgtg atggatatct gcagaattcg 60
 cccttcctat gtacttggtt ctaagcaacc tctccttctt ggagatttgg tataccacag 120
 cagcagtgcc caaagcaccg gccatcctac tggggagaag tcagaccata tcatttacia 180
 gctgtctttt gcagatgtac tttgttttct cattaggctg cacagagtac ttcctcctgg 240
 cagccatggc ttatgaccgc tgtcttgcca tctgctatcc tttacactac ggagccatca 300
 tgagttagcct gctctcagcg cagctggccc tgggctcctg ggtggtgtgg tttcgtggcc 360
 attgcagtgc ccacagccct catcagtggc ctgtccttct gtggttcccg tgccatcaaa 420
 cacttcttct gtgacattgc accctggant gccctggcct gcaccaaacac cacaggcagn 480
 aagagcttgt ggcctttgng aatgccttgn tggggctanc cttngtcat gccctnatca 540
 cctttntcn nctatgngt acantcatta agncceaatc nctcatggga tccccttttg 600
 cnagtggccc ggcgngcnaa ngncctnctc cccgtncen 639

<210> 136
 <211> 654
 <212> DNA
 <213> Homo sapiens

<220>

<221> variation

<222> 3, 108, 186, 216, 221, 252, 322, 329, 339, 344, 346, 350, 370, 376, 379, 385, 388, 391, 398-400, 404, 409, 418, 422, 428-429, 433, 437, 455-456, 462, 465, 474-476, 493, 496, 498, 503, 506, 515, 521, 527, 538, 540, 542, 548, 554, 561, 563, 565, 586, 595, 598, 612, 628, 639, 646

<223> n = any nucleotide

<400> 136

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tgnccctcta gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc 60
cttccgatgt atttgtttct agccaacctg tcattaactg atgcttgntt cacttctgcc 120
tccatcccca aaatgctggc caacattcat acccagagtc agatcatctc gtattctggg 180
tgtctngcac agctatattt cctccttatg tttggnggcc ntgacaactg cctgctggct 240
gtgatgccat angaccgta tgtggccatt tgccaaccac cccattacag cacatctatg 300
agtccccagc tctgtgcaat antgctgcnc gtgtgctgng tgcnanccan ttgtctgcct 360
gctgcacatn ctgttncnc cccnccngg nctctttnnn ccgnaccnc cctacaantc 420
cntatcannt tcnctnccc tttcttctcc cccnnttct tncnccttc ctcnnnccta 480
ctttctctc tcnccntnct canatnatca gtcenacctc nccttcttt cttcactnan 540
tctctcnct cccnctcacc ngntngtcta gtctgctgc gcccnctgc tatcnctncc 600
cccctctccg cntccctga tctctctngt ctaccctcnc catctnatcc ctcc 654

```

<210> 137

<211> 658

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 334, 346, 350, 352, 357, 360, 369, 376-379, 389, 394, 397, 400, 401-402, 411, 414, 421, 435, 438, 447-449, 460, 466-467, 474, 476, 480, 486, 500, 504, 510, 512-513, 515, 517, 521, 525, 528, 543, 551, 554-555, 557, 559, 569-570, 572-573, 585, 587, 591, 593-594, 600-601, 606-607, 612, 615, 617, 621, 623, 628-629, 631, 633, 636-637, 640, 655

<223> n = any nucleotide

<400> 137

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ctctagatgc atgctcgagc ggccgccagt gtgatggata tctgcagaat tcgcccttcc 60
aatgtatttt tttctaagca acctctcctt cctggagatt tggatatacca cagcagcagt 120
gcccaaagca ctggccatcc cactggggag aagtcagacc atatcattta caagctgtct 180
tttcagatg tactttgttt tctcattagg ctgcacagag tacttctctc tggcagccat 240
ggcttatgac cgctgtcttg ccatctgcta tcctttacac tacggagcca tcatgagtag 300
cctgctctca gcgcagctgg cctggggctc ctggncgtgn ggcttngtgn cnttgengcn 360
ctcctagcnc tcatgnnnnc cttgccttnt gggnccntgn nnatcaccct ntttctctgt 420
nacacttgta cctcncgnet tgcctnnnc tgccttctaan tccttngtt gtantnctn 480
gccttntctc cccttgcetn gttnatcttn anntnctnctc nctntnctc ctctcctctg 540
ttngaccct ntannncnc tcttctctnn anntccctc tatcncnccg ntannctcctn 600
ntgtcnccg antangntac ntntcactnt ntntcnnctn ctctcctaac tcttncg 658

```

<210> 138

<211> 670

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 342, 347, 358, 376, 383, 401, 403, 409, 448, 451, 455, 463, 470, 474, 478, 481-482, 484, 487, 489-490, 492, 499, 511, 514, 516, 518, 522, 525, 534,

536, 548, 556, 565, 577, 581, 585, 587, 589, 592, 598, 604, 607-609, 624-626,
628, 636, 639, 645, 651, 655, 660, 661-663, 667-668

<223> n = any nucleotide

<400> 138

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ggccccctag atgcatgctc gagcggggcgc cagcgtgatg gatatctgca gaattcgccc 60
ttcccatgta ttgttttcta agcaacctct ccttcctgga gatttggtat accacagcag 120
cagtgcceaa agcactggcc atcctactgg ggagaagtca gaccatatca ttacaagct 180
gtcttttgca gatgtacttt gttttctcat taggctgcac agagtacttc ctctggcag 240
ccatggctta tgaccgctgt cttgccatct gctatccttt aactacgga gccatcatga 300
gtagcctgct ctacgcgcag ctggccctgg gctcctgggt gngtggnttc gtggccantg 360
tagtgcceac agcccntatc agnggcctgt ccttttggg ncnccegtnc catcaacccc 420
ttctttctgt gacatttgcc cccctgcntt nccntggcc ctncceaan cacngcang 480
nngnttnenn gnetcggcnc cccctttgac ntantncntt gntgngcgt tatnctgag 540
tttaatgncc ttaatnaaac tctcncctct catgttnttc nttntntng gnaccaante 600
ttcnaannna cccttttttc catnnncng tctacntcnc tctcnccttc ntcnggtttt 660
nnngtcnccc 670
```

<210> 139

<211> 635

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 303, 314, 331, 339, 341, 360, 373, 379, 386, 395, 400, 406, 416, 419,
423, 433, 435, 452, 456, 463, 473, 480-481, 487, 490, 493, 499, 501, 504-505,
509, 511, 514, 517, 519, 522, 523, 534, 535, 543, 544, 554, 560, 563, 565,
567, 579, 584, 593, 596-597, 599, 605-608, 611-612, 619-620, 624, 632, 634
<223> n = any nucleotide

<400> 139

```
gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttccgatgt 60
atTTTTTct aagcaacctc tccttcctgg agatttggtat taccacagca gcagtgcceca 120
aagcactggc catcctactg gggagaagtc agaccatatc atttacaagc tgtcttttgc 180
agatgtactt tgttttctca ttaggctgca cagagtactt cctcttgga gccatggctt 240
atgaccgctg cttgccatct gctatccttt aactacgga gccatcatga gtagcctgct 300
ctnagcgcag ctgncctggg ctctgggtg ngtgggtcng ngccattcag cgccacang 360
cttcatcagt ggncttgtn tctgngccc ccgncatcn aaccantttc tctgngana 420
atngtaccce tgnanttgcc ctggcctgt anccancaca tangetcgt tngcttctn 480
ntggcncenn tgnctcgent ngtnnccng ntancngnc tnnacgtcct ttcnnacact 540
ttnnctctat gtntcaacn tcnngncta ttcgtcang atanccactc ttcnannent 600
cggannnnta nctttccnn acntcttct cntnc 635
```

<210> 140

<211> 709

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 357, 369, 379, 382, 414, 430, 441, 458, 462, 468, 474, 481, 486, 494,
505, 507-509, 514, 520, 533, 546, 551, 555-556, 563, 570, 574, 589, 600, 602,
606, 613, 615-616, 622-623, 628, 638, 644, 653, 669, 671, 677, 679, 680-681,
689, 691, 696-698

<223> n = any nucleotide

<400> 140

```
atgacctct agatgcatgc tcgagcggcc gccagtgtga tggatatctg cagaattcgc 60
```

```

ccttcctatg tatttatttc taagcaacct ctcttctctg gagatttggg tataccacag 120
cagcagtgcc caaagcactg ggccatccta ctggggagaa gtcagaccat atcatttaca 180
agctgtcttt tgcagatgta ctttgttttc tcattaggct gcacagagta ctctctcctg 240
gcagccatgg cttatgaccg ctgtcttgcc atctgctatc ctttacacta cggagccatc 300
atgagttagc tgctctcagc gcaagctggc ctgggctcct ggggtgtgtg tttcggnggc 360
cattgcagng cccacagcnc tnatcagtgg gctgtccttt ctgtgggccc ccgngcccat 420
tcaacccacn tttctttttg nggatattgg caaccccntg gnatttgncc cctnggccct 480
ngcacncaaa ccancaccag ggtcngnnna caanctttgn cgggccccct ttntgaaatt 540
ggcctnggtg ngggnnntaat tcnctttggn tttnaatgcc cttccaatna acctttttgn 600
cnttctatg ggngnnccct tnnattcnag caccacanc ttanggggaa ccnccttttt 660
gtcaagtngg nccggttnnn naaaagccnt ntccnnntg cccccccc 709

```

<210> 141

<211> 671

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 1, 18, 368, 374, 375, 386, 392, 404, 405, 414-415, 420-422, 445-446, 449-450, 452, 460, 467-468, 471, 484, 488, 490, 512, 514, 531, 536-537, 541-542, 549, 562, 568, 572, 574-575, 577, 585, 588, 592-593, 595, 599, 617, 619, 627, 636, 639, 647, 658-659, 661-662, 665-667, 669

<223> n = any nucleotide

<400> 141

```

ntgggccctg agatgcangc tcgagcgggc gccagtgtga tggatatctg cagaattcgc 60
ccttcccatg tatttttttc taagcaacct ctcttctctg gagatttggg ataccacagc 120
agcagtcccc aaagcactgg ccatcctact ggggagaagt cagaccatat catttacaag 180
ctgtcttttg cagatgtact ttgttttttc attaggctgc acagagtact tcctcctggc 240
agccatggct tatgatcgct gtcttgccat ctgctatcct ttacactacg gagccatcat 300
gagtgcctg ctctcagcgc agctggccct gggctcctgg gtctgtgggt tcgtggccat 360
tgaagtgncc acanngcctc atcagntggc cntgtccttc tgcnnccccc cgtnnccatn 420
nncacttctt tcgtgacatt gccannctnn tnttgccctn gtccttnncc natcatccat 480
ggcngttngn gctgttggcc ctttcgctca cncngtctgc gcccattctc nctgtnncaa 540
nngcctcent ctactctctg cnttctanct antnnncct ctttctncc tnnantctnt 600
cctcgatctc ctttcangnc tccgctncac tgcctnctna acgtcctttt ctccctnnt 660
ntcnnntnc g 671

```

<210> 142

<211> 739

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 5-6, 23, 232, 235, 349, 353, 358, 374, 397, 400, 406, 423-424, 427, 431, 434, 436-437, 440, 445, 448, 450, 452, 467, 471, 477, 488-489, 497-498, 506, 510-512, 518-520, 525, 528, 547, 550, 557-558, 560, 562-563, 566, 569, 590-591, 604-605, 613, 619, 631, 638-639, 642, 646, 649-650, 654, 660-661, 664, 670, 677, 679, 687, 690, 692, 694-695, 701, 714, 716, 722, 725, 731, 739

<223> n = any nucleotide

<400> 142

```

gggcnncttt gggatgcct tgncccttag atgcatgctc gagcggccgc cagtgtgatg 60
gatattctga gaattcgccc ttccaatgta cttatttcta gccaacctgt cattaactga 120
tgccgttttc acttctgcct ccatccccaa aatgctggcc aacattcata ccagagtca 180
gatcatctcg tattctgggt gtcttgca gctatatttc ctcttatgt tngnggcct 240

```

```

tgacaactgc ctgctggctg tgatggcata tgaccgctat gtggccatct gccaaaccact 300
ccattacagc acatctatga gtccccagct ctgtgcacta atgctgtgng tgngetgngt 360
gctaaccaac tggngctgcc tgatgcacac actgttnctn atccnngcgc tttcttggtc 420
ccnntangcc nctnctnctn ttccttntn tntctctacc tctccenteg ngctctnccc 480
cttccccnnt cttcctnntg tactenctan nnetgttnnn cccententt ctctctctcc 540
ttctctntcn ctttcgnncn tnnttctnct tcttgctccct acctgtcccn ntcatacctt 600
ttcnaatcg ctntctatcnc cgcctatagt ncaattcnc tncctnctnn attncctacn 660
nccntcctcn ccatcantnc taacctnctn cntnntctct ntctctgtcc tcanctctc 720
gnccnatttc nttttccn 739

```

<210> 143

<211> 611

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 497, 528, 536, 540, 543, 551, 557, 563, 565, 570, 582, 589, 600, 605

<223> n = any nucleotide

<400> 143

```

gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttgatagat 60
aattgggttc agcatggggg tcaccacagt gtacatcata gccatgacag tgtccttttag 120
agtagaacta ttagctgatg agcataagta gagaccaata acggttccat agaacagtga 180
caccacagac aggtggggagc cacaagtaga gaaggccttg cagataccct tagaagaagg 240
gaccttgagg atggaggaga caattcttgc ataggaccga aggatgagta ggaatgggat 300
gacaagaatg agccctccca tgataaatat caccattca ttaactcgag tgtcagagaa 360
ggccagcttc agcagagcag acatatcaca gaaaaagtgg gggatcacat tgtctgcaca 420
aaaacacaac ctggccatga gtaaagtgtg taacatggca tgggaagggtg tcagcaccca 480
ggacagcgcc accaggncca gacagagcat ggggctcatg atggcgnggt agtgcngggg 540
gangcagatg nccacantag tgntnatagn ccatggtcac angggaggna gctttcaggg 600
ctttnaataa c 611

```

<210> 144

<211> 641

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 242, 263, 289, 315, 353, 357, 360, 372, 376, 385, 392, 397, 407, 416, 420, 422, 425, 429, 431, 433, 439, 446-449, 454, 465-466, 471, 479, 485, 492, 499, 501, 512, 516, 524, 528-529, 532, 534, 539, 543, 545, 547, 549, 561, 563, 565, 572-573, 575, 578, 582, 584-586, 596, 602, 604, 613, 615, 617, 622, 627-628, 632, 636-637, 639

<223> n = any nucleotide

<400> 144

```

gcgtgctcga gcggccgcca gtgtgatgga tatctgcaga attcgccctt gttgcgcaaa 60
gagtacatga aggggttaag tgaaggagtg cccactgcat agaagagacc aaagaacttg 120
ccctccctt gggcatacgg atttttgggc tggaggtaga cagcaatgac tgagctgtag 180
aagaggggtga ccacagttag atgggaggag cagggtccaa aggcctttct ccatgctgtg 240
gnagagttaa tcctcagcac tgntctgggca gtggctccat aagaggcang gatgaggctg 300
agaggcacaa ccacngaaga tgacactgta cacagccaac tgtattttat tgnaggnggn 360
atctccacag gngagnccaa tcagntgatg gntccnccc atttcanaag tcaactnatn 420
tntntttgnc ngncacgang gtcctnnng agcngttctt gtcenntctt nactatcgnt 480
taccntccct cntccctent ntttcttct cncctnctc ttenttttnc cntntccent 540
gtncnctnt atcttcccta ntntcttct tnntnctnt tngnnnccct cctctntctt 600
tnntccctc tcnantat cnettggncc cncnntnct c 641

```

<210> 145
 <211> 837
 <212> DNA
 <213> Homo sapiens

<220>

<221> variation

<222> 8-9, 12, 330, 350, 364, 367, 387, 390-391, 393-395, 398, 399-400, 403, 406, 409, 411, 413, 416, 428-429, 438, 449, 454, 464-465, 475, 481, 486, 488, 492, 500-501, 504, 506-507, 515, 523, 532, 538, 548, 556, 562, 565, 567, 573-575, 578, 582-583, 589, 592, 598, 599-600, 604, 608, 612, 629, 637-639, 643, 645, 647, 652, 663, 666, 668, 672, 679, 686-687, 689-690, 693, 699, 710, 715, 717, 719, 721-722, 724, 732-734, 748-751, 763-764, 772-773, 780, 783, 791, 811, 818, 828, 834, 836

<223> n = any nucleotide

<400> 145

```

ggttgccnnc gnttaggcat tgggccctct agatgcatgc tcgagcggcc gccagtgtga 60
tggatatctg cagaattcgc ccttccgatg tatttgtttc taagcaacct ctcttctctg 120
gagatttggt ataccacagc agcagtgcc aaagcactgg ccatactact ggggagaagt 180
cagaccatat catttacaag ctgtcttttg cagatgtact ttgttttctc attaggctgc 240
acagagtact tcttcttggc agccatggct tatgaccgct gtcttgccat cctgctatcc 300
tttacactac ggagccatca tgagtagccn tgctctcagc tgcagctggn cctgggctcc 360
tggntgngct gggtttctcgc cctattnttn ncnnnacnnn ccntantcng ncncntctct 420
ctttcttntt tcccttttnc tcaactcatnc ctncctctct tttntgtgcc tcttnataac 480
nttgtntntc gnttctcccn ntentnntct ctctnttgct tcnctctcct cntttcgnat 540
ccctttgntc tctacnctct tncgnantca ctnnnatntc tnttcacng cctcctcnnn 600
gatnttcncc tncctactgc tactctctnc tatactnnnc ttntntncat anttcgtctg 660
ctnactnanc tntactent toccannnnc tcnctgtcnt ctgactctcn cctentntnt 720
nntnctcac cnnntacatg gtctctttnn ntccatctcg tcnntctctc cmtatacgn 780
ttncatactc netaacttct ctccatcatc ntcacntnc tttctttntc cctngnc 837

```

<210> 146
 <211> 639
 <212> DNA
 <213> Homo sapiens

<220>

<221> variation

<222> 16, 340, 379, 394, 401, 425, 428, 433, 435, 437-438, 446, 457, 463-464, 487, 504-505, 508, 510-511, 517-518, 529, 542, 546-547, 549-550, 552-553, 555, 561, 567, 569, 573, 576, 582, 584-586, 590, 594, 597, 599-600, 604, 611, 618, 623, 631, 634, 636

<223> n = any nucleotide

<400> 146

```

gatgatgctc gagcgnccga gtgtgatgga tatctgcaga attcgccctt ccaatgtatt 60
tatttctagg caccactgac ttcttctctt tggccgtcat gtctctggat cgttacctgg 120
caatctgccg accactccgc tatgagaccc tgatgaatgg ccatgtctgt tcccaactag 180
tgctggcctc ctggctagct ggattcctct gggtcctttg cccactgtc ctcatggcca 240
gcctgccttt ctgtggcccc aatggtattg accatttctt tcgtgacagt tggcccttgc 300
tcaggctttc ttgtggggac accacactgc tgaactggn ggctttcatg ctctctacgt 360
tgggtgtact gggccacng gctctgacct cagntttcta ngcccgcatt cttgccactg 420
ttctnagngc ccncnanngc ttgcngagc gaagcanaag atnnttttca cattgcgcac 480
tcggaantta aagggggtgg cgcnnancn nctgggmgc ttcatctnt ctttttactt 540
tnccanngnn tntnngctca ntccctntnc tentencaat cntnnnggcn ctentgntnn 600
gtanactgcc nttaattnga ccnctttccc nacnncac 639

```

<210> 147

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 347, 411, 415, 418, 435, 441-442, 445, 451, 466, 482, 506, 508, 513, 515-516, 526-527, 531-532, 534, 536, 552, 561, 564, 571, 574, 581, 583, 586-588, 591-592, 616

<223> n = any nucleotide

<400> 147

```

catagatgca tgctcgagcg gccgcagtgt gatggatatc tgcagaattc gcccttccga 60
tgtaagtctt tctaggcac cactgacttc ttccctcttg ccgtcatgtc tctggatcgt 120
tacctggcaa tctgccgacc actccgctat gagaccctga tgaatggcca tgtctgttcc 180
caactagtgc tggcctcctg gctagctgga ttccctctgg tcctttgccc cactgtcctc 240
atggccagcc tgcctttctg tggccccaat ggtattgacc acttctttcg tgacagtggg 300
cccttgctca ggctttcttg tggggacacc cactgctga aactggnggc ttcatgtc 360
tctacgttgg tgttactggg ctactgggt ctgacctcag nttcntange ctgcattctt 420
gtcactgtct caggncctt nnagntgctg ngcgaaggaa agcgcntttc acttgcgcct 480
cnatcttaca ggggtggcat catctnangg ggngnntgca tccttnncta nntnncagg 540
tcccagctat antccaaagt nctnaaaaca ngancctcgg nangannnct nntattctac 600
ccttcttctg aacctncc                                     618

```

<210> 148

<211> 633

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 2, 11, 33-34, 36, 38, 346, 352, 370, 406, 412, 414, 417, 420, 423-424, 427, 434, 437, 440, 449, 452-453, 474-475, 477, 486-487, 491, 496, 499-500, 505-506, 515, 517-518, 533, 535, 537, 540, 543, 547, 549, 556, 558, 563, 568, 570, 571, 575, 577, 580, 588, 590, 593-594, 598, 607, 612, 623, 626

<223> n = any nucleotide

<400> 148

```

cntagatgca ngctcgagcg ggcgccagcg tgnngnanat ctgcagaatt cgcccttcca 60
atgtattttt tctcactaac ttgtctttcc tagatctctg cttcaccacc agttctatcc 120
cccagctgct tttcaatcta ggcagcccag gcaagactat cagccacacg ggctgtgcca 180
tccagctctt catgttctct ggcctgggtg gcaagagtgt attctcttgg cagccgtggc 240
ctatgaccgc ttcattgcaa tctgcaagcc ccttcaactat tctgtcatta tgcacctca 300
gctgtgctgg aagtgggtgt ctgtggcccg ggggtgttgg actccncagt tntctaggta 360
tgctcctgn gactatgaag cttgtcacga tgcggaagat gtaagnttgc ancnttncn 420
ttntngnat gccngntcn tataaaaanc annctgggcg ggtcacagt cttngnata 480
gcattngtc ncttnatnn catcnnattt gcctngnngt ccctcgttcc cantntncan 540
tcnttctnng gcttancntt ctncaccngn ncttncntan ctactcctn ttnnttctc 600
cttctancct tncatcttcc ttncntcca tcc                                     633

```

<210> 149

<211> 624

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 433, 456, 511, 513, 516, 533, 541, 543-544, 557-558, 561-562, 567, 573, 582, 597, 604, 606, 609, 617, 619

<223> n = any nucleotide

<400> 149

```

gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttgttccta 60
agactataca tgaatgggtt tagcatcggg ttgaaagaac tgtaaaatag aaaaaggacc 120
ttctgtctgt cctcaggatg gcgggactta ggggccatgt acatgacgat ggcgctgcc 180
aagaagagtc ccactacgca gaggtgggag gagcagggtg agaaggcctt tctgcggccc 240
tcccagact ggatcctcag gatggccgcc aggatgtgtg agtaggagac cagcaccagg 300
cagagtggtc ccaccaggat gaacatgcag gctgcaaaga tgaccacctg gttgagccag 360
gtatcagcac agccagcct gaggacagac aggatttcac aagaagaagt ggttgatttc 420
acgaggccca canaaagggc agtcttagga tgaggntcac atggaccata gccaggaggg 480
agccacattg tcccaggaag ngntgnccag agtgatgcag acttttcagg tcntgatgat 540
ngnnttattc ggagagnntg nnagacnggt cancgttccc gntcgtagga caattancac 600
ccancngng ccttcantna tgtc 624

```

<210> 150

<211> 611

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 449, 480, 506, 555, 578-579, 601, 608, 610-611

<223> n = any nucleotide

<400> 150

```

gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc cttccaatgt 60
atatttttct ctctgacctc tcttcttggt acctctgctt taccacaagt tgtgtccccc 120
agatgctggg caacctctgg ggcacaaaga agaccatcag cttcctggga tgctctgtcc 180
agctcttcat cttcctgtcc ctggggacca ctgagtgcac cctcctgaca gtgatggcct 240
ttgaccgata cgtggctgtc tgccagcccc tccactatgc caccatcatc ccccccgcc 300
tgtgtgggca gctggcatct gtggcctggg ttatgagtct ggttcaatcg atagtccaga 360
catcatccac cctccacttg cccttctgtc cccaccagca gatagatgac tttttatgtg 420
aggteccatc tctgattcga ctctcctgng gagatacctc ctacaatgaa atccagttgn 480
ctgtgtccag tgtcatcttt ggtggntgtg cctctcagcc tcctccttgc ctcttatgga 540
gccactgccc aggcnggggc tgaggattaa ctttgccnna gccatggaag aaaggtcttt 600
nggacctngn n 611

```

<210> 151

<211> 619

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> 415, 417, 427, 516, 524, 536, 544-545, 558, 561, 575, 580, 582, 584, 590, 607, 610, 615

<223> n = any nucleotide

<400> 151

```

gatgcatgct cgagcggccg ccagtgtgat ggatatctgc agaattcgcc ctttctttat 60
ttcgaagagt atacctagt ggattgaaga gaaacaaata cataggaagg gcgaattcca 120
gcacactggc ggccgttact agtggatccg agctcggtag caagcttgat gcatagcttg 180
agtattctaa cgcgtcacct aaatagcttg gcgtaatcat ggtcatagct gtttcctgtg 240
tgaaattgtt atccgctcac aattccacac aacatacgag ccggaagcat aaagtgtaaa 300

```

```

gcctggggtg cctaagtagt gagctaactc acattaattg cgttgcgctc actgtccgct 360
ttccagtcgg gaaacctgtc gtgccagctg cattaatgaa tcggccaacg cgcgngnaga 420
ggccggnttg cgtattgggc gctcttccgc ttctcgctca ctgactcgct gcgctcggga 480
cgtccggctg cggcgagcgg tatcagctta ctcaanggcc gtantacggt tattcncagg 540
aatnnggggt taacgccngg naaagaacat tgtgngccan angncaagcn taatgccag 600
gaaccgntan aacgntccc 619

```

<210> 152

<211> 959

<212> DNA

<213> Homo sapiens

<220>

<221> variation

```

<222> 139, 203, 209, 211-213, 216, 221, 225, 234, 243, 245, 248, 253, 255,
261, 277-279, 287, 296, 302, 311, 318, 321, 344, 348, 350, 353, 376, 379,
381, 383, 395, 397, 402, 406-407, 414, 420, 429, 436, 438, 448, 450, 452,
463, 476, 481, 483, 496, 499, 502, 517, 520, 523, 527, 530, 535, 537, 539,
542, 549, 550, 558, 570, 571, 579, 580, 584, 587, 596, 605, 609, 634-635,
637-638, 640, 644, 648-649, 663, 665-666, 671, 675, 677, 681, 692, 699, 705,
715, 718, 721, 736, 745, 750, 758, 766, 778-779, 791, 793, 797, 811, 816,
821, 829, 831, 832, 837, 839, 840, 843, 846, 846, 851, 858, 883, 889, 892,
895, 897, 898, 917, 923, 928, 935, 945, 956

```

<223> n = any nucleotide

<400> 152

```

ctcgagcggc gcagtgtgat ggatatctgc agaattcgcc ctccctatgt attattttctc 60
cataatattat ctattgccga tatctgcttc tcttccatca cagcgcccaa ggttctggcg 120
gaccttctgt ctgaaagana gaccatctcc ttcaatcatt gctccactca gatgtttcta 180
ttccacctta ttggaggggc gngtgtatnt nnnccntggt ncccnatgcg cctncttttc 240
ccntntcttt tcnantcttt negcctcctc tcatgcnnnc ccttccntct tattcntgtc 300
gnaatacgct ntctccgnct nctgtctgct catccttgct gttncgtntn canctcatcg 360
ctgtctgtcg tacctnttnc ntncgtgtgc tgcgngntca tncacnntct caancgtctn 420
ccctcaactnc tctttntctg ctctctctn cncctgtgtc tancctcttg ccctgntacg 480
nncgcgcgct catatncgng tncgtggtat ccctctnatn ttnttctctn cctctnttnc 540
cntctcacnn acttctctngt ctctctccan ncttgcacnn ctncctnctc tccacnacgc 600
actntctctn ctatatccgc tcttaccgct ctcnncnnan cacncttnc tctgcatact 660
agntntcttc ncacnencat nttcttctca cncttctcnc tgtcncacag atctntcnct 720
nctctgctct cgttgntccc cctgncactn cgcaatcnca catatncgtc tctctctnnt 780
cgccacttat ntngcanctt tctctgctgt nctctnecat ntccctcnc nntctcncnn 840
ctnatnatcg nttattcnaa tcatactcgg tactgtttct gtncctctnt cntgncnct 900
agcttctctc tattcantct acnttctntt cgctntctat ccacnctctt cactcncct 959

```

<210> 153

<211> 375

<212> DNA

<213> Unknown (H38g1 nucleotide)

<220>

<223> Synthetic construct

<400> 153

```

ttggcctgtg ctgacacatc cttagcccag aggggtgagct tccccgacgt tggcctcata 60
tctcttgtct gctttctgct aattctttta tcctacacta gaatcacaat atctatctta 120
agcattcgta caactgaggg ccgtcgccgt gccttctcca cctgcagtgc tcacctcatt 180
gccatcctct gtgcctatgg gccatcctc actgtctacc tgcagcccac acccaacccc 240
atgctgggaa ccgtggtaca aattctcatg aatctggtag gaccaatgct gaaccctttg 300
atctatacct tgaggaataa ggaagtaaaa acagccctga aaacaatatt gcacaggaca 360
ggccatgttc ctgag 375

```


<210> 154
 <211> 965
 <212> DNA
 <213> Unknown (H38g2 nucleotide)

<220>
 <223> Synthetic construct

<400> 154
 cacacagagc cacggaatct cacagatgtc tgagaattcc tcctcctggg actctcagag 60
 gatccagaac tgcaaccggg cctcgttttg ctctccctgt ccctgtccat gtatctgggc 120
 acggtgatga ggaacctgct cagcatcctg actgtcagct ctgtctctcc cctccacacc 180
 cccatgtact tcttcctctc caacctgtgc tgggctgaca tcggtttcac ctcgccacg 240
 gttcccacga tgattgtgga catgcagtcg catagcagag tcatccctca tgcgggctgc 300
 ctgacgcaga tgtatttctt ggtctttttt gcatgtatag aaggcatgct cctgactgtg 360
 atggcctatg actgctttgt agccatctgt cgccctctgc actaccagct catcgtgaat 420
 cctcacctct gtgtcttctt cgttttgggt tccttttttc ttagcctgtt ggattcccag 480
 ctgcacagtt gaattgtgtt acaattcaac atcatcaaga atgtggaaat ctctaatttt 540
 gtctgtgacc cctctcaact tctcaactt gctgttctg acagcgtcat caatatcatt 600
 ttcataatatt tcgatagtac tatgtttgct tttcttccca tttcaggat cctatggctt 660
 actataaaat cgtccctccc attctaagga tttcatcgtc agatgggaag tataaatcct 720
 tctccacctg tgcctctcac ctacgagttg tttgctgatt tgatggaca ggcattggca 780
 tgtacctgac ttcagctgtg tcaccacccc ccaggaatgg tgtgggtggc tcagtgatgt 840
 acgctgtggg ccccccatg ctgaaccttt tcatctatag cctgagaaac aggaacatac 900
 aaagtgcctt gcggaggctg cgcagcagaa cagtcgaatc tcatgatctg ttccatcgtt 960
 tttct 965

<210> 155
 <211> 936
 <212> DNA
 <213> Unknown (H38g3 nucleotide)

<220>
 <223> Synthetic construct

<400> 155
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 ggaaatgtgc tcatcatcct ggccatcagc tctgattccc acctgcacac ccccatgtac 180
 ttcttctctg ccaacctctc cttactgac ctcttctttg tcaccaacac aatccccaag 240
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 ttctcctga ccagggtgac cttctgtggg cctcagaga tccactacct cttctgtgac 540
 atgtacatcc tgctgtggct ggcattgtcc aacaccaca tcattcacac agcgttgatt 600
 gccactggct gcttcatctt cctcaccccc ttaggggttc tgaccacatc ctatgtacgt 660
 attgtcagaa ccatacctca aatgccctcg gcctctaaga aatacaaaac cttctctacc 720
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 cagccctccc atactactc catgaaggac tcagtagcca cagtgtgta tgcgtgtctg 840
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 ggaagagtcc tatggagacc ctttcagagg cctaaa 936

<210> 156
 <211> 914
 <212> DNA
 <213> Unknown (H38g4 nucleotide)

<220>
 <223> Synthetic construct

<400> 156
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 ttactcatcc ttatagcgat tgtttcttca cactcctatg tatttcttct tgggacgcct 180
 gtctactttt gacatattgt tcccatctgt aacatgtccc aagatgctat tgtatctctc 240
 tggccagagc ccagtcattt cttttaaggg atgtgcttca cagctcttct tctatcagtt 300
 gctgggttct gctgaaggct gcctctattc tgtgatgtct tatgatcgct ttgttgccat 360
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 ggtgccgggt tgggtgggtg tcttcacgcc accattctga cctcctttac ctttcagttg 480
 tctactgtg gccccaatca ggtggactac ttcttctgtg acattcctgc tgttttacct 540
 ctggcttgta ctgacagtgc cctggcccag aggggtgggtt ccataaatgt tggctttctg 600
 gctttaacac ttttgatcag tgtctgtgtc tgctacacta gcattgggat tgccatcttg 660
 agaatccgct catcagaggg caggcagaaa gccttctcca cctgcagtgc tcacctgtt 720
 gcaatcctct gtgcctatgg acctgtaatc atcatctatc tgaagtccac acccaacccc 780
 ttgcttggtg ccagggtcaa atattaaata atgttgtctc acccatgctg aactcgtaa 840
 tctattcctt aaggacaacg gaagtgaataa ggtccctgaa aagagtattc tgaaatgtt 900
 tacttactgt ttgt 914

<210> 157

<211> 951

<212> DNA

<213> Unknown (H38g5 nucleotide)

<220>

<223> Synthetic construct

<400> 157
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 gggaaactgtc tcattgtcct tctgatcaga ctggacagcc gactccacac tcccatgtat 180
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 ctgctggcac attttcttgc agaacataaa gccatcccat tccagagctg tgcagcccag 300
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 gaccgctatg tggctgtgtg tgatgccctg cgatactcgg ccatcatgca tggagggctg 420
 tgtgctaggt tggccatcac atcctgggtc agtggcttca tcagctctcc tgtgcagact 480
 gctatcacct ttcagctgcc catgtgcaga aacaagttta ttgatcacat atcctgtgaa 540
 ctctagctg tggtcaggct ggcttgtgtg gacacctcct ccaatgaggt caccatcatg 600
 gtgtctagca ttgttcttct gatgacacc ttctgcctgg ttcttttgtc ctacatccag 660
 atcatctcca ccatcctaaa gatccagtc agagaaggaa gaaagaaagc tttccacacg 720
 tgtgcctctc acctcacagt ggttgccctg tgctatggtg tggccatttt cacttacatc 780
 cagccccact ccagtccttc tgccttcag gagaagttgt tctctgtctt ttatgccatt 840
 ttaacaccaa tgctgaaccc catgatttac agcctaagga ataaagaggt gaagggggcc 900
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<210> 158

<211> 1025

<212> DNA

<213> Unknown (H38g6 nucleotide)

<220>

<223> Synthetic construct

<400> 158
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 ctggagaaac tgctcatcat catggcagtc agccctgact tccacctcca ccccccatg 180
 tacttcttcc tctccaacct gtccttgccct gacatcggtt tcacctccac acgggtcccca 240
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gtgtttctgt	ggcttccaag	atttgttgtc	cctgtttttt	tttctttttt	tttttttttc	480
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gatgtggaaa	tttctaattg	cttctgggaa	ccttctcaac	tccccatct	tgcattgtgt	600
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tcaaa						1025

<210> 159

<211> 936

<212> DNA

<213> Unknown (H38g7 nucleotide)

<220>

<223> Synthetic construct

<400> 159

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ggcaacctga	gcatgatcac	tctaataagg	ttcagttctc	acctgcacac	ccccatgtac	180
catttctcca	gcagtctgtc	cttcattgat	ctctgccagt	cttctgtcat	taccccaaaa	240
atgctgggtga	attttgtgtc	agagaggaat	attatctcct	accagcatg	catgactcag	300
ctctacttct	tccttgttct	tgtcatatct	gaatgtcaca	tgttggctgc	aatggcttat	360
gaccactaca	ttgccatatg	taacccactg	ctttaccatg	tcgccatgtc	ttatcagggtc	420
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agtctgcatg	ctaagagtgc	ttttctgtaa	ggctgatgta	atcaaccatt	acttctgtga	540
tcttttccca	ctactggagc	tctcccgcct	cagtatttct	atcaatgaaa	tagtagtttg	600
tgcttcagtg	catttaatat	ccttttccgc	agcctcacca	tccttagctc	ttacatcttc	660
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tgcagctccc	acatctcggc	tgtttctggt	ttctttgggt	ctgcagcatt	catgtacctg	780
cagccatcat	ccgtcagctc	catggaccag	gggagtgtct	tctgtgtttt	atgctactgt	840
tgtgcccattg	ctgaaccccc	aatctacagc	ctgaggaata	aagatgtcaa	agttgcctta	900
attaagttcc	ttgaaaaaag	aagtttctctg	tgaagg			936

<210> 160

<211> 985

<212> DNA

<213> Unknown (H38g8 nucleotide)

<220>

<223> Synthetic construct

<400> 160

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agtgattggg	gcattcaggt	atccctcttc	gccctgatcc	tggccatgta	tttgggtgact	120
attttaggaa	acaccctcat	tcttcttctg	atcagactgg	acaacaggct	tcataacccc	180
atgtacttct	cccttagtgt	tctgtcattt	gtggactttt	gttatacaaa	gagtattgtc	240
ccacaaatgc	tgtcccactt	gctctcagcc	cgaaagtcca	tcccattcta	cagttgtgtg	300
ctccagctct	atgtttctct	ggcatttgtt	gggtctgagt	tcttctgct	gggggccatg	360
gcctatgacc	gctacgtggc	cgtgtgccac	ccactgcact	acacggatcat	catgcatgga	420
gggctgtgcc	tggggctggc	ggccagccgc	ctgggtggctg	gcttctcaaa	ttccctgatg	480
gaaacaatta	tcaccttcca	gcttctctgtg	tcacgggtgtt	atcaatcact	ttgtctgtga	540
gaccttagca	gtgctacagc	tagcctgtgt	ggatgtcccc	ttcaacaagg	tcatgggtggc	600
catctcaggg	tttctgggtga	tcttgccttc	ctgttccctg	gttctattct	cctatgcttg	660
catagttgcc	accattttgt	gcattcgctt	taccaggta	cgtgcaaaag	cctttgggac	720
ctgtgcctct	cacctcatgt	tggtttgcat	gtgctttggg	gctaccatct	gcacctacct	780
ggggccacag	ttggcctcct	cagcagagga	agagaagatg	attgctctct	tctatggagt	840

gggtgtacccc atgttgaacc ccttgatcta cagcttgagg aataaggaag ttacggctgc	900
tgtccggaaa gttttagaaa gatgcagata aagggtcaag actctaagaa cctcttgta	960
tctatcatca aaacaaaaa ggaga	985

<210> 161

<211> 954

<212> DNA

<213> Unknown (H38g9 nucleotide)

<220>

<223> Synthetic construct

<400> 161

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ccaaaaatgg agatgatcct gtcaggagtt gtcgccatct tctacttaat tacattgggtg	120
ggtaacacag ccattcattct tgcattctct ctggattccc agcttcatac accaatgtac	180
tttttccca gaaatttate ttccctagat ctatgtttca caaccagcat catccctcag	240
atgctgggtca acttggtggg acctgataag accatcagct atgtgggttg tatcatccaa	300
ctctatgttt acatgtggtt gggctcagtt gaggccttc tcctggctgt tatgtcctat	360
gacgtgttta cagctatatg taagcccttg cattattttg tagtcatgaa cccacatcta	420
tgtctaaaga tgattatcat gatctggagt attagtttgg ccaattctgt agtattatgt	480
acactcactc tgaatttgcc cacatgtgga aacaacattc tggatcattt cttgtgtgag	540
ttgccagctc tggtaagat agcttgtgta gacaccacaa cagttgaaat gtctgttttc	600
gcttttaggca ttataattgt cctcacacct ctcacctta ttcttatatc ctatggctac	660
attgccaaag ctgtgctgag aacgaagtc aaagcaagcc agcgaaaagc aatgaatacc	720
tgtggatctc atcttactgt agtgtctatg ttctatggaa ctattatcta catgtacctg	780
caaccaggta acagggcttc caaagaccag ggcaagttcc tcacctctt ttacaccgtc	840
atcactccaa gtctcaaccc gtcattttac accttaagaa ataaggacat gaaggatgcc	900
ctgaagaaac tgatgagatt tcaccacaaa tctacaaaaa taaagaggaa ttgc	954

<210> 162

<211> 970

<212> DNA

<213> Unknown (H38g10 nucleotide)

<220>

<223> Synthetic construct

<400> 162

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gatccagagc tgcagtcggt cctcgctttg ctgtccctgt ccctgtccac gtatctggcc	120
acgggtgctga ggaacgtgct caacatcctg gctgtcagct ctgactcccc cctccacacc	180
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gttcccaaga tgattgtgga catgcagtcg tatagtagag tcattctctca tgagggtgc	300
ctcacacaga tgtctttctt ggtccttttt gcatgtatag aaggcatgat cctgactgtg	360
atggcctatg actgctttgt agccatctgt cgccctctgc attaccagat catcgtgaat	420
cctcacctct gtgtcttttt cgtttttggt tcctttttcc ttagcctgtt ggattcccag	480
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acgctgtggt ccccccatg ctgaaccttt tcatctacag cctgagaaac agggacatac	900
aaagtgcctt gcggaggctg ctccagcaga cagtcgaatc tcatgatctg ttccatcgtt	960
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<210> 163

<211> 933

<212> DNA

<213> Unknown (H38g11 nucleotide)

<220>

<223> Synthetic construct

<400> 163

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gaaaacgtga	tcatcatcct	attggtgctg	caaaatcggc	cactgcacaa	gcctatgtac	180
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cgagttatcc	atgcccttcaa	catgaacaaa	attatttcca	tcttctatgc	cattgtcact	840
ccttctctca	accctttcat	ttattgccta	agaaaccgag	aggtcaagga	agctctgaag	900
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<210> 164

<211> 939

<212> DNA

<213> Unknown (H38g12 nucleotide)

<220>

<223> Synthetic construct

<400> 164

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accaatgcaa	tcatcatttc	caccattgtg	ctggacagag	cccttcatac	tcccatgtac	180
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ctacgaagaa	caatcggccca	aactttctat	cctcttagt			939

<210> 165

<211> 954

<212> DNA

<213> Unknown (H38g13 nucleotide)

<220>

<223> Synthetic construct

<400> 165

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cttttgggaa	atgttatatt	caggaccctt	gtttgttctt	tgggatttca	cacatcatgc	180
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<210> 166

<211> 998

<212> DNA

<213> Unknown (H38g14 nucleotide)

<220>

<223> Synthetic construct

<400> 166

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tgggagatcc agctcctcct cctagtgttt tctctgtgac tctatgtggc aagcattact 120
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ttctgaatcc agttgtctat acattcagga ataaggagat gaaggcagca ataaagagag 900
tatgcaaaac gctagtgtt tacaagaaga tctcataaat gatacaataa gcccttctcg 960
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<210> 167

<211> 966

<212> DNA

<213> Unknown (H38g15 nucleotide)

<220>

<223> Synthetic construct

<400> 167

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ttcatatatt tcgatagtac tatgtttggt tttcttccca tttcagggat cctatggtct 660
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ttctccacct	gtgcctctca	cctagcagtt	gtttgctgat	tttatggaac	aggcattggc	780
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tacgctgtgg	tcacccccc	gctgaacctt	ttcatctaca	gcctgagaaa	cagggacata	900
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<210> 168

<211> 837

<212> DNA

<213> Unknown (H38g16 nucleotide)

<220>

<223> Synthetic construct

<400> 168

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cgcttcgaca	ccccatgta	cttcttcttc	agcaacatgt	cctttgtgga	caactgcttc	120
tccaccaccg	tccccaagat	gctggccaat	cacatactca	ggactcaaac	catctccttc	180
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aagatgaccc	atcagctctg	tgccctgctg	gtcactggat	catgggtggt	tgccaactcg	360
aatgctctgc	tgcacaccct	gctgatggct	cgactctcat	tctgtgcaga	caacaccatc	420
ccccacatct	tctgcgatgt	gactccccct	ctgaaactct	cctgttcaga	cacacacctc	480
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tggaaagcct	tctccacctg	tggtccccc	ctggctgtgg	ttctctctct	ctatggcacc	660
atcatgtctc	catatttcag	aacttcaccc	tcccactcag	ctcagagaga	tatagcagct	720
gctgtgaggt	tcacagtggg	gactcccgtg	atgaatcctt	tgatctacag	cctgaggaac	780
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<210> 169

<211> 770

<212> DNA

<213> Unknown (H38g17 nucleotide)

<220>

<223> Synthetic construct

<400> 169

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cttggtgctt	atctctgcat	actggtggac	aacatctcaa	ttattgtggt	acccagggga	120
tattttaggg	gagcaccaaa	tgcattcattt	tagctgtgac	gtctttggat	ccttacattg	180
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tggccatggc	atggctaagc	agtttggcca	actctacttc	agtcattcct	tgccgtccag	300
ctgccactag	gcggttaaaa	ggtaggacgac	tttctgtgtg	aggtctcagc	gatgatcaag	360
atatcacgtt	ttgacaccac	attcaatgta	tctatgtctt	ccattgtgag	gatatttttag	420
tccctcgttc	tctaataaat	tatctttgct	tactgtggat	tcattgtagc	tactgtgctg	480
aggattcagt	cctcaggggg	aaagaaggag	gtcttcaaca	catgtggttc	tcataattgta	540
tctctctctt	atgggcctgt	aattagcatg	tatgtacagc	cctctgccaa	ctcccaggac	600
aaaaacaaat	tcattgtccct	gttctacagt	ttggtgactc	ctatgcttaa	cccttttctc	660
tacactttga	gcaacaggga	cataaaaggg	gcaatgagga	ggcttcttgt	ctttttgtat	720
caccaggaag	agaacaaaag	taattatttt	tatactccac	attcttcata		770

<210> 170

<211> 1003

<212> DNA

<213> Unknown (H38g18 nucleotide)

<220>

<223> Synthetic construct

<400> 170

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cctatgtccg	gtttgtagcc	atctgtcacc	ctctatatca	ttcagccatc	atgaacccgt	420
gtttctgtgg	cttcttactt	ttgttgctt	ttttttttct	cggctcttta	gacgcccagc	480
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tcatgtattt	ccctgctgcc	gtatttggtt	tccttcccat	ctcggggacc	cttttctctt	660
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aagtgtcctg	cggcagccgc	acggcagcac	ggtctaattc	caagaccttc	ttatctgttc	960
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<210> 171

<211> 998

<212> DNA

<213> Unknown (H38g19 nucleotide)

<220>

<223> Synthetic construct

<400> 171

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tgggagatec	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaacatcc	tcattgtatt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
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atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcat	tgggtggtgt	gagatgggtc	tgctcatagc	catggccttt	360
gacagttatg	tggccctatt	aagccccctc	actatctgac	cattatgagc	ccaagaatgt	420
gcctttcatt	tctggctgtt	gcctggaccc	ttggtgtcag	tactcctctg	ttccaactgg	480
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ttctgaatcc	agttgtctat	acattcagga	ataaggagat	gaaggcagca	ataaagagag	900
tatgcaaaac	gctagtgtat	tacaagaaga	tctcataaat	gatacaataa	gcccttcttg	960
ttaaacatga	tatggcttta	tgtttctttc	tttgatat			998

<210> 172

<211> 1018

<212> DNA

<213> Unknown (H38g20 nucleotide)

<220>

<223> Synthetic construct

<400> 172

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gatccagaac	tgcagccggg	cctcgctggg	ctgttcctgt	ccatgtgcct	ggtcacgggtg	120
ctcaggaacc	tgctcatcat	cctggccatc	agccctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtcctttcct	gacagtcgtt	tcacctccac	cacagtcctc	240
aagatgattg	tggacatcca	gtctcacagc	agagtcattc	cctatgcagg	ctgcctgact	300
cagatgtctc	tctttgccat	ttttggagac	atggaagaga	gacatgttcc	tgagtgtggt	360


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ggcctatgac cggttttag ccatctgtca ccctttatat cgttcagcca tcttaaacc 420
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<210> 173

<211> 942

<212> DNA

<213> Unknown (H38g21 nucleotide)

<220>

<223> Synthetic construct

<400> 173

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ccagagctcc agctttttct gttcctgtc tgccatca tgtacatgat aatcctcctg 120
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aaacccaagt caaagaacac taatacatct gatgagatta ttgggctgtc ttatggagtg 840
gtaagcccaa tgttaaattc catcatctat agcctcagga ataaagaggt caaagagggt 900
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<210> 174

<211> 958

<212> DNA

<213> Unknown (H38g22 nucleotide)

<220>

<223> Synthetic construct

<400> 174

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gaagaacaca tttttggtgc tactgagatc atcctgctga cagtgtatggc ctgtgacaac 360
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ctcctagtgg tagtggcctg gataggagga tttctccatg caaatattca gattctattt 480
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cctttgttaa aacttgtttg cctggacact catacccttg gtctctttgt tgcgtccaac 600
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agatgtttaa agaactatat cttggagggg aggggtaaaag cccctccac ctgtatttct 720
cacatcataa tagttgtctt attctttgtg ccttgtatat ttgtgtatct gcacccagtg 780
acaaactctg cccattgata aagctgctgc tgtattttat actatggtgg tcccaatgtt 840

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aaatcctttg atctacacac tcagaaatgc tgaggtaaaa agtgcaataa ggaagctttg 900
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<210> 175.

<211> 933

<212> DNA

<213> Unknown (H38g23 nucleotide)

<220>

<223> Synthetic construct

<400> 175

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ctggagacta ttctgttggt cctgtttttg tccttctaca tcttcacct tatggggaac	120
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gcccacctca ccgccatcct gcttttttac attgccagtgg tctcattta cctgaggcct	780
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<210> 176

<211> 906

<212> DNA

<213> Unknown (H38g24 nucleotide)

<220>

<223> Synthetic construct

<400> 176

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gtacagagag ttctctttgt ggtctttttg ctgatctatg tggtcacggg ttgtggcaac	120
atgctcattg tggctactat cacctccagc cccacgctgg cttcccctgt gtattttttc	180
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tctactttac ctatagacaa aaatatggca ttattttatg gtattctgac acctatgttg	840
aatccactca tttataccct gagaaatgaa gaggtaaaaa atgccatgag aaagctcttt	900
acatgg	906

<210> 177

<211> 798

<212> DNA

<213> Unknown (H38g25 nucleotide)

<220>

<223> Synthetic construct

<400> 177

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tttgcgacag	agaagaacat	catctcctac	cctgaatgca	tggtcagct	ctattttatc	180
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gccatctgca	gccccttgct	gtacaatgtc	atcatgtcct	atcaccactg	cttctggctc	300
acagtgggag	tttacatttt	aggcatcctt	ggatctacaa	ttcataccag	ttttatgttg	360
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tttaacatcc	tgatgcctgc	cttaaccatc	cttgcttctt	acatctttat	cattgccagc	540
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<210> 178

<211> 954

<212> DNA

<213> Unknown (H38g26 nucleotide)

<220>

<223> Synthetic construct

<400> 178

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ggaaatggag	tcatacatcat	tgtgagtgtt	tatgacaccc	acttgcacac	ccccatgtac	180
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aagcccaagg	ctaaagactc	ttctggtgca	gacaaagaac	aagtcacaga	caaaatcatc	840
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<210> 179

<211> 984

<212> DNA

<213> Unknown (H38g27 nucleotide)

<220>

<223> Synthetic construct

<400> 179

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ccagaactgc	agaaattctt	gtttgttatg	tttttaatac	cctacttgat	cacattggca	120
ggtaacctgt	tcatactcagt	catcatcttc	atcagcccag	ccctgggttc	ccccatgtac	180
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atgaactttg	acttgatctc	tgaaaagaac	accatactct	tcaatggctg	catgactcag	300
ctcttcacag	aacatttctt	tacagaacat	ttctttgagg	cagctgagat	catcttatta	360
agtgtcatgg	cctatgacca	ctatgtggcc	atccgtaagc	ccttgcaacta	tgcaaccatc	420
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gggaccttga	ttgctgccaa	cagtgggtca	ctgtgtttcc	tcattttttc	catgctgggt	660
gcttcctatg	tcatactcct	gtgcttcctg	aggactcata	gctctgaagg	gcgtcgcaaa	720
gctctgtcta	gttgtgcctc	tcatactctc	attgtcatct	tattctttgt	ccctttttca	780
tacctgtatc	taagacctaa	cctccttccc	cactgacaaa	gctgtgactg	tgttttgac	840
cctatttaca	cctatgttga	accctttaat	ctacacctc	aaaaataaag	aagtgaaaaa	900
tgtcattaag	aagctctgga	agcaaataat	gacaactgat	gataaataag	tcttgtgaca	960
caaacattta	ggcaagaata	tctg				984

<210> 180

<211> 954

<212> DNA

<213> Unknown (H38g28 nucleotide)

<220>

<223> Synthetic construct

<400> 180

atggaatggg	aaaaccacac	cattctgggtg	gaattttttc	tgaagggact	ttctggtcac	60
ccaagacttg	agttactctt	ttttgtgctc	atcttcataa	tgtatgtggt	catccttctg	120
gggaatggta	ctctcatttt	aatcagcatc	ttggacctc	accttcacac	ccctatgtac	180
ttctttctgg	ggaacctctc	cttcttggac	atctgctaca	ccaccacctc	tattccctcc	240
acgctagtga	gcttcctttc	agaaagaaag	accatttccc	ttcttggctg	tgcagtgcag	300
atgttcctcg	gcttggccat	ggggacaaca	gagtgtgtgc	ttctgggcat	gatggccttt	360
gaccgctatg	tggctatctg	caacctctg	agatatccca	tcatcatgag	taaggatgcc	420
tatgtacca	tggcagctgg	gtcctggatc	ataggagctg	tcaattctgc	agtacaatca	480
gtgtttgtgg	tacaattgcc	tttctgcagg	aataacatca	tcaatcattt	cacctgtgaa	540
attctggctg	tcatgaaact	ggcctgtgct	gacatctcag	acaatgagtt	catcatgctt	600
gtggccacaa	cattgttcat	attgacacct	ttgttattaa	tcattgtctc	ttacacgtta	660
atcattgtga	gcatacttcaa	aattagctct	tccgagggga	gaagcaaagc	ttcctctacc	720
tgttcagccc	atctgactgt	ggtcataata	ttctatggga	ccatcctctt	catgtacatg	780
aagcccaagt	ctaaagagac	acttaattcg	gatgacttgg	atgctaccga	caaaattata	840
tccatgttct	atgggggtgat	gactcccatg	atgaatcctt	taatctacag	tcttagaaac	900
aaggatgtga	aagaggcagt	aaaacacctc	ctgaacagaa	ggttctttag	caag	954

<210> 181

<211> 792

<212> DNA

<213> Unknown (H38g29 nucleotide)

<220>

<223> Synthetic construct

<400> 181

atggtagaca	acctaatacat	tgtggtgaca	atcaccacca	gccagccct	ggactcccc	60
gtgtattttt	ttctgtcttt	cttttccttc	atagatggct	gctcctcttc	taccatggcc	120
cccaaaatga	tatttgactt	actcactgaa	aagaaaacta	tttccttcag	tgggtgcatg	180
accagctct	ttgtagaaca	tttctttggg	ggagttgaga	tcattctgct	cgtggtgatg	240
gcctatgact	gctatgtggc	catctgcaag	cccctgtact	acctgatcac	aatgaacagg	300
caggatgtg	gcctcctggg	ggccatggca	tgggtcgggg	gatttcttca	cgctctgatt	360
caaatgcttt	taatagtctg	gctgcccttc	tgtggcccca	atgtcattga	ccatttcac	420
tgtgaccttt	tcctctgct	aaaactctcc	tgcactgaca	ctcacgtctt	tggactcttt	480
gttgccgcca	acagtgggct	gatgtgtatg	ctcatttttt	ctattcttat	tacctcttac	540
gtcctaatac	tctgtcaca	gcggaaggct	ctctctacct	gcgccttcca	tatcactgta	600
gtcgtcctat	tctttgttcc	ctgtatattg	gtgtaccttc	gacctatgat	caccttccct	660
attgataaag	gtgtgtctgt	gttttatact	gtggtaacac	ccatgttaaa	ccctttaate	720
tacacctca	gaacacaga	ggtgaaaaat	gccatgaagc	agctctggag	ccaaataatc	780
tggggttaaca	at					792

<210> 182

<211> 936
 <212> DNA
 <213> Unknown (H38g30 nucleotide)

<220>
 <223> Synthetic construct

<400> 182

atgtggccca	atattactgc	agcccccttt	ttgctgactg	gttttccagg	gctggaggca	60
gctcatcact	ggatctccat	ccccttcttt	gctgtttatg	tgtgcatcct	tctgggcaat	120
ggcatgctcc	tctacctcat	caagcatgac	cacagtcttc	atgagcccat	gtactacttc	180
ctcaccatgc	tggcaggcac	agacctcatg	gtgacattga	ccacgatgcc	tactgtaatg	240
ggcatcctat	gggtgaatca	cagggagatt	agcagtgtgg	gctgcttcct	acaggcttac	300
tttattcact	ccctttctgt	tgtggaatca	ggttccctcc	tggcaatggc	atatgatcgt	360
ttcattgcc	tccgcaatcc	tttgagatat	gcttccattt	tcaccaatac	tagagtcata	420
gcgttaggag	tgggagtggt	tctaaggggt	tttgtatcca	tcctgcctgt	aattttgcgt	480
cttttttcat	tttcatattg	caaatctcat	gttatcacac	gtgctttctg	cctccaccaa	540
gaaatcatga	gactggcttg	tgctgacata	actttcaata	gactttaccc	tgtaatattg	600
atctctttta	caatcttcc	agactctctg	atcatcctct	tctcctatat	tctaattcct	660
aatactgtca	taggcattgc	ctctggtgaa	gagagagcca	aagccctcaa	tacctgtatc	720
tcccacatta	gttgtgttct	tatcttctat	gttacggtga	tggttttgac	attcatttac	780
agatttggga	agaatgtgcc	agaggttgct	cacattatca	tgagttacat	ctacttcctc	840
tttctcctt	taatgaaccc	tgtcatctac	agcatcaaaa	ccaagcaaat	acaatatggc	900
attatccgcc	ttttatctaa	acataggttt	agtagg			936

<210> 183
 <211> 854
 <212> DNA
 <213> Unknown (H38g31 nucleotide)

<220>
 <223> Synthetic construct

<400> 183

gacacagagc	cacagaatct	cacagctgtc	tcagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagcccat	cctcgctggg	ctcttctcgt	ccatgtacct	ggtcacgggtg	120
ctgggggaac	tgtcatttat	cctggccatc	ggctctgact	cccacctcga	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatcggtt	tcacctcggc	cacgggtcccc	240
aagatgattg	aggagatgca	atcgcatagc	agagtcac	accatgggga	ctgctgacac	300
agatgtcttt	ctttgtcctt	tttgcattga	aggatgacat	gatcctgact	gtgatggcct	360
atgactgggt	tgtggccatc	tgtaaccccc	tgaactaccc	aggcatcatg	aatcctcacc	420
tctgtgtctt	attagttttg	gtgccttttt	tccttagcct	gttggattcc	cagctgcaca	480
atgtgattgt	gttacaattc	atctgcttca	agaatgtgga	aatctcctaat	tttttctgtg	540
acccgtttca	acgtctcaac	cttgccctgtt	ctgacagtga	catcaataac	atatacatat	600
atttagatag	tactatattt	ggttttcttc	gcatttcagg	gacccctttg	tgttactata	660
cagttgtctt	ccccattcta	agaattccat	cctcagatgg	gaattataaa	gccttctcca	720
cctgaggctc	tcgcctggca	gttgtttgct	tattttatgg	aacaggcatt	ggcgtgtacc	780
tgacttccgc	tgtgtcatca	tccccagga	atgatgtggt	ggcgtcagta	atgtacgctg	840
tggtgggtcac	cccc					854

<210> 184
 <211> 951
 <212> DNA
 <213> Unknown (H38g32 nucleotide)

<220>
 <223> Synthetic construct

<400> 184

atgggtgaga	ttaaccagac	acttgtgtca	gaattttctc	ttctgggtct	ttctgggatac	60
ccaaagattg	agattgttta	ctttgtcttc	attctagtta	tgtacctagt	gattctaatt	120

ggcaatgggtg	ttctaatacat	agccagcattc	tttgattctc	atcttcacac	accaatgtac	180
ttcttcctgg	gcaacctctc	tttcctggat	atctgctata	catcctcctc	tggtccctca	240
acattgggtga	gcttaatactc	aaagaaaaga	aacatttcct	tctctggatg	tgcatgtcag	300
atgttctttg	ggtttgcaat	ggggtcaaca	gaatgtctgc	ttcttggcat	gatggcattt	360
gatcggtatg	tggccatctg	caaccactg	agatacccca	tcacccctgag	caaggtggcg	420
tatgtattga	tggcttctgt	gtcctggctg	tccggtggaa	ttaattcagc	tgtgcaaaaca	480
ttacttgcca	tgagactgcc	tttctgtggg	aataatatta	tcaatcattt	cgcatgtgaa	540
atattagctg	tcctcaagct	ggcctgtgct	gatatatccc	tcaatattat	caccatgggtg	600
atatcaaata	tggccttcct	ggttcttcca	ctgatgggtca	tttttttctc	ctatatgttc	660
atcctctaca	ccatcttgca	aatgaattca	gccacaggaa	gacgcaaggc	attttccacg	720
tgctcagctc	acctgactgt	ggtgatcata	ttttacggta	ccatcttctt	tatgtatgcg	780
aaaccgaagt	ctcaagacct	gattggggaa	gaaaaattgc	aagcattaga	caagctcatt	840
tctctgtttt	atggggtagt	gacacccatg	ctgaatccca	tactctatag	cttgagaaat	900
aaggatgtaa	aagctgctgt	aaaatatttg	ctgaacaaaa	aaccaattca	c	951

<210> 185

<211> 927

<212> DNA

<213> Unknown (H38g33 nucleotide)

<220>

<223> Synthetic construct

<400> 185

atgggtgcca	agaacaatgt	gactgagttt	gttttatttg	gcctttttga	gagcagagag	60
atgcagcata	catgctttgt	ggtattcttc	ctctttcatg	tgctcactgt	cctggggaac	120
cttctgggtca	tcataccat	caatgctaga	aagacctga	agtctcccat	gtatttcttc	180
ctgagccagt	tgtcttttgc	tgacatatgt	tatccatcca	ctaccatacc	caagatgatt	240
gctgacactt	ttgtggagca	taagatcatc	tccttcaatg	gctgcatgac	ccagctcttt	300
tctgcccact	tctttgggtg	cactgagatc	ttcctcetta	cagccatggc	ctatgaccgc	360
tatgtggcca	tctgtaggcc	cctgcactac	acagccatca	tggattgccc	gaagtgtggc	420
ctgctagcgg	gggctcctcg	gttagctggc	ttcctgcatt	ccatcctgca	gaccctcctc	480
acgggttcagc	tgcctttttg	tggggccaat	gagatagaca	acttcttctg	tgatgttcat	540
cccctgctca	agttggcctg	tgcagacacc	tacatggtag	gtctcatcgt	gggtggccaac	600
agcgggtatga	tttcttttagc	atcctttttt	atccttatca	tttctatgt	tatcatctta	660
ctgaacctaa	gaagccagtc	atctgaggac	cggcgtaagg	ctgtctccac	atgtgggtca	720
cacgtaatca	ctgtcctttt	ggttctcatg	ccccccatgt	tcatgtacat	tcgtccctcc	780
accaccctgg	ctgctgacaa	acttatcatc	ctctttaaca	ttgtgatgcc	acctttgctg	840
aaccctttga	tctatacact	aaggaacaac	gatgtgaaaa	atgccatgag	gaagctgttt	900
agggtcaaga	ggagcttagg	ggagaag				927

<210> 186

<211> 987

<212> DNA

<213> Unknown (H38g34 nucleotide)

<220>

<223> Synthetic construct

<400> 186

gctacttgcc	acttgatgaac	acacaatgag	gctccttttt	tgctgcctgg	cttttcagta	60
ctggaggcaa	cttatcactc	gatctccatc	cccttctttg	ctgtttatgt	gtgcgtcctt	120
cttggcaatg	cgaagctcct	ctacctcatc	aagcatgacc	acagtcttca	cgaacctatg	180
tactgtttcc	ttgccacact	gaggcaagac	ctcatggtga	aattgacct	gatgccact	240
gtaatgggag	tcttgtggat	gaatcacaaa	gagggtatcc	atggggcctg	cttcttgag	300
gtttacatta	tcactccca	ttatccactt	gcagaatcag	gtattctcct	gtcaatggcc	360
tatgaccgtt	tcattatcat	ccacatgctt	ctcaggtata	actctatttc	tactaaatct	420
tgggtgaaga	tagaactgtg	gctatttatg	agggactttt	tatccctcgt	gcctccaatt	480
ctgccactcc	attgcttccc	atattgtcat	tcccatgttc	tcttccacac	cttttttctc	540
catcaagatg	tcctgaaact	tgccgtgct	gatattacat	tcaatcactt	ataccagct	600
attctgggtg	ctttgatatt	cttcctagac	gctctgatca	ttgtcttttc	ttatatcctg	660

atccttaaaa	cagttatagg	tattgcctcc	agaaaagagc	aagccaaagc	tctcaacatg	720
tgtgtctccc	atatcagctg	tgtcttggtg	tttcacatca	ccgtgatcag	tgagactttc	780
attcacaggt	tgggaaaca	tgaccacat	gtggtgcaca	ttaccgtgag	ctaagtactc	840
atttcttttt	cctccattca	tgaaccctat	tatatacagc	atcaaaacca	gcagatccaa	900
agaagcattg	ttgcctatt	ttctgggcac	agaatggctt	gagccctttt	ttcagaattt	960
tgtgatcttc	atgatttctg	ggccttt				987

<210> 187

<211> 887

<212> DNA

<213> Unknown (H38g35 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(887)

<223> n = A,T,C or G

<400> 187

ctgctgctcc	tgggtgctct	gctgcccacg	ttcctgctga	gtcttntggg	gaacntgctc	60
atcatctcca	ctgtgctgtc	ctgctcccgc	ctccacaccc	ccatgacttc	ttcttggtgca	120
acctctctat	cctggacatc	ctcttcacct	cagtcattct	tccaaaagtg	ttggccaact	180
taggactag	ggataaaacc	atctcctttg	cggatgtat	caccagtg	tatttctact	240
ttttcttggg	cacagttgag	ttcctcctgc	tgacggtc	gtcctatgac	tgctatgccg	300
ccatctgctg	ccccctg	tacaccacca	tcatgagacc	ttatgtctgc	attgggaccg	360
ttgtgttctc	ttgggtggga	ggcttcctgt	ctgtgctctt	tccaaccatc	ctcatctccc	420
agctgccctt	ctgtggctcc	aatatcatta	accacttctt	ctgtgacagt	ggacccttgc	480
tggccctggc	ctgtgcagac	accactgcca	tgcagctgat	ggattttatg	ctttcttcca	540
tggtcatcct	ctgtgcata	gtcctcgtgg	cctatttcta	tacgtacatc	atcttgacca	600
taatgcgcat	tccttctgca	agtgaagga	agaaggcctt	taatacctgt	gcttcccacc	660
tgaccatagt	catcatttct	agtggcatca	ctgtgtttat	ctatgtgact	ccctcccaga	720
aagaatatct	ggagatcaac	aagatccctt	cgttcttgag	cagtttggtg	actccatttc	780
tcaaccctt	tatatatact	ctgaggaatg	acacagtgc	gggagtcctc	agggatgtgt	840
gggtcagggt	tcgaggaggt	ttcgaaga	ggatgagggc	agtgtctg		887

<210> 188

<211> 930

<212> DNA

<213> Unknown (H38g36 nucleotide)

<220>

<223> Synthetic construct

<400> 188

atgtgggtata	acaacagtgc	tggcccttc	ttgtgactg	gcttcttggg	ctcagaggca	60
gttcaactacc	ggatctctat	gtccttcttt	gtcatctact	tctccgtcct	ttttggaaat	120
ggcactcttc	ttgtcctcat	ttggaatgat	cacagcctcc	atgagcccat	gtactacttc	180
ctggctatgc	tggcagacac	ggaccttggg	atgacattca	ctacaatgcc	cacagtcctg	240
ggtgtcctgc	tgctagacca	gagggagatt	gcccattgctg	cctgtttcac	ccaatccttc	300
attcattcac	tggccattgt	agaatcaggt	atcttgcttg	ttttggccta	tgactgtttc	360
attgccatcc	gcacaccact	gaggtacaac	tgcattctta	ccaattccc	agtgtatgaac	420
ataggactgg	gggtactgat	gagaggtttt	atgtccattt	tgcccataat	tctttcactc	480
tactgtctacc	catattgtgg	ttcccgtgcc	ctcttgacac	cattttgcct	ccatcaagat	540
gtcataaaac	tcgcctgtgc	tgatatcacg	tttaatcaca	tatatccaat	tattcagact	600
tctttgactg	tctttttaga	tgtcttaatc	atcatctttt	cttatatact	aatccttaag	660
acagtgtatg	gcattgcgtc	tggacaagag	gaagctaaat	ctctcaacac	ttgtgtctcc	720
catattagct	gtgtcctagt	atttcacatc	actgtatggg	gactgtcatt	cattcacagg	780
tttgggaaac	atgcacctca	tgtgggtccc	attaccatga	gctatgtcca	ttttctcttt	840
cctccattcg	tgaatcctat	catttatagc	atcaagacca	agcagattca	aagaagcatt	900
attgccttat	tttctgggca	gagtagggct				930

<210> 189
 <211> 996
 <212> DNA
 <213> Unknown (H38g37 nucleotide)

<220>
 <223> Synthetic construct

<400> 189
 cacacagagc cacggaatct cacagggtgc tgagaattcc tcctccttgg actcccagag 60
 gatccagaac tgcagccggg tctcgttttg ctctccctgt cctgtgccat gtatctgggc 120
 acgggtgctga ggaacctgct catcactctg gctgtcagct ctgtctctcc cctccacacc 180
 cccatgtact tcttctcttc caacctgtgc tgggctgaca tcggtttcac ctgggccacg 240
 gttcccaaga tgattgtgga catgcagtcg catagcagag ccactctctca tgcgggctgt 300
 ctgacgcaga tgtcttttct gttccttttt gcatgtatag aaggcatgct cctgactgtg 360
 atggcctatg actgctttgt agccatctgt cgccctctgc actaccagc catcgtgaat 420
 cctcacttct gtgtcttctt cgttttggtg tcctttttcc ttagcctgtt ggattcccag 480
 ctgcacagtt ggtattgtgt acaattcacc atcttcaaga atgtggaaat ctctaatttt 540
 gtctgtgacc cctctcaact tctcaaactt gcctgttctg acggcgctcat caatagcata 600
 ttcatatatt ttgatagtac tatgtttggt ttccttccca tttcagggat cctatggtct 660
 tactataaaa tcgtcccttc cattctaagg atttcatcgt cagatgggaa gtataaagcc 720
 ttctccacct gtggtctctca ccaggcagtt gtttgctgat tttatagaac aggcattggc 780
 atgtacctga cttcagctgt gtcaccaccc cccaggaatg gtgtgggtggc atcattgata 840
 tacgctgttg tcaactccat gctgaacctt ttcactaca gcctgagaaa caggacata 900
 caaagtgcc tgcggaggct gctcagcaga acagtcgaat ctcatgatct gttccatcct 960
 ttttcttggg gggtagagaa gggcaaccac attaaa 996

<210> 190
 <211> 930
 <212> DNA
 <213> Unknown (H38g38 nucleotide)

<220>
 <223> Synthetic construct

<400> 190
 atgggagaca atataacatc catcagagag ttcctcctac tgggatttcc cgttggccca 60
 aggattcaga tgetctctt tgggctcttc tccctgttct acgtcttcac cctgctgggg 120
 aacgggacca tactggggct catctcactg gactccagac tgcacgcccc catgtacttc 180
 ttcctctcac acctggcggg cgtcgacatc gcctacgcct gcaacacggg gccccggatg 240
 ctggtgaacc tcctgcatcc agccaagccc atctcctttg cgggcccgcg gatgcagacc 300
 tttctgtttt ccacttttgc tgtcacagaa tgtctctcc tgggtggtgat gtcctatgat 360
 ctgtacgtgg ccacttgcca cccctccga tatttgcca tcatgacctg gagagtctgc 420
 atcacctcg cggtgacttc ctggaccact ggagtccttt tatccttgat tcatcttggt 480
 ttacttctac ctttaccctt ctgtaggccc cagaaaattt atcacttttt ttgtgaaatc 540
 ttggctgttc tcaaacttgc ctgtgcagat acccacatca atgagaacat ggtcttggcc 600
 ggagcaattt ctgggctggg gggacccttg tccacaattg tagtttcata tatgtgcac 660
 ctctgtgcta tccttcagat ccaatcaagg gaagttcaga ggaaagcctt ccgcacctgc 720
 ttctcccacc tctgtgtgat tggactcgtt tatggcacag ccattatcat gtatgttggg 780
 cccagatatg ggaaccccaa ggagcagaag aaatatctcc tgctgtttca cagcctcttt 840
 aatcccatgc tcaatccctt tatctgtagt cttaggaact cagaagtga gaatactttg 900
 aagagagtgc tgggagtaga aagggcttta 930

<210> 191
 <211> 968
 <212> DNA
 <213> Unknown (H38g39 nucleotide)

<220>
 <223> Synthetic construct

<400> 191

cacacagagc	cacggaatct	cacgggtgtc	tgagaattcc	tcctcctggg	aatctcagag	60
gatccagaac	tgagcccgt	cctcgctggg	ctgaccctgt	ccatgtacct	ggtcacgggtg	120
ctgaggaacc	tgctcatcat	cctggctgtc	agctctgact	cccacctcca	cacctccatg	180
tacttcgtcc	tctccaacct	gcgctgggtt	gacatcggtt	tcacctcggc	cacggttccc	240
aagatgattg	tgacatgca	gtcgcatagc	agagtcacct	cttatgcggg	ctgcctgaca	300
cagatgtctt	tcttggtctt	ttttgcatgt	atagaagaca	tgctcctgac	tgtgatgtcc	360
tatgaccaat	ttttggccat	ctgtcacccc	ctgcactacc	cagtcacgt	gaatcctcac	420
ttctgtgtct	tcttagtttt	ggtgtccttt	ttccttagcc	tgttggattc	ccagctgcat	480
agatggattg	tgttacaatt	caccttcttc	aagaatgtgg	aaatctctaa	ttttgtctgt	540
gagccatctc	aacttctcaa	ccttgctgt	tctgacagcg	tcataaatat	catattcata	600
tatttagata	gtactatgtt	tggttttctt	cccatttcag	ggatcctttt	gtcttactat	660
aaaattgtcc	cctccattct	aaggatgtca	ttgtcagatg	tgaagtataa	agccttctcc	720
acctgtggct	ctcacctggc	agttttttgc	ttattttacg	gagcaggcat	tggcgtgtac	780
ctgacttcag	ctgtgtcacc	accttccggc	aatgggtgtg	tggcttcagt	gatgtacact	840
gtggtcacc	ccatgctgaa	ccctttcatc	tacagcctga	gaaacaggga	cattcaaagt	900
gccccgtgga	ggctgcgag	cacaacagtt	gaatctcatg	atctcttcca	tcctttttct	960
tgtgtctg						968

<210> 192

<211> 960

<212> DNA

<213> Unknown (H38g40 nucleotide)

<220>

<223> Synthetic construct

<400> 192

cacacagagc	cacagaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgagcccgt	cctggctggg	ctgtccctgt	ccatgtacct	ggtcacgggtg	120
ctgaggaacc	tgctcatcat	cctggctgtc	agctctgacc	cccacctcca	cacccccatg	180
tgcttcttcc	tctccaacct	gtgctgggct	gacatcggtt	tcaccttggc	cacggttcct	240
aagatgattg	tgacatgca	gtctcatacc	agagtcacct	cttatgaggg	ctgcctgaca	300
cggatatctt	tcttggtcct	ttttgcatgt	atagaagaca	tgctcctgac	tgtgatggcc	360
tatgactgct	ttgtagccat	ctgtcgccct	ctgcactacc	cagtcacgt	gaatcctcac	420
ctctgtgtct	tcttcttttt	ggtatacttt	ttccttagct	tgttggattc	ccagctgcac	480
agttggattg	tgttacaatt	caccatcatc	aagaatgtgg	aaatctctaa	ttttgtctgt	540
gacccctctc	aacttctcaa	acttgctgt	tctgacagcg	tcataaatag	catattcatg	600
tatttccata	gtactatgtt	tggttttctt	cccatttcag	ggatcctttt	gtcttactat	660
aaaatcgtcc	cctccattct	aaggatttca	tcacagatg	ggaagtataa	agccttctcc	720
acctgtggct	ctcacttggc	agttgtttgc	tgattttatg	gaacaggcat	tggcgtgtac	780
ctgacttcag	ctgtgtcacc	acccccagg	aatgggtgtg	tagcgtcagt	gatgtacgct	840
gtggtcacc	ccatgctgaa	ccttttcatc	tacagcctga	gaaacaggga	catacaaagt	900
gcctgcgga	ggctgctcag	cagaacagtc	gaatctcatg	atctgttcca	tcctttttct	960

<210> 193

<211> 980

<212> DNA

<213> Unknown (H38g41 nucleotide)

<220>

<223> Synthetic construct

<400> 193

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gatccagaac	tgagccgggt	cctcgctggg	ctgttcctgt	ccatgtgcct	ggtaaggtg	120
ctggggaacc	tgctcatcat	cctggccatc	agccctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatcggtt	tcacctccac	catgggtccc	240
aagatgattg	tggaaatccaa	tctcacagca	gagtcattctc	ctatgcaggc	tgctgtactc	300
agatgtctct	ctttgccatt	tttggaggca	tggaaagagag	acatgtctct	gagtgtgatg	360

gcctatgacc	ggtttgtagc	catctgtcac	cctctatata	attcagccat	catgaacccg	420
tgtttctgtg	gcttcctagt	tttgctgtct	tttttttctt	tctttttctc	agctgcacaa	480
cttgattgcc	ttaaaaatga	cctgcttcaa	gaatgtggga	attcctaatt	tcctctgtga	540
cccttctcaa	ctccccatc	tcacatgttg	tgacaccttc	accaatcaca	taatcatgta	600
tttccccgct	gccatatttg	gtttttcttc	catctcgggg	acccttttct	cttaccatgt	660
aattgtttcc	tccattctga	gggtttcatc	atctgtggga	ggtgtaaagc	cttccccatc	720
tgtgagttgt	ttgctgatat	tatggaacag	gctttggagg	gtacctcagt	tcagatgtgt	780
catcttccct	gagaaaggct	gcagtggcct	cagtgatgta	catggtggtc	acacccatgc	840
tgaacccctt	catctacagc	ctgagaaaca	gggatattaa	aagtgtcgtg	cagcggccgc	900
atggcagcac	ggtctaattc	caatatcttc	ttatctgttc	cattcctttt	gtagtgtggg	960
ttaaaaaagg	cagcaaggtc					980

<210> 194

<211> 939

<212> DNA

<213> Unknown (H38g42 nucleotide)

<220>

<223> Synthetic construct

<400> 194

atgggaaact	ggagcactgt	gactgaaatc	accctaattg	ccttcccagc	tctcctggag	60
attcgaatat	ctctcttcgt	ggttcttctg	gtaacttaca	cattaacagc	aacaggaaac	120
atcaccatca	tctccctgat	atggattgat	catcgccctg	aaactccaat	gtacttcttc	180
ctcagtaatt	tgtcctttct	ggatatctta	tacaccactg	tcattacccc	aaagtgtgtg	240
gcctgcctcc	taggagaaga	gaaaaccata	tcttttctgt	gttgcatgat	ccaaacatat	300
ttctacttct	ttctggggac	gggtggagtt	atcctcttgg	cgggtgatgtc	ctttgaccgc	360
tacatggcta	tctgcgaccc	actgcactac	acggtcatca	tgaacagcag	ggcctgcctt	420
ctgctggttc	tgggatgctg	gggtgggagc	ttcctgtctg	tggtgtttcc	aaccattgta	480
gtgacaaggc	tacccttactg	taggaaagaa	attaatcatt	tcttctgtga	cattgcccct	540
cttcttcagg	tggcctgtat	aaatactcac	ctcattgaga	agataaaact	tctcctctct	600
gcccttgta	tcctgagctc	cctggcattc	actactgggt	cctacgtgta	cataatttct	660
accatcctgc	gtatccccctc	cacccagggc	cgtcagaaag	ctttttctac	ctgtgcttct	720
cacatcactg	ttgtctccat	tgcccacggg	agcaacatct	ttgtgtatgt	gagacccaat	780
cagaactcct	cactggatta	tgacaagggtg	gccgctgtcc	tcacacacagt	ggtgaccctt	840
ctcctgaacc	cttttatcta	cagcttgagg	aatgagaagg	tacaggaagt	gttgagagag	900
acagtgaaca	gaatcatgac	cttgatacaa	aggaaaaact			939

<210> 195

<211> 737

<212> DNA

<213> Unknown (H38g43 nucleotide)

<220>

<223> Synthetic construct

<400> 195

atgggaaata	tcaacataag	tcttgaaaat	tactttattc	tactgggtct	ttctaattga	60
cctcctctgg	aaatagttat	ttttgtagtt	ctcttgatat	tctgcttcat	gacactgata	120
ggcaagctgt	tcagcatcat	tctgtcatac	ctggactccc	atccccacac	tctcgggtact	180
tattctcttt	tctggatttc	tgctacacca	tcagttccat	cttttaatta	cagtacaatc	240
tctggggccc	acagaagaac	atctcttatg	ccagtgggtat	gattcaaatt	tattttgttc	300
tcacactggg	aacctgggat	tgcgctctac	tggtgggtgat	gtccaggact	gtgatgcagc	360
tggacacaga	cacttgccct	atactgttgt	tatggctgtg	gctttttggg	taagtagctt	420
taccaactca	gcatttgatt	ccttttttac	cttctgggta	accctgtgtg	gacatcacta	480
ttatgcttac	atctttatat	ttacatcatt	gttagtataa	agatggttca	ttaacagaaa	540
gaaacagtct	gtgttctcac	tgaatcatgc	agctttatta	acattatctt	ttccattata	600
aaatgactgc	ttccaggaga	ttgaaaagaa	catgttaaga	aaagcacagc	attggagaaat	660
ctgaaagcat	gtgatcttgt	tcaattaaac	caagtatcaa	aaacatgcat	ttttatgaga	720
ctatttttagg	aaattca					737

<210> 196
 <211> 949
 <212> DNA
 <213> Unknown (H38g44 nucleotide)

<220>
 <223> Synthetic construct

<400> 196
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 cagcttcaaa tttccctttt ggcagtcctc tggtttactt atatgcttac tctaacagga 120
 aacggttgcca tcatttccct aacatgtgag aatcatcgcc tccaaacccc aatgtacttc 180
 ttcctcagta attggtcaat ttgggacatt tttttacca cctcagttat cccaaagcta 240
 ttagcctgtc tcctgcagga caagaagacc atatctttgg ctgggtgcat caccctaaact 300
 tatttccttg gttttctggg ggacagtggg gtttatcctc tgggcagtga tgccttttga 360
 ctgctacgtg gccatctgtg acccctgca ctacaccatt atcatgaaca gcagggcctg 420
 cctcctacta gttctgggct gctgggttgg agccttcctg tctgtgttgt gcccaccat 480
 tgtggtgtcc agattgcctt tctgttataa ggaaattagt cacttcttct gtgacatcac 540
 cctctgcta catgtgtcct gtatagacac tcatttcac gagatgataa acttcctctt 600
 atcttccctc atcctcctga cctcactggt gctcaccact gtgtcctaca tctacatcat 660
 ttctaccatc ctgcacatcc cctcagccca aggacgtcgg aaggcctttt ccacgtgctc 720
 tccccacatc accgtcattt ccatcgctta tataagcaac atcttcaggt atgtgaggcc 780
 cagccagagt cattcaatgg gttttgacaa ggtgacagct gtccccacaa tgggtgacccc 840
 tcttctgaat ccttctactt atagtctaag aaatgaaaag gtaaaggcag tcttgaaaga 900
 agcagtcagc aaaattatgt cctcatggca caggagaact taaaacttt 949

<210> 197
 <211> 930
 <212> DNA
 <213> Unknown (H38g45 nucleotide)

<220>
 <223> Synthetic construct

<400> 197
 atggaaccac agaaccacac acaggtatca atgtttgtcc tcttaggggtt ttcacagacc 60
 caagagctcc agaaattcct gttccttctg ttcctgttag tctatgttac caccattgtg 120
 ggaaacctcc ttatcatggt cacagtgact tttgactgcc ggctccacac acccatgtat 180
 tttctgctcc gaaatctagc tctcatagac ctctgtctatt ccacagtcac ctctccaaag 240
 atgctggtgg acttcttcca tgagaccaag acgatctcct accagggctg catggcccag 300
 atcttcttct tccacctttt gggaggtggg actgtctttt ttctctcagt catggcctat 360
 gaccgtaca tagccatctc ccagcccctc cggatgtgca ccatcatgaa cactcaattg 420
 tgtgtgggcc tggtagtagc cgcctgggtg gggggctttg tccactccat tgtccaactg 480
 gctctgatac ttccactgcc cttctgtgac cccaatatca tagataaact ctactgtgat 540
 gttccccaag tactgagact tgcctgcact gatacctccc tcctggagtt cctcatgac 600
 ttcaacagtg ggctgctagt tatcatctgg ttctcctccc ttctgatctc ttatactgtc 660
 atcctggtga tgcagaggtc ccactcggga aaggcaagga ggaaggcagc ttccacctgc 720
 accaccaca tcatcgtggt gtccatgac ttcatccct gtatctatat ctatacctgg 780
 ccttccacc cttcctcat ggacaaggct gtgtccatca gctacacagt catgacccc 840
 atgctcaacc ccatgatcta caccctgaga aaccaggaca tgaaagcagc catgaggaga 900
 ttaggcaagt gcctagtaat ttgcaggagg 930

<210> 198
 <211> 932
 <212> DNA
 <213> Unknown (H38g46 nucleotide)

<220>
 <223> Synthetic construct

<400> 198

gaccaagaaa	atcagacttc	tgaagtcacc	ttcatcctct	tgggcttctc	agaatatcca	60
gaccttcaga	cgcccctgtt	cctgggtgtc	ctgaccatct	acacagtcac	tgtgctgggg	120
aatctgggca	tgatcatagt	catcaggatc	agcccaaac	tccacacccc	catgtgcttt	180
ttcctcagcc	acttgcctt	tggtgatttc	tgttattcca	ccacaattac	acccaaactg	240
ctggagaact	tgggtgtgga	agatagaact	atctccttca	caggatgcac	catgcagtta	300
ttctttgtct	gcatatttgt	agtaacagaa	acattcatgc	tggcagtgat	ggcctatgac	360
cgatatgtgg	cgggtgtgta	ccctcttctc	tacacagttg	caatgtacca	gaggctttgc	420
tccttgtttag	tggctacatc	atactgttgg	gggatagtct	gttccctgac	acttacctag	480
tttctactgg	aattatcctt	cagaggaaat	aatatcatta	ataactttgt	ctgtgagcac	540
gctgccattg	ttgctgtgtc	ttgctctgac	ccctgtgtga	gccaggagat	cactttagtt	600
tctgccacat	tcaatgaaat	aagcagcctg	cttccctatgc	tttcattttt	atcactgtca	660
tgaagacgcc	ttccactggg	gggcgcaaga	aagcgttctc	cacgtctgcc	tcccacttga	720
cggccattac	cattttccat	gggactatcc	ttttcctcta	ctgtgttcc	aactccaaaa	780
gttcgtggct	catggccaag	gtggcctctg	tcttttacac	agtggtcatt	cccatgctga	840
accccttgat	ctatagcctc	aggaacaaag	atgtaaaaga	gacagttagg	aggttactca	900
ttaccaaatt	attatgtctc	atattataaa	at			932

<210> 199

<211> 1000

<212> DNA

<213> Unknown (H38g47 nucleotide)

<220>

<223> Synthetic construct

<400> 199

tatgcagacc	cacagaatct	aacagatgtc	tctatatctc	tcctcctaga	agtctcaggg	60
gatccagaac	tgcagccagt	ccttgctggg	ctgttcctgt	ccatgtgcct	ggtcacgggtg	120
ctggggaacc	tgctcatcat	cctggccatc	agccctgact	cccacctcca	caccccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatcgggt	tcacctccac	cacggtcccc	240
aagatgattg	tggacatcca	gtctcacagc	agagtcactc	cctatgcagg	ctgcctgact	300
cagatgtctc	tctttgccat	ttttggaggc	atggaagaga	gacatgctcc	tgagtgtgat	360
ggcctatgac	tggttttag	ccatctgtca	cccgtatat	cattcaccat	catgaacccg	420
tgtttctgtg	cctttctagt	tttgttgtct	tttttttct	cagtctttta	gactcccagc	480
tgcacaactt	gattgcctta	caagtgacct	gcttcaagga	tgtggaaatt	cctaatttct	540
tctgtgaccc	ttctcaactc	tcccatcttg	catgttgtga	caccttcacc	attaacataa	600
tcatgtattt	ccctgctgcc	atatttgggt	ttcttcccat	cttggggacc	cttttctctt	660
tctctaaaat	tgtttctctc	attctgaggg	ttcttctatc	aggtgggaag	tataaagccc	720
tctccacctg	tgggtctcgc	ctgtcagttg	tttgcagagt	ttatggaaca	ggcgttgag	780
ggtacctcag	ttcagatgtg	tcatcttccc	ccagaaaggg	tgcagtggcc	tcagtgtatg	840
acacactggt	caccccatg	ctgacccctt	tcatctacag	cctgagaaac	agggatatga	900
aagggtgtct	gcggcagccg	cacggcagca	cagtctaate	tcaatatctt	atctgttcca	960
ttcctttgta	gtgtgggttc	aaaaaggcag	caaggtcaaa			1000

<210> 200

<211> 921

<212> DNA

<213> Unknown (H38g48 nucleotide)

<220>

<223> Synthetic construct

<400> 200

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cgggagctcc	agcgtttcct	gtttctaatg	ttcctgtttg	tctacatcac	cactgttatg	120
ggaaacatcc	ttatcatcat	cacagtgacc	tctgattccc	agctccacac	acccatgtac	180
tttctgtctc	gaaacctggc	tgctcctagac	ctctgtttct	cttcagtcac	tgctcccaaa	240
atgctagtgg	acctcctctc	tgagaagaaa	accatctctt	accagggtcg	catgggtcag	300
atcttcttct	tccacttttt	gggaggtgcc	atggctttct	tctctcag	gatggccttt	360
gaccgcctca	ttgccatctc	ccggccctc	cgctatgtca	ccgtcatgaa	cactcagctc	420
tgggtggggc	tgggtgtagc	cacctgggtg	ggaggctttg	tccactctat	tgtccagctg	480

gctctgatgc	tcccactgcc	cttctgtggc	cccaacattt	tggataactt	ctactgtgat	540
gttccccaag	tactgagact	tgctgcact	gacacctcac	tgctggagtt	cctcaagatc	600
tccaacagtg	ggctgctgga	tgtcgtctgg	ttcttcctcc	tcctgatgtc	ctacttattc	660
atcctggtga	tgctgaggtc	acatccaggg	gaggcaagaa	ggaaggcagc	ttccacctgc	720
accaccaca	tcacgtgggt	ttccatgac	ttcgttccaa	gcatttacct	ctatgcccgg	780
cccttcactc	cattccctat	ggacaagctt	gtgtccatcg	gccacacagt	catgaccccc	840
atgctcaacc	ccatgatcta	taccctgagg	aaccaggaca	tgcaggcagc	agtgagaaga	900
ttaggagagc	accggctggg	t				921

<210> 201

<211> 947

<212> DNA

<213> Unknown (H38g49 nucleotide)

<220>

<223> Synthetic construct

<400> 201

cacacagagc	cacagaatct	cacagatgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgacagccgt	cctcgctttg	ctctccctgt	ccctgtccat	gtatctgggc	120
atggtgctga	ggaacctgct	cagcctcctg	gctgtcagct	ctgtctctcc	cctccacacc	180
cccacctgtg	ctgggctgac	atcggtttca	ccttggccac	ggttcccaag	atgattgtgg	240
acatgcagtc	gcatagcaga	gtcatctctc	atgcgggctg	tctgacgcag	atgtctttct	300
tcctcctttt	tgcatgtata	gaaggcatgc	tcctgactgt	gatggcctat	gactgctttg	360
tagccatctg	tcgcccctctg	cactaccctg	tcctcgtgaa	tcctcacctc	tgtgtcttct	420
tcgttttggg	gtcctttttc	cttagcctgt	tggattccca	gctgcacagt	tgaattgtgt	480
tacaattcac	catcatcaag	aatgtggaaa	tctctcattt	ttctctgtac	ccctctcaac	540
ttctcaaact	tgctgtttct	gacagcgtca	tcaatagcat	attcatatat	ttcgatagta	600
ctatgtttgg	ttttcttccc	atttcaggga	tcctatgggc	ttactataaa	atcatccctc	660
ccattctaag	gatttcatca	tcatatggga	agtataaagc	cttctccaca	tgtgcctctc	720
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tgctgaaccc	tttcatctac	agcctgagaa	acagggacat	acaaagtggc	ctgcggaggg	900
tgctcagcag	aacagtcgaa	tttcatgac	tggtccatcc	tttttct		947

<210> 202

<211> 369

<212> DNA

<213> Unknown (H38g50 nucleotide)

<220>

<223> Synthetic construct

<400> 202

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atgatctgct	ttgccctcac	tgtcctctct	tacatccgca	tcttggccac	agtgggttcag	120
atccgttcag	cagccagccg	ccggaaggcc	ttctccacct	gttcttccca	cctgggcatg	180
gtgctcctgt	tctatggcac	cggcagctcc	acctacatgc	gacccaccac	ccgctactcc	240
ccgctggaag	ggcgcttggc	tgtgtcttct	tactccatcc	tcataccacc	cctgaatccg	300
ctcatctaca	gcctgaggaa	ccaggacatg	aagagagccc	tgtggaagct	ctatctccag	360
gtgccatac						369

<210> 203

<211> 1068

<212> DNA

<213> Unknown (H38g51 nucleotide)

<220>

<223> Synthetic construct

<400> 203

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atgatcaatg atagccactt cagtgggttt atactccttg gattcacagg gcagcctcag      60
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atggccatca tectattgtc ttctctagat gaccatctcc aagtcccat gtactttctc      180
cttagaaatt tggccatctt ggatctctgt tataccacaa atatagtccc acaaatgttg      240
gtcagtatct ggggcaaaga caaaagaatt acctttggtg ggtgtgcctt tcaacttttc      300
attgatgtgg cactgtactc agttgaatgc atccttctgt ccatgatgtc atatgatcga      360
ctcaatgcta tctgcaagcc tctgcatcat atgaccataa tgaacctcca actctgccag      420
ggccttggtg tcatctcctg ggtagttggt gtgattaatt gcatcatacc ttccccctat      480
gccacgagtc ttctcctgat taggaaccac cacctagacc acttttttgt gtgtgtgaaa      540
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acatttgcca tgtgcctgat tatagttctt gtctctcttc ttcttattct tgtgtcatat      660
ggtttcattg ctgtggctgt actcaagatc aagtctgcag caggaagaca aaaagcattt      720
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tatatacagc caggaaacag tccaaatcag aatgagggca aacttctcag tatattttac      840
tccattgtta ctcccagctt gaacccatta atttatacgg taaggaataa ggagttcaag      900
ggggccatga agaggctaac tggaaaagaa aaagattgca tggaaaaaag aggacattga      960
ttcttctctc cagcaatttc taatatggca attgatcttc ccaatctaaa atgtagacaa     1020
tttattttgt aaataaattg tctacacctg agataaagat aatatcca      1068

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<210> 204

<211> 949

<212> DNA

<213> Unknown (H38g52 nucleotide)

<220>

<223> Synthetic construct

<400> 204

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atggttcctta tctgctgccc attactggat aaacatctcc aaaccccat atatttcttt      180
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actaatgtga cgctatgcac ggttgaatgt atgcttctgg ctgtgatgtc atatgaccca      360
ttcaatgctg tctgcaagcc tctggactat atgaccataa tgaaccccca actctgtcaa      420
ggcctgggtg ccatgacctg gttaattggt gtcactaatt gcatgatact ttccccctgt      480
cctgtgagtc ttctcctgat cggagaccac cacctggatc actatttttg tgaatatctt      540
gcaatggcta aaattgcatg tggggctacc acagtcatgg aggaaaaacc ttatttgcac      600
tgtgtgtgtg ttgttgtttt catttctctt gcatcacttc ttctcattct tgtgtcatat      660
ggcttcattg ctgtggctgt actcaagatc aagtctgcag caggaagaca aaaagcattt      720
gggacctgtt tctcccatct catttgtgta tccatcttct atgggactgt tagatatatg      780
tatatagagc caggaaacag tccatctcag gatgagggca aacttctcca tatattttac      840
tccattgtta ctcccacctt gaacccatcc cactaaggaa taaggagttc aagtgggcca      900
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<210> 205

<211> 936

<212> DNA

<213> Unknown (H38g53 nucleotide)

<220>

<223> Synthetic construct

<400> 205

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ctggaaagga ctctcttctg ggttgtcttc acttctctacc tcctaaccct agtgggcaac      120
acactcatca tctgctgtgc tgcgctggac cccaagctcc actctccaat gtactttttc      180
ctctccaacc tctcttcttt ggacctctgt ttccaccaga gttgtgttcc ccaaatgctg      240
gtcaacctct ggggcccaaa gaagaccatc agcttctctg actgctctgt ccagatcttc      300
atcttctctg ccctggggac aactgagtgc atcctcttga cagtgatggc ttttgatcgc      360
tacgtggctg tctgccagcc cctccactat gccaccatca tccacccccg cctgtgctgg      420

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cagctggcat	ctgtggcctg	ggtcattggg	ctagtggagt	cagtgggtcca	gacaccatcc	480
accctgcacc	tgcccttctg	ccccgatcgg	caggtggatg	atcttgtctg	tgagggtccca	540
gctctaattc	gactctcctg	tgaagacacc	tcctacaatg	agatccaggt	ggctgttgcc	600
agtgtcttca	tcttggttgt	gcctctcagc	ctcatccttg	tctcttacgg	agccattacc	660
tgggcagtgc	tgaggattaa	ctctgcaaaa	gggcggagga	aagcttttgg	gacctgctcc	720
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ccttcactta	accctctcat	atacaccctg	aggaacaagg	aggttaaccag	ggcattcagg	900
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<210> 206

<211> 1030

<212> DNA

<213> Unknown (H38g54 nucleotide)

<220>

<223> Synthetic construct

<400> 206

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ctggaaagga	ctctctttgt	agttgtcttc	acttctacc	tcctaaccct	ggtggactca	120
tcacctctgt	gtctgtgctg	gacccagggc	tcactctctc	aatgtacttt	ttcctctcca	180
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gaaggaaatg	gggctcatat	aaagttgagg	gagagctgtt	taatgtgctt	tctaaattaa	960
gaagaaatta	tttatccttt	tgtgaacaag	tttgagctcc	caagtatact	acctttcata	1020
caccatcac						1030

<210> 207

<211> 873

<212> DNA

<213> Unknown (H38g55 nucleotide)

<220>

<223> Synthetic construct

<400> 207

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ctggccttgg	tagacgcggg	cttcaactact	agcgtgggtg	cgccgctgct	ggccaacctg	180
cgcggaaccg	cgctctggct	gcccgcgagc	cactgcacgg	cccagctgtg	cgcatcgctg	240
gctctgggtt	cggccgaatg	cgctcctcctg	gcgtgtgatg	ctctggaccg	cgcgcccaag	300
aaagtgaagg	gggcagcgag	gaggctgctg	cggagtctgg	ggagaggcca	ggctgggcag	360
agcgctcct	ggctaagcgg	cctcaccaac	tcggttgctg	aaaccgcgct	cctggctgag	420
cggcgctgt	gcgcgccccg	cctgctggac	cacttcatct	gtgagctgcc	ggcgttgctc	480
aagctggcct	gcggaggcga	cggagacact	accgagaacc	agatgttcgc	cgcccgctg	540
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cgctacaacc	aggcacgggg	caagttcgta	tcgctcttct	acaccgtggg	cacacctgct	780
ctcaaccgcg	tcactctac	cctcaggaat	aagaaagtga	agggggcagc	gaggaggctg	840

ctgcggagtc tggggagagg ccaggctggg cag

873

<210> 208

<211> 921

<212> DNA

<213> Unknown (H38g56 nucleotide)

<220>

<223> Synthetic construct

<400> 208

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gccctgtggt	gtgaccggcg	acttcacact	ccatgtaca	tggtcctggg	agatttctcc	180
tttttagaga	tatggtatgt	cttttctaca	gttccaaga	tggtggtcaa	cttcctttca	240
gagaaaacaa	acatctcctt	tgctggattg	ctttctccag	atctatttct	tcttctcttt	300
gatacatcag	aatgcttgct	tttgactgtg	atggcctttg	atcagaacct	tgctatctgc	360
cggcccttgc	actatcctaa	tatcatgact	gggcactctc	gtgccaaact	ggccatactg	420
tgtggggttt	gtggctttct	gtggttctcg	atccccattt	tctcatctct	cagatgccct	480
tctgtggccc	aaacattatt	gacatgttg	tgtgtgacct	agggccacta	tttgcatggg	540
attgtgtttc	tgccccaga	atccaactgt	tttgcacac	tctaagctca	ttagttattt	600
ttggttaactt	cctctttatt	attggatcct	atactattgt	cctgaaagtt	gtgttgggta	660
cgccttcaag	cactgggaga	cataaggcct	tctctacctg	tggttctcat	ttggctgtgg	720
tatcactgtg	ctatggctct	cttatgggtca	tgtagtgtag	cccaggactc	ggacattcta	780
cggagatgca	gaaaattgta	actttgttct	atgctatggt	gacctcactc	ttcaatcccc	840
ttatctatag	gcctccagaa	taaggagata	aaggcagcct	tgaggaaagt	tctggtgagt	900
tccaacataa	tctaaggcat	a				921

<210> 209

<211> 660

<212> DNA

<213> Unknown (H38g57 nucleotide)

<220>

<223> Synthetic construct

<400> 209

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gccctctgca	ttaccagtc	atcgtgaatc	ctcacctctg	tgtcttcttc	gttttgggtg	120
ccttctcatt	agcatgtagg	ttcccagctg	cacagttgaa	ttgtgttaca	attcaccatc	180
atcaagaatg	tggaatctc	taattttgtc	tgtgaccctc	ctcaatttct	caaacttgcc	240
tggtctgaca	gcgtcatcaa	tagcatattc	acgtatttcc	atagtactat	gttttggttt	300
cttcccattt	cagggatcct	tttgtcttac	tttaaaatcg	tcaccttcat	tctctggatt	360
tcactctcag	atgggaagta	ttaaagcctc	tccacctgtg	actctcacct	agcagttgtt	420
tgctgatttt	atggaacagg	cattggcgtg	tacttgactt	cagctctgtc	accaccccc	480
aggaatgggtg	tgatggcgtc	agtgatgtac	gctgtgggtca	cccccatgct	gaaccttttc	540
atctacagcc	tgagaaacag	ggacatacaa	agtgcctgtg	ggaggctgct	cagcagaaca	600
gtcgaatctc	atgatctgtt	ccatcctttt	tcttgtgtgg	gtaaggggcaa	ccacattaaa	660

<210> 210

<211> 942

<212> DNA

<213> Unknown (H38g58 nucleotide)

<220>

<223> Synthetic construct

<400> 210

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cccaaatggg	agattcccct	ctttctgggtg	tttctgagtt	tctacctagt	cacccttctt	120
gggaatgtgg	ggatgattat	gttaatccaa	gtagatgtca	aactctacac	cccaatgtac	180

ttcttctga gccacctctc cctgctggat gcctgttaca cctcagtcac caccctcag	240
atcctagcca cattggccac aggcaaacg gtcactctct acggccactg tgctgccag	300
ttctttttat tcaccatctg tgcaggcaca gactgctttc tgctggcagt gatggcctat	360
gacgctatg ctgccattcg caaccactg ctctataccg tggccatgaa tcccaggctc	420
tgctggagcc tgggtgtagg agcctatgtc tgtgggggtg caggagccat cctgcgtacc	480
acttgacact tcacctctc cttctgtaag gacaatcaaa taaacttctt cttctgtgac	540
ctccacccc tgctgaagct tgcctgcagt gacacagcaa acatcgagat tgctcatc	600
ttctttggca attttgtgat tttggccaat gcctccgtca tcctgatttc ctatctgctc	660
atcatcaaga ccattttgaa agtgaagtct tcagggtggca gggccaagac tttctccaca	720
tgtgcctctc acatcactgc tgtggccctt ttctttggag cccttatctt catgtatctg	780
caaagtggct caggcaaatc tctggaggaa gacaaagtcg tgtctgtctt ctatacagt	840
gtcatcccca tgctgaacct tctgatctac agcttaagaa acaaagatgt aaaagacgcc	900
ttcagaaagg tcgctaggag actccagggt tccctgagca tg	942

<210> 211

<211> 941

<212> DNA

<213> Unknown (H38g59 nucleotide)

<220>

<223> Synthetic construct

<400> 211

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gcccaacacc ctgaaatcca gactgccttc ttcttggaaac tactgttttt ctactagtca	120
cagcgtttga gaacatcctt atcggtgctg tagtgagatg agattctcga cttcatactc	180
ctatgggatt tttttttcct cagtaccta tcctcccttg aaatgtgta cttcatcagc	240
tgggagctat aagtcttggc tcaatgcac aaggacttcc ccaccatctc ctataacagc	300
tgttctgttc agatgatcac acacctctt ctggggatga cagtgtctcc tccttgcctg	360
catggcttac aacagggttg ttgaaatctc ttatctctc cattacacta ttattatgag	420
caatcgggtc tgtatacagt tggccttggg aatctggacc catgccttct tagtagcagt	480
cacactaatc attgcaattc ctgctagtta ttatggacac aatgtcatca accattttac	540
cttgagatcc aggcctgct gaagctcgtc tgctcagaca cccttgctcag cctgattcag	600
ggtctggtta tcagtgtgtt cacactgccc ctgccttca cattcatcct catctcctaa	660
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atctgactgg agtcaccata ttttatgggg cagccatctg catgtacttg aaacctcagt	780
caaaggggaa ccagggaagag gataaagttg tctcaaaact ttatggagca gttactccca	840
tgtaaatcc cccaatttac attcagagaa ataaggatat aaaagggtgca cttagaaagt	900
tagccaaagg aatgaaaaa tcctaacagt tctctttaa c	941

<210> 212

<211> 1049

<212> DNA

<213> Unknown (H38g61 nucleotide)

<220>

<223> Synthetic construct

<400> 212

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tacaaccatc caaaatttca gattgccttt tatcgacca tggtagtggt ctacctgac	120
acatttgttg gtagcagtct cattattggt gtggttaaag ttgatgggtg gcttcacact	180
cctatgtgtt ttttctaag caacctgtcc ttcttgata tctgtactc cagcaattca	240
gtaccttttt tgttgttcaa tggcttaaga gactacccca ccatttcta taacagctgt	300
tatgccaga tgaccagtgc ttttttctg gggatgcacag ggtgtcttct ccttgcctg	360
atggcttatg agagatttgt tgtgatctcc aatccctgc gctacatcat cattatgaac	420
aataaggctc gcatacagtt ggccatgggt acctgggcca gtgccttctt tatgtcatta	480
atacaataat tgcaataata cattgcaata atacattaat tgcaatgatt gcattgcaat	540
tcctgcccac ttttgtggac acaatgtcat caaccatttt acctgtgagg tgcagggaatt	600
gttgaagctt gtctgtcag acatcccagg cagcctcctc ctgggtctag tcatcggcat	660
attcacttgc tccctgcctc tcaccttgc cctgccttc accttcatcc tcttcgccta	720

tgctcacatt	gtggttgctg	tgctgaggat	caactctgca	gaggccagac	tcaaagcttt	780
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gtacttgaaa	cctcagtcaa	gggaatccca	agatgagggt	aaagtcattc	ctgtattttt	900
tttgaaagta	gagaagcaac	atcaaaatga	tagcatctct	gtattttatg	gtgttgtagc	960
ccctatgttg	aacccccctc	tttacacctt	gagagacaag	gatgcaaaa	tgctctaaga	1020
aaaataatta	ggaagaaaga	gtcctaaaa				1049

<210> 213

<211> 954

<212> DNA

<213> Unknown (H38g62 nucleotide)

<220>

<223> Synthetic construct

<400> 213

atggacaaga	taaaccagac	atttgtgaga	gaattcattc	ttctgggact	ctctggttac	60
cccaaacttg	agatcatttt	ctttgctctg	attctagtta	tgtacgtagt	gattctaatt	120
ggcaatgggtg	ttctgatcat	agcaagcatc	ttggattctc	gtcttcacat	gccccgttac	180
ttcttccctg	gcaacctctc	tttctgggat	atctgctata	caacctcctc	cattccctca	240
acactgggtga	gcttaattctc	aaagaaaaga	aacattttcct	tctctggatg	tgcatgacag	300
atgttctttg	ggtttgcaat	gggttcaaca	gaatgtttcc	tccttggcat	gatggcattt	360
gategttatg	tggccatctg	taacctctctg	agatacccca	tcacatgaa	caagggtggg	420
tatgtactgc	tgacttctgt	atcatggctt	tctgggtgaa	tcaattcaac	tgtgcaaaaa	480
tcacttgcca	tgcatggcc	tttctgtggg	aacaatatta	ttaatcattt	cttatgagag	540
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gtgtcaaaaa	ttgctttcct	agttcttctc	ctgctcgtga	tttttttctc	ctatatgttc	660
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aaacctaagt	cccaggacct	ccttgggaaa	gacaacttgc	aagctacaga	ggggcttggt	840
tccatgtttt	atgggggtgt	gacccccatg	ttaaaccca	taatctatag	cttgagaaat	900
aaagatgtaa	aagctgctat	aaaatatttg	ctgagcagga	aagctattaa	ccag	954

<210> 214

<211> 957

<212> DNA

<213> Unknown (H38g63 nucleotide)

<220>

<223> Synthetic construct

<400> 214

atgttcccgg	caaattggac	atctgtaaaa	gtatttttct	tcctgggatt	ttttcactac	60
cccaaagttc	aggtcatcat	atttgcggtg	tgcttgctga	tgtacctgat	caccttgctg	120
ggcaacattt	ttctgatctc	catcaccatt	ctagattccc	acctgcacac	ccctatgtac	180
ctcttccctc	gcaatctctc	ctttctggac	atctgggtact	cctcttctgc	cctctctcca	240
atgctggcaa	actttgtttc	agggagaaac	actatttcat	tctcaggggtg	cgccactcag	300
atgtacctct	cccttgccat	gggtccact	gagtgtgtgc	tcctgcccac	gatggcatat	360
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caaaccccca	tgttgaaatc	tatcatctat	agtctacgga	acaaagaggt	gaaagtggcc	900
ttgaaaaaat	tgtctgattg	aaatcatttt	aatactgcct	tcatttccat	cctcaaa	957

<210> 215

<211> 930

<212> DNA

<213> Unknown (H38g64 nucleotide)

<220>

<223> Synthetic construct

<400> 215

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gggaacttag	agatgattat	tctgatcctc	atggatcacc	agctccacgc	tccaatgtat	180
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gaccgtact	tggtgtgtg	ccagccctg	ctttatgtca	ccatcctgac	acagcaggcc	420
cgcttgagtc	ttgtgctgg	ggcttacgtt	gctggtctca	tcagtgcctt	ggtgaggaca	480
gtctcagcct	tcactctctc	cttctgtgga	accagtgaga	ttgactttat	tttctgtgac	540
ctccctcctc	tggtaaagtt	gacctgtggg	gagagctaca	ctcaagaagt	gctgattatt	600
atgtttgcca	tttttgtcat	ccctgcttcc	atggtggtga	tcttgggtgc	ctacctgttt	660
atcatcgtgg	ccatcatggg	gatccctgct	ggaagccagg	ccaagacctt	ctccacctgc	720
acctcccacc	tcactgtgtg	gtcactcttc	tttggtaacc	tcacttctcat	gtacttgaga	780
ggtaactcag	atcagtcttc	ggagaagaat	cgggtagtgt	ctgtgcttta	cacagaggtc	840
atccccatgt	tgaatccctt	catctacagc	ctgaggaaca	aggaagtga	ggaggccctg	900
agaaaaattc	tcaatagagc	caagttgtcc				930

<210> 216

<211> 964

<212> DNA

<213> Unknown (H38g65 nucleotide)

<220>

<223> Synthetic construct

<400> 216

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catcctgcct	tccccgggct	tctctttgca	atagtcttct	ccatctttgt	ggtgggtata	120
acagccaact	tggtcatgat	tctgtctatc	cacatggact	cccgcctcca	cacacccatg	180
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aagatgctcc	aggacctcct	gtccaaggac	aagaccattt	ccttcctggg	ctgtgcagtt	300
cagatcttcc	tctacctgac	cctgattgga	ggggaattct	tcctgctggg	tctcatggcc	360
tatgaccgct	atgtggctgt	gtgcaaccct	ctacgggtacc	ctctcctcat	gaaccgcagg	420
gtttgcttat	tcattgggtgt	cggtcctctg	gttgggtggt	ccttggatgg	gttcatgctg	480
actcctgtca	ctatgagttt	ccccttctgt	agatcccag	agatcaatca	ctttttctgt	540
gagatcccag	ccgtgctgaa	gttgtcttgc	acagacacgt	cactctatga	gacctgatg	600
tatgcctgct	gcgtgctgat	cgctgcttat	ccctctatct	gtcatctctg	tctcctacac	660
gcacatcctc	ctgactgtcc	acaggatgaa	ctctgctgag	ggccggcgca	aagcctttgc	720
tacgtgttcc	tcccacatta	tggcgggtgag	cgttttctac	ggggcagcct	tctacaccaa	780
cgtgctgccc	cactcctacc	acactccaga	gaaagataaa	gtgggtgtctg	ccttctacac	840
catcctcacc	cccattgtca	acccactcat	ctacagcttg	aggaataaag	atgtggctgc	900
agctctgagg	aaagtactag	ggagatgtgg	ttcctcccag	agcatcaggg	tggcgactgt	960
gatac						964

<210> 217

<211> 933

<212> DNA

<213> Unknown (H38g66 nucleotide)

<220>

<223> Synthetic construct

<400> 217

atggctcaca	caaatgaatc	gatgggtgtct	gagtttgtac	ttttgggact	ctctaattcc	60
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tggggacttc	aacttttctt	tttcgccatc	ttctctatag	tctatgtgac	atcagtgcta	120
ggcaatgtct	taattattgt	cattatttct	tttgactccc	atttgaactc	tcctatgtac	180
ttcttgctca	gtaatcttct	tttcattgat	atctgtcagt	ctaactttgc	cacccccaag	240
atgcttgtag	acttttttat	tgagcgcaag	actatctcct	ttgagggttg	catggcccag	300
atattcgctt	ttcacagttt	tgttgggagt	gagatgatgt	tgcttgtagc	tatggcatat	360
gacagattta	tagccatag	taagcctctg	cactacagta	caattatgaa	cgggaggctc	420
tgtgtaattt	ttgtgtctat	ttcctgggcg	gtgggcgttc	ttcattctgt	gagccacttg	480
gcttttacag	tggacctgcc	attctgtggt	cccaatgagg	tggatagctt	cttttgtagc	540
cttcccttgg	tgatagagct	ggcttgcatg	gatacatatg	aaatggaaat	tatgacccta	600
acgaacagtg	gcctgatatc	attgagctgt	ttcctggcct	taattatttc	ctacaccatc	660
attttgatcg	gtgtccgatg	caggtcctcc	agtgggtcat	ctaaggctct	ttctacatta	720
actgccacac	tcacagtggg	cattcttttc	ttcgggcctt	gcatttattt	ctatatatgg	780
ccttttagca	gacttcctgt	ggacaaattt	ctttctgtgt	tctacactgt	ttgtactccc	840
ttgttgaaac	ccatcatcta	ctctctgagg	aatgaagatg	ttaaagcagc	catgtggaag	900
ctgagaaacc	gtcatgtgaa	ctcctggaaa	aac			933

<210> 218

<211> 936

<212> DNA

<213> Unknown (H38g67 nucleotide)

<220>

<223> Synthetic construct

<400> 218

atggatcaga	aaaatggaag	ttctttcact	ggatttatcc	tactgggttt	ctctgacagg	60
cctcagctgg	agctagtcct	ctttgtgggt	cttttgatct	tctatatctt	cactttgtctg	120
gggaacaaaa	ccatcattgt	attatctcac	ttggaccac	atcttcacac	tcctatgtat	180
tttttcttct	ccaacctaa	ctttttggat	ctgtgttaca	caaccggcat	tgttccacag	240
ctcctgggta	atctcagggg	agcagacaaa	tcaatctcct	atggtgggtg	tgtagttcag	300
ctgtacatct	ctctaggctt	gggatctaca	gaatgcgttc	tcttaggagt	gatggatttt	360
gaccgctatg	cagctgtttg	caggcccctc	cactacacag	tagtcatgca	cccttgctctg	420
tatgtgctga	tggcttctac	ttcatgggtc	attggttttg	ccaactccct	attgcagacg	480
gtgctcatct	tgcttttaac	actttgtgga	agaaataaat	tagaacactt	tctttgtgag	540
gttcctccat	tgctcaagct	tgctgtgtgt	gacactacta	tgaatgaatc	tgaactcttc	600
tttgtcagtg	tcattattct	tcttgtagct	gttgcatata	tcatattctc	ctatagtcag	660
attgtcaggg	cagtcagtag	gataaagtta	gcaacagggc	agagaaaagt	gtttgggaca	720
tgtggctccc	acctcacagt	ggtttccctg	ttctacggca	cagctatcta	tgtttacctc	780
cagcccggca	acaactactc	tcaggatcag	ggcaagttca	tctctctctt	ctacaccatc	840
attacacca	tgatcaacct	cctcatatat	acactgagga	acaaggatgt	gaaaggagca	900
cttaagaagg	tgctctggaa	gaactacgac	tccaga			936

<210> 219

<211> 939

<212> DNA

<213> Unknown (H38g68 nucleotide)

<220>

<223> Synthetic construct

<400> 219

atgtgctcag	ggaatcagac	ttctcagaat	caaacagcaa	gcactgattt	caccctcacg	60
ggactctttg	ctgagagcaa	gcatgctgcc	ctcctctaca	ccgtgacctt	ccttcttttc	120
ttgatggccc	tactgggaa	tgcctctctc	atcctctctc	tccactcaga	gccccgcctc	180
cacacccccca	tgtacttctt	catcagccag	ctcgcgctca	tggatctcat	gtacctatgc	240
gtgactgtgc	ccaagatgct	tgtgggcccag	gtcactggag	atgataccat	ttccccgtca	300
ggctgtggga	tccagatgtt	cttcacactg	accctggctg	gagctgaggt	tttctctctg	360
gctgccatgg	cctatgaccg	atatgctgct	gtttgcagac	ctctccatta	cccactgctg	420
atgaaccaga	gggtgtgcca	gtcctgtgtg	tcagcctgct	gggttttggg	aatgggtgat	480
ggtttgttgc	tcacccccat	taccatgagc	ttcccccttt	gccagtctag	gaaaatcctg	540
agttttttct	gtgagactcc	tgcctgtgct	aagctctcct	gctctgacgt	ctcctcttat	600

aagatgetca	cgtacctgtg	ctgcatcctc	atgctttctca	cccccatcat	ggatcatctcc	660
agctcataca	ccctcatcct	gcattctcatc	cacaggatga	attctgccgc	cggccgcagg	720
aaggccttgg	ccacctgtct	ctccccacatg	atcatagtgc	tgctgctctt	cgggtgcttcc	780
ttctacacct	acatgctccc	gagttcctac	cacacagctg	agcaggacat	gatgggtgtct	840
gccttttaca	ccattcttcac	tcctgtgctg	aacccctca	tttacagtct	ccgcaacaaa	900
gatgtcacca	gggctatgag	gagcatgatg	cagtcaaga			939

<210> 220

<211> 942

<212> DNA

<213> Unknown (H38g69 nucleotide)

<220>

<223> Synthetic construct

<400> 220

atggatgtgg	gcaataagtc	taccatgtct	gaatttggtt	tgctggggct	ctctaattcc	60
tgggaactac	agatgttttt	ctttatgggtg	ttttcattgc	tttatgtggc	aacaatgggtg	120
ggtaacagcc	tcatagtcat	cacagttata	gtggaccctc	acctacactc	tcctatgtat	180
ttcctgctta	ccaatctttc	aatcattgat	atgtctcttg	cttctttcgc	caccccaaag	240
atgattacag	attacctaac	aggtcacaaa	accatctctt	ttgatggctg	ccttaccag	300
atattctttc	tcacaccttt	cactggaact	gagatcatct	tactcatggc	catgtccttt	360
gataggtata	ttgcaatatg	caagccctg	cactatgctt	ctgtcattag	tccccagggtg	420
tgtgttgctc	tcgtgggtgg	ttcctggatt	atgggagtta	tgcatccaat	gagtcaggtc	480
atatttgccc	tcacgttacc	attctgtggt	ccctatgagg	tagacagctt	ttctgtgac	540
cttctgtggt	tggtccagtt	ggcttgtgtg	gatacttatg	ttctgggcct	ctttatgatc	600
tcaacaagtg	gcataattgc	gttgctctgt	tttattgttt	tatttaattc	atatgttatt	660
gtcctgggtta	ctgtgaagca	tcattcttcc	agaggatcat	ctaaggccct	ttctacttgt	720
acagctcatt	tcattgttgt	cttcttggtc	tttgggccat	gcattctcat	ctacatgtgg	780
ccactaagca	gctttctcac	agacaagatt	ctgtctgtgt	tttataccat	ctttactccc	840
actctgaacc	caataatcta	tactttgagg	aatcaagaag	taaagatagc	catgaggaaa	900
ctgaaaaata	ggtttctaaa	ttttaataag	gcaatgcctt	ca		942

<210> 221

<211> 930

<212> DNA

<213> Unknown (H38g70 nucleotide)

<220>

<223> Synthetic construct

<400> 221

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aggattcaga	tgctcctctt	tgggctcttc	tccctgttct	acgtcttcac	cctgctgggg	120
aacgggacca	tactggggct	catctcactg	gactccagac	tgacgcgcc	catgtacttc	180
ttcctctcac	acctggcggt	cgctgcacatc	gcctacgcct	gcaacacggg	gccccggatg	240
ctgggtgaacc	tcctgcatcc	agccaagccc	atctcctttg	cgggcccgc	gatgcagacc	300
tttctgtttt	ccacttttgc	tgtcacagaa	tgtctcctcc	tggtggtgat	gtcctatgat	360
ctgtacgtgg	ccatctgcca	ccccctccga	tatttggtcca	tcatgacctg	gagagtctgc	420
atcacctctg	cggtgacttc	ctggaccact	ggagtccctt	tatccttgat	tcattctgtg	480
ttacttctac	ctttaccctt	ctgtaggccc	cagaaaattt	atcacttttt	ttgtgaaatc	540
ttggctgttc	tcaaaacttg	ctgtgcagat	accacatca	atgagaacat	ggctcttgcc	600
ggagcaattt	ctgggctggg	gggacccttg	tccacaattg	tagtttcata	tatgtgcac	660
ctctgtgcta	tccttcagat	ccaatcaagg	gaagttcaga	ggaaagcctt	ccgcacctgc	720
ttctcccacc	tctgtgtgat	tggactcggt	tatggcacag	ccattatcat	gtatgttgga	780
cccagatatg	ggaaccccaa	ggagcagaag	aaatatctcc	tgctgtttca	cagcctcttt	840
aatcccatgc	tcaatccctt	tatctgtagt	cttaggaact	cagaagtga	gaatactttg	900
aagagagtgc	tgggagtaga	aagggtttta				930

<210> 222

<211> 969

<212> DNA

<213> Unknown (H38g71 nucleotide)

<220>

<223> Synthetic construct

<400> 222

cacacggagc	cacggaatct	cacaggtgtc	tgagaattcc	tcttcctggg	actctcagag	60
gatccagaac	tgctgccggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctggtc	120
atggtgctga	ggaacctgct	cagcatcctg	gctgtcagct	ctgactcccc	tccacacccc	180
cgtgtacttc	tctctctcca	acctgtgctg	ggctgacatc	ggtttcacct	cgcccacggt	240
tcccaagatg	attgtggaca	tgcagtcgca	tagcagagtc	atctctcatg	cgggctgcct	300
ggcacagatg	tctttcttgg	tcttttttgc	atgtatagaa	gacatgctcc	tgactgtgat	360
ggcctatgac	agctttgtag	ccatctgtca	ccctctgcac	taccagtc	tcatgaatcc	420
tcacctctgt	gtcttctctg	ttttggtgtc	ctttttcctt	agcctgttgg	attcccagct	480
gcacggttgg	attgtgttac	aattcaccat	catcaagaat	gtggaaatct	ctaattttct	540
ctgtgacccc	tctcaacttc	tcaaacttgc	ctgttctgac	agcgtcacca	atagcatatt	600
catatatatt	gatagtacta	tgtttggttt	tcttcccat	tcagggatcc	ttttgtctta	660
gtataaaatt	gtcccctcca	ttctaaggat	gtcatcgcca	gatgggaagt	ataaagcctt	720
caccacctgt	ggctctcacc	tagcagttgt	ttgctgattt	gatggaacag	gcattggcat	780
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cgctgtggtc	acccccatgc	tgaacctttt	catctacagc	ctgagaaaca	gggacataca	900
aagtgcctcg	cggaggctgc	gcagcagaac	agtggaaatct	catgatctgt	tccatccttt	960
ttcttgtgt						969

<210> 223

<211> 945

<212> DNA

<213> Unknown (H38g72 nucleotide)

<220>

<223> Synthetic construct

<400> 223

atggcctgga	gcaatcagtc	tgcggttaacc	gaattcatac	tacggggtct	gtccagttct	60
ttagaactcc	agattttcta	cttcctgttt	ttctccatag	tctatgcagc	cactgtgctg	120
gggaaccttc	ttattgtggg	caccattgca	tcagagccac	accttcattc	ccctacgtac	180
ttctgtctgg	gcaatctctc	cttcattgac	atgtccctgg	cctcatttgc	cacccccaaa	240
atgattgcag	acttccttag	agaacacaaa	gccatctctt	ttgaaggctg	catgacccag	300
atgttcttcc	tacatctctt	agggggtgct	gagattgtac	tgctgatctc	catgtccttt	360
gataggtag	tggtatctg	taagcctcta	cattacctaa	caatcatgag	ccgaagaatg	420
tgtgttgggc	ttgtgatact	ttctgggatt	gtcggcatct	tccatgctct	gagtcatgta	480
gcatttacag	tgaatctgcc	cttctgtgga	cccaatgaag	tagacagttt	cttttgtgac	540
ctcccttttg	tgattaaact	tgcttgtgtc	gacacatata	ttctgggggt	gttcatgac	600
tcaaccagtg	gcatgattgc	cctgggtgtc	ttcatctct	tggtgatctc	ttacactatc	660
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cctttcacaa	atttcccaat	agacaaagta	ctctcagtat	tttataccat	atacactccc	840
ctcttgaatc	cagtgtatcta	taccgtagg	aataaagatg	tcaagtattc	catgaggaaa	900
ctaagcagcc	atatcttta	atctaggaag	actgatcata	ctcct		945

<210> 224

<211> 963

<212> DNA

<213> Unknown (H38g73 nucleotide)

<220>

<223> Synthetic construct

<400> 224

atgaaaaagt	acatggaaag	gactaattga	acaactgagt	ttgagttgat	tctcataagt	60
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ctatgagtag	tcataagttg	acaaaaactc	ctttttgtca	catgcttagt	ggtgtatcta	120
gtgaccctct	tggggaacag	aatacagatc	atcccaacac	tccttggttc	ccacctatat	180
ttatgccatg	gcaatccctc	cttcctggat	atcgggctta	cgcccttttt	actccctcta	240
tcctaataaa	cttcctatca	gagggaaaaa	aactctcttt	cacagattgt	attatacaaa	300
tgtctatctt	ctattccatg	gggtccacgg	agtgtgtgct	cctagcagtg	atggcatatg	360
ataactgtgt	ggtcatcagc	aaattccctga	gataccctct	catcataaat	aagggtgaata	420
aaataaaaaa	ggtgctttgt	gttttcatgg	ctactgtctc	ttatgaatta	ggattttctca	480
acagacaaaa	tgtattaata	gttacatatg	aatgcacttt	tgtggaaaac	acatcattaa	540
tcatttttat	aaaatattac	agttaatggc	tctggcttgc	atagatattt	ccttgaatga	600
gaatataata	atattgggca	aagtaaactt	tccatttact	ttattactac	catttcagtt	660
cttttatctc	agttttttat	attttcacca	tctatgctgt	attgaaatca	attcagctga	720
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ccggacaatc	ctcttcatgt	acataaagtc	aacatcta	ggcactactt	cagagaaact	840
gggtgacctg	ttctgctggg	tagtaatgct	catgctcaat	cttatcatct	atagcctggg	900
gaatatggag	gtgcttgggg	ttatgaagaa	attgatcagt	atgagtagac	cctggtgctg	960
gaa						963

<210> 225

<211> 974

<212> DNA

<213> Unknown (H38g74 nucleotide)

<220>

<223> Synthetic construct

<400> 225

cacacggagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggg	cctcgctttg	ctgtccctgt	ccctgtccat	gtccatgtat	120
ctgggtcacg	tgctgaggaa	cctgctcagc	atcctggctg	tcagctctga	ctcccaactc	180
cacacccccca	tgtacttctt	cctctccaac	ctgtgctggg	ctgacatcgg	tttcacctcg	240
cccattgggtc	ccaagatgat	catggacatg	cagtcgcata	gcagagtcac	ctctcatgcg	300
ggctgcctga	cacggatgtc	tttcttggtc	ctttttgcat	gtatagaaga	catgctcctg	360
actgtgatgg	cctatgactg	ctttgtagcc	atctgtcgcc	ctctgcacta	cccagtcac	420
atgaatcctc	acctctgtgt	cttcttcggt	ttggtgtcct	ttttccttag	cctgttggat	480
tcccagctgc	acagttagat	tgtgttacia	ttcactttct	tcaataatgt	ggaaattgct	540
aattttgtct	atgagccatc	tcaacttctc	aaccttgact	gttctgacac	cgatcatcaat	600
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tcttagtata	aaattgtccc	ctccattcta	aggatgtcat	cgtcagatgg	gaagtataaa	720
gccttcgcca	cctgtggctc	tcacctagca	gttgtttgct	gatttgatgg	aacaggcatt	780
ggcatgtacc	tgacttcagc	tgtgtcacca	ccccccagga	atggtgtggc	ggcgtcagtg	840
atgtacgctg	tggtcacccc	catgctgaac	cttttcatct	acagcctgag	aaacagggac	900
attcaaagtg	ccctgcagag	gctgagtagc	agaacagtgg	aatctcatga	tctgttccat	960
cctttttctt	gtgt					974

<210> 226

<211> 957

<212> DNA

<213> Unknown (H38g75 nucleotide)

<220>

<223> Synthetic construct

<400> 226

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gaggtggagc	tgtgtctcct	ggtgtcctct	ctgcccacgt	tcctgtctgac	tcttctgggg	120
aacctgtctc	tcatctccac	tgtgtgtgct	tgtctccgcc	tccacacccc	catgtacttc	180
ttcttgtgca	acctctctat	cctggacatc	ctcttcacct	cagtcactct	tccaaaagtg	240
ttggccaact	taggatctag	ggataaaaac	atctcctttg	ccggatgtat	caccagtgct	300
tatttctact	ttttcttggg	cacagttgag	ttctcctctg	tgacgggtcat	gtcttatgac	360
cgttatgccca	ccatctgctg	ccccctgcgg	taccaccaca	tcagtagacc	ttctgtctgc	420
attgggaccg	ttgtattctc	ttgggtggga	ggcttcctgt	ctgtgtctct	tccaaccatc	480

ctcatctccc	agctgccctt	ctgtggctcc	aatatcatta	accacttctt	ctgtgacagt	540
ggacccttgc	tggccctggc	ctgtgcagac	accactgcca	tcgagctgat	ggattttatg	600
ctttcttcca	tggtcatect	ctgtgcata	gtcctcgtgg	cctattccta	tacgtacatc	660
atcttgacca	tagtgcgcat	tccttctgca	agtgggaagga	agaaggcctt	taatacctgt	720
gcttcccacc	tgaccatagt	catcattcct	agtggcatca	ctgtgtttat	ctatgtgact	780
ccctcccaga	aagaatatct	ggagatcaac	aagatccctt	tggttctgag	cagtgtggtg	840
actccattcc	tcaaccctt	tatatatact	ctgaggaatg	acacagtgc	gggagtcctc	900
agggatgtgt	gggtcagggt	tcgaggagtt	tttgaaga	ggatgagggc	agtgcgtg	957

<210> 227

<211> 939

<212> DNA

<213> Unknown (H38g76 nucleotide)

<220>

<223> Synthetic construct

<400> 227

atggaaactg	caaattacac	caaggtgaca	gaatttggtc	tcactggcct	atcccagact	60
cgggaggtcc	aactagtcct	atttggtata	tttctatcct	tctatttggt	catcctacca	120
ggaaatatcc	ttatcatttg	caccatcagg	ctagaccctc	atctgacttc	tcctatgtat	180
ttcctgttgg	ctaactctggc	cctccttgat	atttggtact	cttccattac	agccccataa	240
atgctcatag	acttctttgt	ggagaggaag	ataatttcct	ttggtggatg	cattgcacag	300
ctcttcttct	tacactttgt	tggggcttcg	gagatgttct	tgctcatagt	gatggcctat	360
gaccgctatg	ctgctatctg	ccgacccttc	cactatgcta	ccatcatgaa	tcgacgtctc	420
tgctgtatcc	tggtggctct	ctcctggatg	gggggcttca	ttcattctat	aatacagggtg	480
gctctcattg	ttcgacttcc	tttctgtggg	cccaatgagt	tagacagtta	cttctgtgac	540
atcacacagg	ttgtccggat	tgccctgtgcc	aacaccttcc	cagaggagtt	agtgatgatc	600
tgtagtagtg	gtctgatctc	tgtgggtgtg	ttcattgctc	tgtaaatgtc	ctatgccttc	660
cttctggcct	tgctcaagaa	acattcaggc	tcagatgaga	ataccaacag	ggccatgtcc	720
acctgctatt	cccacattac	cattgtgggtg	ctaattgttg	ggccatccat	ctacatttat	780
gctcgcccat	ttgactcatt	ttccctagat	aaagtgggtg	ctgtgtttca	tactgtaata	840
ttccctttac	ttaatcccat	tatttacaca	ttgagaaaca	aggaagtaaa	ggcagccatg	900
aggaaggtgg	tcaccaaata	tattttgtgt	gaagagaag			939

<210> 228

<211> 940

<212> DNA

<213> Unknown (H38g77 nucleotide)

<220>

<223> Synthetic construct

<400> 228

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atacaaatat	ttgtttttgt	gttcttattt	tgtaatgttg	ccatcttggt	gggaaacttt	120
ctgatcctta	tctctatttg	atgtagtcct	ctttttaacc	aaccaatgca	ctattttctc	180
aggctatatg	aatatctact	atacctcctg	tgtcacaccc	aaaataattg	gtgatctagt	240
agtgggaaga	ataaacatct	cctatgatag	gagtccttcc	catgcacttc	tttggaatca	300
ttgaaatctt	catccttaca	gtcatggctt	ttgatcacta	tggtgccatc	tgcaaaccctc	360
cccgtacct	aattatcatg	aataggacaa	aatacaatac	tctaattctcg	gttgcttggc	420
tggtggggct	ttccattctt	tgtttcagtt	ttctatgaaa	atctggttgc	ctttctgtgg	480
ctccaacaaa	gttgatgact	aatattaaga	tatttttcct	ttactgaaag	tcgcttgtac	540
tgatacctgc	atcactggtg	tcctcgtggg	tgccaattct	ggaatgtttg	ccttggtaac	600
cttggttctgt	cgtttggctc	ttatgtcatt	atactattcc	ccttaaaaaa	tcattcagta	660
gaggggaagat	gcaaagccct	ctctacctgt	ggatctcata	tcaccatggg	aatctttttc	720
ttcgaaacctt	caacttttgc	ctaccttaga	ccttctcact	tttctgagg	acaaaatatac	780
tgctctgttt	tactactatta	ttgtcccaat	gttcaaccac	ctaactctata	acctgagaaa	840
tacagagatg	aaaaaggcca	tgagaaaagt	ttggtaccaa	atatcatttt	cagaagaaaa	900
acagctgatt	tgtcctactt	agtgtactaa	agaactttat			940

<210> 229
 <211> 912
 <212> DNA
 <213> Unknown (H38g78 nucleotide)

<220>
 <223> Synthetic construct

<400> 229
 atgagaaatg gcacagtaat cacagaattc atcctgctag gctttcctgt tatccaaggc 60
 ctacaaacac ctctctttat tgcaatcttt ctcaacctaca tattaaccct tgcaggcaat 120
 gggcttatta ttgccactgt gtgggctgag ccagggtac aaattccaat gtacttcttc 180
 ctttgtaact tgtctttctt agaaatctgg tacaccacca cagtcacccc caaactgcta 240
 ggaacctttg tagtggcaag aacagtaatc tgcattgctt gctgcctgct gcaggccttc 300
 ttccacttct tcgtgggcac caccgagttc ttgatcctca ctatcatgtc ttttgaccgc 360
 tacctacca tctgcaatcc ccttcaccac ccaccatca tgaccagcaa actctgcctg 420
 cagctggccc tgagctcctg ggtgggtggc ttcaccattg tctttgtca gacgatgtg 480
 ctcattccagt tgccattctg tggcaataat gttatcagtc atttctactg tgatgttggg 540
 ccagtttga aagcgcctg catagacacc agcattttgg aactcctggg cgcatagca 600
 accatccttg tgatcccagg gtcacttctc tttaatatga tttcttatat ctacattctg 660
 tccgcaatcc tacgaattcc ttcagccact ggccaccaa agactttctc tacctgtgcc 720
 tcgcacctga cagttgtctc cctgctctac ggggctgttc tgttcattga cctaagaccc 780
 acagcacact cctcctttaa gattaataag gtggtgtctg tgctaaatac tatectcacc 840
 ccccttctga atcccttat ttatactatt agaaacaagg aggtgaaggg agccttaaga 900
 aaggcaatga ct 912

<210> 230
 <211> 963
 <212> DNA
 <213> Unknown (H38g79 nucleotide)

<220>
 <223> Synthetic construct

<400> 230
 atgacaattc ttcttaatat cagcctccaa agagccactt tcttcctgac gggcttccaa 60
 ggtctagaag gtctccatgg ctggatctct attcccttct gcttcactca cctgacagtt 120
 atcttgggga acctcaccat tctccacgtc atttgtactg atgccactct ccatggaccc 180
 atgtactatt tcttgggcat gctagctgtc acagacttag gcctttgcct ttccacactg 240
 cccactgtgc tgggcatttt ctggtttgat accagagaga ttggcatccc tgctgtttc 300
 actcagctct tcttcaccca cacttgtct tcaatggagt catcagttct gttatccatg 360
 tccattgacc gctacgtggc cgtctgcaac ccactgcatg actccaccgt cctgacacct 420
 gcatgtattg tcaagatggg gctaagctca gtgcttagaa gtgctctctc catcctcccc 480
 ttgccattcc tcctgaagcg cttccaatac tgccactccc atgtgctggc tcatgcttat 540
 tgtcttcacc tggagatcat gaagctggcc tgccttagca tcattgtcaa tcacatctat 600
 gggctctttg ttgtggcctg caccgtgggt gtggactcac tgctcatctt tctctcatac 660
 gccctcatcc ttcgcaccgt gctcagcatt gcctcccacc aggagcgact ccgagccctc 720
 aacacctgtg tctctcatat ctgtgctgta ctgctcttct acatccccat gattggcttg 780
 tctcttgtgc atcgcttttg tgaacatctg ccccgcttg tacacctctt catgtcctat 840
 gtgtatctgc tgggtaccac ctttatgaac ccatcatct acagcatcaa gaccaagcaa 900
 attcgccagc gcatcattaa gaagtttcag ttataaagt cacttaggtg tttttggaag 960
 gat 963

<210> 231
 <211> 968
 <212> DNA
 <213> Unknown (H38g80 nucleotide)

<220>
 <223> Synthetic construct

<400> 231

atggggaacc	acaccaccgt	caccgagttt	gtcctgctgg	ggctctcaga	gacctgtgag	60
ctgcagatgc	tcacttctct	ggggctcctc	ctgacctacc	tcctcacact	gctggggaat	120
ctggtcacgc	tggtcacac	cctcatggac	aggcgctcc	acaccaccat	gtactacttc	180
ctccgcaact	ttgtgtccc	ggagatctgg	ttcacctcgg	tcactcttcc	caagggtgctg	240
gccaacatcc	tcacaggata	caagaccatt	ccctcccagg	ctgcttctctg	caaagtttgc	300
tctatttttt	cttgggcacc	acagagttct	tcctcctggc	ggtgatgtcc	tttgacaggt	360
acgtggccgt	atgtaaccct	ttgcattatg	ccaccatcat	gagcaaaagg	gtctgtgtcc	420
agctagtcc	ctgttagtgg	atgacaggat	tccttctcat	cattattcca	agttttcttg	480
tccttcagca	gccattctgt	ggccccaaca	tcattaacca	tttcttctgt	gacaactttc	540
ccctcttgaa	actcatttgt	gcagacatga	ctctgataga	gctcctgggt	tttggtatag	600
ccaacgtcag	cttactgggc	actctgtcta	tgacggccac	ttgctatggc	cacatcctcc	660
acgccattct	gcacatcccc	tcagccaaag	agaagcagaa	agccttctcc	gcctgctcct	720
cccacatcat	tgtcgtgtct	ctcttctatg	gcagctgcat	cttcagtac	attcagtcag	780
gcaagagtga	ccagaaggaa	gacaggaaca	aggtggcggc	attgcttaac	accgtggtga	840
ccctgatgct	caaccccttc	atctacaccc	tgaggaacaa	acaggtgaaa	caggtgttta	900
ggcagcaggt	gagcaaacctc	ctcatataaa	gctgtgtaaa	aaaaaaactg	aagctcagca	960
tccccaga						968

<210> 232

<211> 949

<212> DNA

<213> Unknown (H38g81 nucleotide)

<220>

<223> Synthetic construct

<400> 232

gaaataaaga	tagcaaacaa	cacagtagtg	acagaattta	tcctccttgg	tctgactcag	60
tctcaagata	ttcagctctt	ggtctttgtg	ctgatcttaa	ttttctacct	tatcatectc	120
cctggaaatt	tcctcatcat	tttcaccata	aagtcagatc	ctgggctcac	agcaccctc	180
tatttcttcc	tgggcaactt	ggccttctctg	gatgcacct	actccttcat	tgtggtccc	240
cggatgttgg	tggacttctt	ctctgcgaag	aatgtaatct	cctacagagg	ctgcatcact	300
cagctctttt	tcttgcaact	ccttgaggga	ggagagggat	tactccttgt	gatgtagcct	360
ttgaccgcta	catcgccatc	tgccggcctc	tgcactattc	tactctcatg	aaccccagag	420
cttgctatgc	aatgatgttg	gctctgtggc	ttgggggttt	tgtccactcc	attatccagg	480
tggtcctcat	cctccgcttg	cctttttgtg	gccccaaacca	gctggacaac	ttcttctgtg	540
atgtcccaca	ggtcatcaag	ctggcttgca	ccgacacgtt	tgtggtggag	cttctgatgg	600
tcttcaacag	tggcctgatg	acactcctgt	ctttctgggg	cttctggcct	cctatgcagt	660
catectgtgc	catgttcgta	aggcagcttc	tgaattgaag	aacaaggcca	tgtccacgtg	720
caccactcat	gtcattatta	tacttcttat	gtttggacct	gctatcttca	tctacatgca	780
ccccttcagg	gccttaccag	ctgacaaggt	ggtttctttc	tttcacacag	tgatctttcc	840
attgatgaat	cctatgattt	atacccttcg	aaaccaggaa	gtgaaaactt	ccatgaagag	900
gttattgagt	cgacatgtag	tctgtcaagt	ggactttata	ataagaaac		949

<210> 233

<211> 857

<212> DNA

<213> Unknown (H38g82 nucleotide)

<220>

<223> Synthetic construct

<400> 233

gtcatacgaa	accagacaat	ggtaactgaa	ttcaccgggt	ctcccttctt	gctgtccagg	60
agcttcagat	ttggctatgt	gtccttctct	ggctggttca	tatgtccacc	ataacaggaa	120
acctttctgt	cattttctta	acgtggacag	ataattgtct	ccaaacccca	atggacttgt	180
tccttagaaa	aaagtcatat	cgttctcttg	ctgcatcacc	caaataatatt	tctacttctt	240
tctagggaca	gtggcgttta	tccccttggc	agtgacatcc	ttcaaact	gcatggcaac	300
ctgtgacccc	ctgtgcagca	ccatcattgc	aaaaagcagg	gcctgcctcc	tgtggctct	360
gggatgctgg	atgggaacct	tcctggctgt	gttgccctg	actattgtgg	tgtccaggtt	420

gccagactgt	actgaaaaaa	ttagtccctt	cttctgtgac	attgcctctt	tactgcagg	480
ggcctgtatt	gatattcatt	tcattgagat	gataagcttc	ctttgatcat	ctcttatgg	540
cctgacctcg	ctgggtctta	atgccacatc	ctacgcctac	atcattttctc	cctcctgtgc	600
atccccctcag	cccaaggatg	tcaggaggcc	ttttccacct	gtgcttcaca	catcaccatc	660
atctttattg	cctgcccga	ctccatctcc	acgtgtgtga	ggcctaacc	gaggtattag	720
ctggattttg	acaaagtgc	agctatcctc	actatagtag	tgacttcttt	tctgaatccc	780
cgcatttata	gcttgaggta	aaggaagtat	gaagggagtc	aatttgcaca	atactgtcac	840
cacattccaa	aggaaca					857

<210> 234

<211> 921

<212> DNA

<213> Unknown (H38g83 nucleotide)

<220>

<223> Synthetic construct

<400> 234

atggaaagcg	agaacagaac	agtgataaga	gaattcatcc	tccttgggtct	gacccagtct	60
caagatatcc	agctcctgg	ctttgtgcta	gttttaatat	tctacttcat	catcctccct	120
ggaaattttc	tcattatatt	caccataaag	tcagacctg	ggctcacagc	ccccctctat	180
ttctttctgg	gcaacttggc	cttcctggat	gcactcctact	ccttccactgt	ggctccccgg	240
atgttgggtg	acttcctctc	tcggaagaag	ataatctcct	acagaggctg	catcactcag	300
ctctttttct	tgcacttcct	tggaggagg	gagggattac	tccttgttgt	gatggccttt	360
gaccgttaca	tcgccatctg	ccggcctctg	cactatccta	ctgtcatgaa	ccctagaacc	420
tgctatgcaa	tgatgttggc	tctgtggctt	gggggttttg	tccactccat	tatccagggtg	480
gtcctcatcc	tccgcttgcc	tttttgtggc	ccaaaccagc	tggacaactt	cttctgtgat	540
gtcccacagg	tcatcaagct	ggcctgcacc	gacacatttg	tgggtggagct	tctgatggtc	600
ttcaacagtg	gcctgatgac	actcctgtgc	ttcttggggc	ttctggcctc	ctatgcagtc	660
attctttgtc	gcatacgagg	gtcttcttct	gaggcaaaaa	acaaggccat	gtccacgtgc	720
atcacccata	tcattgttat	attcttcatg	tttggacctg	gcacttctcat	ctacacgcgc	780
cccttcagg	ctttccacgc	tgacaagggtg	gtttctctct	tccacacagt	gatttttccct	840
ttgttgaatc	ctgtcattta	tacccttcgc	aaccaggaag	tgaaagcttc	catgaaaaag	900
gtgtttaata	agcacatagc	c				921

<210> 235

<211> 927

<212> DNA

<213> Unknown (H38g84 nucleotide)

<220>

<223> Synthetic construct

<400> 235

atggaaaatc	aaaacaatgt	gactgaattc	attcttctgg	gtctcacaga	gaacctggag	60
ctgtggaaaa	tattttctgc	tgtgtttctt	gtcatgtatg	tagccacagt	gctggaaaa	120
ctacttattg	tggtaactat	tatcacaagt	cagagtctga	ggtcacctat	gtattttttt	180
cttaccttct	tgtccctttt	ggatgtcatg	ttctcatctg	tcgttgcccc	caagggtgatt	240
gtagacaccc	tctccaagag	cactaccatc	tctctcaaag	gctgcctcac	ccagctgttt	300
gtggagcatt	tctttgggtg	tgtggggatc	atcctcctca	ctgtgatggc	ctatgaccgc	360
tacgtggcca	tctgtaagcc	cctgcactac	acgatcatca	tgagtccacg	ggtgtgctgc	420
ctaattgtag	gaggggcttg	ggtgggggga	tttatgcacg	caatgataca	acttctcttc	480
atgtatcaaa	tacccttctg	tggctcta	atcatagatc	actttatatg	tgatttgttt	540
cagttgttga	cacttgcttg	cacggacacc	cacatcctgg	gcctcttagt	taccctcaac	600
agtgggatga	tgtgtgtggc	catctttctt	atcttaattg	cgctctacac	ggcatccta	660
tgctccctga	agtcttacag	ctctaaaggg	cggcacaaaag	ccctctctac	ctgcagctcc	720
cacctcacgg	tggttgtatt	gttctttgtc	ccctgtattt	tcttgtacat	gaggcctgtg	780
gtcactcacc	ccatagacaa	ggcaatggct	gtgtcagact	caatcatcac	acccatgtta	840
aatcccttga	tctatacact	gaggaatgca	gaggtgaaaa	gtgccatgaa	gaaactctgg	900
atgaaatggg	aggctttggc	tgggaaa				927

<210> 236
 <211> 933
 <212> DNA
 <213> Unknown (H38g85 nucleotide)

<220>
 <223> Synthetic construct

<400> 236

gtagaggata	tggtgccatt	ctctatgagg	atttctggca	tttttcaa	attcatttta	60
cggctatcat	caccttatct	actaatatc	tgtactgaca	tgtgtaccat	ttcagtttac	120
atattctcat	atagtaaaat	gttaactgca	agggaaatta	cctcaaacc	aaaccattaa	180
cgtaacttca	gagacaatat	ggattaagat	tatccatgat	ttccttcacg	aaccaagac	240
tatctccttt	gagggtgca	tggcccagat	attcttggtc	catgtctttg	ctggtggtga	300
gatggtgctc	ctttagacca	tggcatatga	catatatgta	gccatatgca	aacctctcca	360
ttatgcaacc	atcatgaact	tgtgcacatg	tacaggccta	gtggtaggat	cttgggtcac	420
tggagttatg	cactccctga	gccagttagc	tttactgta	agtttgccct	tctgtggccc	480
aaacatagtg	gacagttatt	attgtgacct	tactttggtc	atcaaacttg	cctgtacaga	540
tacttatatc	cctgaagcgt	tgatgctttt	ggacagtggg	cttatggggg	tgacttcatt	600
ttgcttttgc	tgatctccta	cacggtcatt	ctgattactg	tgcagcgacc	ttcctcagca	660
ggtagggcca	aggctgcag	cactctgact	gccacgtga	ctgtggtgac	cctgttcttt	720
gggccttgta	tcttcatcta	tgccctggcct	ttcagcaact	taccagtggg	taacattttg	780
tctgtattct	ctacagtttt	cacacctata	ttaaaccctc	ttatctacac	actgagaaac	840
aaagaggtaa	aatcagcaat	tcataacctg	aagaccctgt	atgtaacttc	caggctgtct	900
tcccagctct	ctctcatagg	actagatttg	ttg			933

<210> 237
 <211> 629
 <212> DNA
 <213> Unknown (H38g86 nucleotide)

<220>
 <223> Synthetic construct

<400> 237

ttgggaaatg	tctcaacaga	gactactttt	atttttggtt	gtttcacaaa	tggacaacaa	60
ttccagcctg	tatgcttctc	ctcattttta	gtgcttggcc	actcagtgtc	tgggctaagt	120
tctctcctca	acatcctggg	gaacttggtc	tcagcttggt	ttcttttggt	tttggttttc	180
agatgtccta	ctcctttgtc	attttaatta	aaatgataat	gaactctata	tctgagaggt	240
acatcaccac	taatttgaag	tgcaagattc	tgcccttggt	tttatctgct	ttgctatcag	300
tgagcactct	aatacttttg	gcttgggggc	actgtgggat	ctgtgtgcct	caggctctgt	360
ctctgacgat	gcttggcctt	cactggggga	ggtattgatg	gtgtcatggc	ccaccagag	420
gcaatgggtc	gtctgtcttt	ctgtgaccgc	agcatcatca	accactgtgt	gtggcacact	480
tcttttctac	aaactctcct	tagagcacct	gcttcacaag	ctgggtgatt	tgtagtcatt	540
gcgtagtgac	tgatcatctt	catctctgac	atactatcct	ttccaccatc	ctccattttc	600
tctttcctga	ggcaaaactc	aaagctttt				629

<210> 238
 <211> 822
 <212> DNA
 <213> Unknown (H38g87 nucleotide)

<220>
 <223> Synthetic construct

<400> 238

atgggggaatc	tgggcatgat	catgggtcatc	aggatcaacc	ccaaactcca	cacccttatg	60
tacttttttc	tcagccactt	gtcctttggt	gatttctgtt	attccaccac	aattacacca	120
aaactgctgg	agaacttggg	tgtggaagac	agaatcatct	ccttcacagg	atgcatcatg	180
caattcttct	ttgcctgtat	atttgtgggt	acagaaacat	tcatgctggc	agcgatggct	240
tatgacagat	ttgtggcagt	gtgtaaccct	ctgctttaca	cagttgcaat	gtcccagagg	300

ctttgtcct	tgtagtg	tgcatcat	tcttgag	tagttgt	ctaacat	360
acatacttt	tgtagttt	atcttttt	aggactaa	tcattaata	ctttgtct	420
gagcacgt	ccattgtg	tggtcctg	tctgacct	acatgagcc	gaaggct	480
ttagtttct	caacattca	tgaaataag	agcctggg	tcattctca	ttcctatg	540
ttcattttt	tcactgtc	gaagatgc	tccactggg	ggcgcaaga	agcgttct	600
acgtgtgc	cccacctg	cgccattac	atcttccat	ggactatcc	ttttctct	660
tgtgttcta	actccaaa	ttcatggc	atgggtcaa	tggtctct	cttttac	720
gtggtcatt	ccatgctg	ccccttgat	tatagcct	ggaacaa	tgtaaaag	780
acagtcagg	agttagtc	taccaaatt	ttatgtcat	aa		822

<210> 239

<211> 1041

<212> DNA

<213> Unknown (H38g88 nucleotide)

<220>

<223> Synthetic construct

<400> 239

atgaccaaca	gcagtgtca	gggagactt	atcctgggt	gtttctctc	tcagcccc	60
ctggaaaaga	tcctctttg	ggctgtttt	atatectat	tccttacc	tgtgggaa	120
acagtaatta	ttctgatct	ctctgtag	cctaaactc	agacaccc	gtattttt	180
ttactcacct	ctccttagt	gatatctgt	ttaccacc	tattgtccc	cagctgct	240
ggaacctaaa	aggacctg	aaaacaat	cattcctgg	ttgtgtcat	cagctctac	300
tctccctggc	attgggtcc	actgagtgt	tctcctggc	tgtaatgg	tttgatcgt	360
atgctgcagt	ttgcaaacc	ctccactat	ccgccgtaa	gaaccctc	ctgtgccag	420
ttctggcagg	ggttgctgt	ctgagtgg	tggaacac	tcttatcc	ggcactgt	480
ccctctggct	tcctcgctg	ggacaccg	tgctccaac	tttctctg	aggtacc	540
catgattaag	cttgcatgt	tggacatcc	tgataatg	gttcagct	ttgttgct	600
actggtcctg	ctcctcttg	ccttagtgc	aatactgct	tcctatgg	atatagcc	660
ggtggtcata	aggatcaag	cagtccagg	ctggtgcaa	ggcctggg	catgtggat	720
ccatttgata	gtagtgtcc	tcttctgtg	gaccatcac	gctgtctac	tccagtc	780
cagttcttat	gcccattgc	atgggaagt	catctccct	ttctatac	ttgtgccc	840
gacctcaat	cctctcat	acacactg	gaataatg	gtgaaagg	cactgcgat	900
atttaacaga	gacttaggc	cataaaaa	gaagcagag	acacagcg	caactttt	960
cacaaagcaa	ctttaaagg	catcttgt	aatttttc	tcaagaact	tgccagct	1020
taaaggaaga	gatgtaatt	t				1041

<210> 240

<211> 957

<212> DNA

<213> Unknown (H38g89 nucleotide)

<220>

<223> Synthetic construct

<400> 240

atggataagt	ccaattctt	agtgggtgt	gaatttgt	tgtagggact	ctgtagtt	60
caaaaactcc	agcttttct	ttttgttt	ttctctgt	tgtatacag	cattgtgct	120
ggaaatctt	tcattatcc	cacagtga	tctgatacc	gcctgactc	ccctatgt	180
tttctcttg	gaaaccttt	ctttgttg	attgtcagg	cttcttttg	taccctaaa	240
atgattgcag	attttctg	tgcacacg	accatatct	tcagtggct	catagccaa	300
attttcttta	ttcaccttt	tactggagg	gagatgggt	tactgttt	gatggcct	360
gacaggtag	tagccatat	caaaccct	tactatgtg	tcatcatg	ccgaaggac	420
tgactgtct	tgtaatgat	ctcctgggt	gtgagcttg	tgcacacatt	aagccagtt	480
tcatttactg	tgaacctgc	ttttgtgga	cctaagtga	tagacagct	ttttgtgat	540
cttctcgag	tcaccaaact	tgctgcctg	gactcttaca	tcattgaa	actaattgt	600
gtcaatagt	gaattcttt	cctaagcact	ttctctct	tggtcagct	ctacatcatt	660
attcttggt	cagtttggt	caagtcttc	gctgcaatg	caaaggcatt	ttctacgt	720
gcttcccata	ttgcagtag	aatattatt	tttgaccct	gcattctcat	ctatgtgtg	780
ccctttacca	tctctcctt	ggataaatt	cttgccatat	tttactctg	tttcacccc	840

gtcctaaacc	ccattatttta	tacactaagg	aatagggata	tgaaggctgc	cgtaaggaaa	900
atttgtgaacc	attacctgag	gccaaggaga	atttctgaaa	tgctactagt	agtgaga	957

<210> 241
 <211> 935
 <212> DNA
 <213> Unknown (H38g90 nucleotide)

<220>
 <223> Synthetic construct

<400> 241	
atgcctgcc	agaactctc
ccgggactcc	agatccccgc
gggaacctgg	gcttgataat
tttttcccc	tcaacttgtc
atgctgatga	gctttgtctc
tttttcttct	gtttctttgt
cgctacgtgg	gcatctgtaa
ttgtctcttt	tactgggtgt
acataatgtt	tatgtccttt
ttcctctcct	tgagctctcc
ttgtgaccgt	tggcattggg
tttccagcat	tctccacatt
gttcccatat	aattgtggta
caccttctat	tctacccctg
tgcccatgtt	taaccatta
ggagaacctt	ttgcagaaaa
	ttagtctctt
	aaaaa
	60
	120
	180
	240
	300
	360
	420
	480
	540
	600
	660
	720
	780
	840
	900
	935

<210> 242
 <211> 1071
 <212> DNA
 <213> Unknown (H38g91 nucleotide)

<220>
 <223> Synthetic construct

<400> 242	
atgaattggg	taaataagag
ccatggctag	agattccacc
ggcaatctga	caataattct
ttttttctta	gcaatctctc
atgctggtaa	acatatgcaa
cttttcattt	tccctggcct
gataggtttg	tagctatttg
tgcttccagt	tggcagctgc
acctggacac	ttaagatgcc
gtccctgctc	tgctcaagtt
ttcatcagt	tgctattcct
attgtccaag	cagtgttgag
tgtggctccc	atctaattgt
caaccacctt	caccagctc
attgcacca	tgctgaatcc
tttaaaagg	tggttgcaaa
agctttgcta	aagacacagt
tttgtcatta	ctatagaaaa
	ctattgtaat
	ctccctcaa
	gaaaatttcc
	t
	60
	120
	180
	240
	300
	360
	420
	480
	540
	600
	660
	720
	780
	840
	900
	960
	1020
	1071

<210> 243
 <211> 959
 <212> DNA
 <213> Unknown (H38g92 nucleotide)

<220>

<223> Synthetic construct

<400> 243

cacacagagc	cacggaatct	cacaggagcc	tgagaactcc	tcctcctggg	actctcagag	60
gatccagaac	tgagcccat	cctcgctggg	ctgtccctgt	ccatgtatct	ggtcacgggtg	120
ctgagggaac	tcctcatcag	cctggctgtc	agctctgact	cccacctcca	cacccaatg	180
tgcttcttcc	tctccaacct	gtgctgggct	gacatcgggt	tcacctcggc	cacgggtccc	240
aagatgattg	tggacatgcg	gtcgcatagc	ggagtcattc	cttatgcgga	ctgcctgaca	300
cggatgtctt	tcttggtcct	ttttgcatgt	gtagaagaca	tgctcctgac	tgtgatggcc	360
tatgactgct	ttgtagccat	ctgtcgccct	ctgcactacc	cagtcacgt	gaatcctcac	420
ctctgtgtct	tcttagtttc	ggtgtccttt	tccttagcct	gttggattcc	cagctgcgca	480
gttggattgt	gttgcaattc	accttcttca	agaatgtgga	aatctctaata	tttgtctgtg	540
acccatctca	acctctcaag	cttgccctgtt	ctgacagcat	catcgatagc	atgttcatat	600
atttcgatag	tactatgttt	ggttttcttc	ccatttcagg	gacccctttg	tcttactata	660
aaattgtccc	ctccattcta	aggatttcat	ctgcagatgg	gtagtataaa	gccttctccg	720
cctgtggctc	tcacctgcca	gttggttgct	tattttatgg	aacaggcatt	ggcgtgtacc	780
tgacttcagc	tgtggcacca	ccctcagga	atggtgtggg	ggcgtcagtg	acgtatgctg	840
tggtcacccc	catgctgaac	cctttcatct	acagcctgag	aaacagggac	attcaaagcg	900
ccctgtggag	gctgcgagc	agaacagtca	aatctcatga	tctgttccat	cctttttct	959

<210> 244

<211> 939

<212> DNA

<213> Unknown (H38g93 nucleotide)

<220>

<223> Synthetic construct

<400> 244

atggaggggt	tcaactgttc	cagagtatct	gaattcatgt	tacttggact	tactgattct	60
cctgaactcc	agagattctt	ttttgtggta	ttttctgtct	tctatttaata	gaccatgttg	120
ggcaactgcc	tgattttgct	cactgtgcta	tcacctcac	accttactc	tcccatgtac	180
ttctgtctca	gcaacctgtc	tctcattgac	atgtgcctgt	cctcctttgc	cacaccaaag	240
atgattatgg	acttttttgc	tctgcgtaag	accatctctt	ttgaaggctg	catttctcag	300
atcttttttt	gcacctcttc	accgggactg	agattgtgct	gctgatctcc	atgtcttttg	360
acaggatata	tgccatatgt	aaacctctcc	attattcaac	aattatgagc	caaagagtgt	420
gtgttgagct	tgtggccgtt	tcttgacag	tgggctttct	gcatacaatg	agccaattag	480
cttttaccct	ctatttgccc	ttctgtggtc	ccaatgttgt	agagtttttt	ctgtgatctt	540
cctttgggtca	tcagctagc	ttgtatggat	atttatgttc	ttgggatctt	catgatttca	600
actagtgggt	tgattgctct	tataagtttt	ctgcttttgc	tcacctccta	catcattgtt	660
cttattactg	tcagggacta	ctcctccaca	ggatcctcca	aggctctttc	tacctgtaca	720
gcacatttta	ttgttgtgtt	aatgttcttt	gggcctgtta	ttttcattta	tgtgtggcct	780
tccacaaact	tcctggtaga	caaaattctc	tctgttttct	ataccatctt	cactcccttt	840
ctgaatccac	ttatctatac	tttgagaaac	caggaagtga	agacagcaat	gaagaagtaa	900
ctgaatattc	agtatttcag	tcttgggaaa	actgtctcgg			939

<210> 245

<211> 1014

<212> DNA

<213> Unknown (H38g94 nucleotide)

<220>

<223> Synthetic construct

<400> 245

atgatattgc	ctgctagctt	ttcttaagga	acaatggaaa	caagcagtgt	aagttctgga	60
acagatttca	tccttctggg	gttttctgat	cgaccccaat	tagagcacat	catctcagtg	120
gttgtcttca	tcattctatat	tgtgactctg	gtaggaaata	caaccatcat	tcttgtatct	180
tatctagaca	cccagctcca	taccttcattg	tattttttct	tatccaattt	gtctttcttg	240

gacctctgtt	atacaactag	cattatcccc	cagatgctgg	caaatcaatg	gggccccaaa	300
aaatctatta	cttatggagg	gtgtgtactc	caattctttt	ttgtccttga	cttgggagcc	360
acagaatgtc	ttctgttggc	tgtgatggcc	tatgatcggt	atgctgctgt	ctgtcaacct	420
cttcactaca	ccttaaaatg	caccctcagc	tttgccactg	cctgggtgag	tggctcttgc	480
agtgccttaa	ttgtttgctc	cttgactttg	aagtgtgcaa	gatgtgggca	ccgggaagtg	540
gataatTTTT	tctgtgagat	gccagcattg	atcaagatgg	cttgtgtcta	ttcaaaagta	600
attgagattg	ttgtctttgc	tttcggagtg	gtatttcttt	tcgtacctct	atcactaatt	660
cttatctcat	atggagttat	cactcaagct	gtaatgagga	tcaagtcagc	aacaagggtg	720
caaaagatcc	ttaatacatg	tggctcccac	ctcacagtag	taattctgtt	ttatggaaca	780
atcattttata	tatacatgaa	gccacagaat	accatatccc	aagatgaagg	gaagttcttc	840
actctttttac	acaatcatca	caccagcct	taaccttccc	atctacactt	taagaacaa	900
agatgtaaag	agtgcactga	agagaatact	gtggatgaaa	aaatcttcag	cagaatcatg	960
aattagatgg	aaaaaagtag	aatgtagagc	actaaagaaa	tattggcatt	tatc	1014

<210> 246

<211> 941

<212> DNA

<213> Unknown (H38g95 nucleotide)

<220>

<223> Synthetic construct

<400> 246

atgcaccaag	gaaattgaac	tactgtctct	aaattctttc	tcctgggaat	cacaacaaag	60
cctaagagc	agcagtttat	cttcatgctg	tttctatgca	cgtatctggt	cactatggta	120
agaaaattac	ttatcatcct	ggcgtttgtc	agtgatgctc	acctccatgg	ccccatatat	180
ttcttccttg	ccaatctatc	tttactaac	gtctgcatca	caaccactac	agtccccaaa	240
atcttggcag	atattcaaag	ccagaattca	accatatcct	ttgaaggatg	ccctgcacaa	300
atgtagtttt	aaatattcct	ggtggatctg	gataatttcc	tattggtaga	catggcatat	360
aattgataca	ttgccatctg	tcacccatta	cactatatgt	ggtagtactg	agtcccaaga	420
actgtgccct	gttggttgtg	actccatggg	ttatctccaa	ccttgtctca	atactgcata	480
tcagtctgct	aagccactta	actttctgtg	atttcacata	tcttctatga	cctggaaccc	540
atttttagggc	ttgcttgctc	agacacccaa	atcaacaact	tgataattac	tgccattggg	600
gaagtagtta	tcttcatccc	ctttaccttc	acattcttgt	ctcctatggc	cttattggca	660
gcactatgct	tggagtcca	tcagccaagg	ggaagtagaa	aacattctct	acatgtgggt	720
cccatctctc	agttgtgccc	caggtcttct	atgggttcat	cattggagtc	tactttctct	780
ccttttttgc	ctactcagca	gaaagggatg	aggtagctgc	tatcatgtat	acaactgtaa	840
ctcacttgat	caaatcattt	atctgtagtc	taagggaacga	ggacatgaaa	ggagcactga	900
ggagaccact	cagcagacaa	ggtttttctg	gagtggtgag	c		941

<210> 247

<211> 941

<212> DNA

<213> Unknown (H38g96 nucleotide)

<220>

<223> Synthetic construct

<400> 247

atgatgaaga	agaaccaaac	catgatctca	gagttcctgc	tcctgggcct	tccatccaac	60
ctgagcagcg	gaatctgttc	tatgccttgt	tcttggccgt	gtatcttacc	acctcctgg	120
ggaacctcct	cgtcattgtc	ctcattcgac	tggactccca	cctccacatg	cctatgtatt	180
tgtgtctcag	caacttgtcc	ttctctgacc	tctgcttttc	ctcggtcaca	atgccccaat	240
tgctgcagaa	catgcagagc	caaaacccat	ccatccctt	tgcggactgc	ctggctcaga	300
tgtactttca	tctgttttat	ggagttctgg	agagcttcc	ccttgtggtc	atggcttata	360
actgctatgt	ggctatttgc	tttctctctg	actacaccac	tatcatgagc	cccaagtgtt	420
gccttggctc	gctgacactc	tcctggctgt	tgaccactgc	ccatgccacg	ttgcacacct	480
tgcttatggc	caggctgtcc	ttttgtgctg	agaatgtgat	tcctcacttt	ttctgtgata	540
catctacctt	gttgaagctg	gcctgctcca	acacgcaagt	caatgggtgg	gtgatgtttt	600
tcattggcgg	gctcatcctt	gtcatcccat	tcctactcct	catcatgtcc	tgtgcaagaa	660
tcgtctccac	catcctcagg	gtcccttcca	ctgggggcat	ccagaaggct	ttctccacct	720

gtggccccc	cctctctgtg	gtgtctctct	tctatgggac	aattattggt	ctctacttgt	780
gccattgac	gaatcataac	actgtgaagg	acactgtcat	ggctgtgatg	tacactgggg	840
tgaccacat	gctgaacccc	ttcatctaca	gcctgaggaa	cagagacatg	agggggaacc	900
ctgggcagag	tcttcagcac	aaagaaaatt	ttttgtctt	t		941

<210> 248

<211> 994

<212> DNA

<213> Unknown (H38g97 nucleotide)

<220>

<223> Synthetic construct

<400> 248

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ccgggactcc	aggtccccgt	cttcttcctg	tttctagggt	tctacgcggg	cacgggtggg	120
gggaacctgg	gcttgataat	cctgataggg	ctcaactctc	gcctgcatac	ccccatgtac	180
ttttccccct	tcaacttgtc	cctcgtagat	tttagtttct	ctacgacct	cattcccaaa	240
atgctgatga	gttttgtctc	aaggaagaac	attatttcct	tcacaggggtg	tatgagtcag	300
ttcttcttct	tctgtttctt	tgtcttttct	gagtccttca	tcctgtcggc	gatgggtgtg	360
gaccgctacg	tgggcatctg	taacccactg	ttgtacacga	tcacatgtc	tccccagggtg	420
tgtttgctcc	ttttactggg	tgtctacggg	atgggggttt	ttggggctgt	ggctcataca	480
ggaaatatag	tgtttctcac	cttttgtgca	gacaaccttg	tcaatcacta	catgtgtgac	540
atccttcccc	ttcttgagct	ctcctgcaac	ggctcttaca	taaatgtcct	ggtcatcttt	600
attgtttgtga	ccgttggcat	tgggggtgcc	attgttgccg	tttttatctc	ttatggtttt	660
attctttcca	gcattctccg	cgtagttct	gctgagggca	ggtctaaagc	cttcagtagc	720
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aaacccccct	ccattttacc	cctggaccag	gggaaagtgt	cctccctgtt	ctataccact	840
gtggtgccca	tgtttaaccc	attaatctac	agcctgagga	ataaggatgt	caaacttgcc	900
ctgaagagaa	ccttttccag	aataagcttt	tcttgaaaaa	aatttttagaa	acagaaaaga	960
gatactagga	tttttttaaa	atcagattgc	tttt			994

<210> 249

<211> 942

<212> DNA

<213> Unknown (H38g98 nucleotide)

<220>

<223> Synthetic construct

<400> 249

atgtcgaatg	aggacatgga	acaggataat	acaacattgc	tgacagagtt	tgttctcaca	60
ggacttacat	atcagccaga	gtggaaaatg	cccctgttct	tgggtgttct	ggtgatctat	120
ctcatcacta	ttgtgtggaa	ccttgggtctg	attgctctta	tctggaatga	cccacaactt	180
cacatcccca	tgtacttttt	tcttgggagt	ttagcctttg	ttgatgcttg	gatattcttc	240
acagtaactc	ccaaaatggt	ggttaatttc	ttggccaaaa	acaggatgat	atctctgtct	300
gaatgcatga	ttcaattttt	ttcctttgca	tttgggtggaa	ctacagaatg	ttttctcttg	360
gcaacaatgg	catatgatcg	ctatgtagcc	atatgcaaac	ctttactata	tccagtgatt	420
atgaacaatt	cactatgcat	acggctgtta	gccttctcat	ttttagggtg	cttcctccat	480
gccttaattc	atgaagtcc	tatatccaga	ttaaccttct	gcaattctaa	cataatacat	540
catttttact	gtgatattat	accactgttt	atgatttctt	gtactgacc	ttctattaat	600
tttctaattg	tttttatttt	gtctggctca	attcagggtat	tcaccattgt	gacagttctt	660
aattcttaca	catttgctct	tttcacaatc	ctaaaaaaga	agtctgttag	aggcgtaagg	720
aaagcctttt	ccacctgtgg	agcccatctc	ttatctgtct	ctttatatta	tggcccactt	780
atcttcatgt	atttgcgccc	tgcattctca	caagcagatg	accaagatat	gatagactct	840
gtcttttata	caatcataat	tcctttgcta	aatcccat	tctacagtct	gagaaataaa	900
caagtaatag	attcattcac	aaaaatggta	aaaagaaatg	tt		942

<210> 250

<211> 939

<212> DNA

<213> Unknown (H38g99 nucleotide)

<220>

<223> Synthetic construct

<400> 250

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ctggaggagc	agaagccccct	ctttgggtcc	ttcctgttca	tgtacttggt	cacgggtggca	120
ggcaacctcc	tcatcattct	agtcattcatt	actgacactc	aactccatac	ccccatgtac	180
ttctttctag	ccaacctctc	ccttgcagat	gcctgctttg	tgtccaccac	agtccctaag	240
atgctggcaa	acatacagat	ccagagtcag	gccatctcct	actcaggggt	tctactacag	300
ttgtattttt	tcatgttatt	tgtgatgctg	gaggcattcc	tcttggcggt	catggcctat	360
gactgctacg	tggccatatg	ccaccactt	cattacattc	tgatcatgag	ccctgggctc	420
tgcattcttc	tcgtgtctgc	atcctggatc	atgaatgccc	tccactccct	tctacacaca	480
cttctgatga	acagcctgtc	cttctgcgca	aaccatgaga	tcccacactt	cttctgtgac	540
atcaatcccc	tcctgagtct	gtcctgcaca	gaccccttca	ccaatgagct	ggtgatcttc	600
atcactgggg	gtctcacagg	actcatttgt	gtgctttgcc	tgattatctc	ttacacgaac	660
gttttctcga	ccatcctgaa	gatcccatca	gctcagggga	agcggaaagc	cttttccacc	720
tgcagctctc	atctctccgt	ggtctctctc	ttctttggga	cttctttttg	tgttgatttc	780
agttctccct	caaccactc	ggcccagaag	gacacagttg	catcagtgat	gtacacagtg	840
gtaaactccaa	tgttgaatcc	ctttatctac	agtttgagga	accaagaaat	aaagtcttcc	900
ctgagaaagt	taatctgggt	tcggaaaatt	cattccct			939

<210> 251

<211> 931

<212> DNA

<213> Unknown (H38g100 nucleotide)

<220>

<223> Synthetic construct

<400> 251

atggaagagg	aaaatgcaac	attgctgaca	gagtttgttc	tcacaggact	tttatatcaa	60
ccacagtgga	aaataccct	gttcttgaca	ttcttggtta	tatatctcat	caccatcatg	120
gggaatcttg	gtctgattgc	tgatcatctg	aaagaccctc	accttcagat	cccaatgtac	180
ttactcctcg	ggaatttagc	ttttgtagat	gcttggtat	catctacagt	gactccaaag	240
atgctgaata	acttcttagc	taagagtaag	atggtatctc	tgctgaaag	caaaatacag	300
tttttttctg	ttgcaatcag	tgtaaccact	gaatgttttc	tcttggcaac	aatggcatat	360
gatcgctatg	tagccatatg	caaaccctta	ctttatccag	ccattatgac	caatggactg	420
tgcattccggc	tatgtagggtg	gtcttcttca	tgctttaatc	catgaaggat	ttttattcag	480
actaaccttc	tgtaactcca	acgtagtaca	ccacatttac	tgtgacatta	tcccattgtc	540
taagatttct	tgtactgatt	cttctattaa	ttttctaatg	gtttttattt	tctcagggtc	600
aattcaagtt	ttcaccattg	ggactgggtc	tatatcttat	acatttgtcc	tctttacaat	660
cttgaaaaag	aaatctgtca	aagggtataag	aaaagccttc	tccacctgtg	gagctcatct	720
cttatctgta	tctttatacc	atgggcccct	cgacttcatg	tatatgggct	ctgcatcccc	780
acaggctgat	gacgaagaca	tgatggagtc	tctattttac	actgtcatag	ttcctttatt	840
aaatcccatg	acctacagcc	tgagaaacaa	aacagtaata	gcttcattca	caaaaatggt	900
caaaagaaat	aatatttaga	tctcttactc	a			931

<210> 252

<211> 690

<212> DNA

<213> Unknown (H38g101 nucleotide)

<220>

<223> Synthetic construct

<400> 252

ttctgtttgt	tcccagccac	agtctccaag	gcagtgggtga	aatttttggc	agagacaatt	60
tccttctcct	attatgtgat	acaaatgctg	gtatttttgt	tctttgtgac	tactgaatgc	120
aatcttttag	cctccctggg	caaggacatt	tatatgcca	tcagacaacc	catgctctat	180

cctgtcacta	tgtcccaagt	ttgttgtatc	caattagtagg	cttcatgtta	cgggcatgga	240
gttatccata	ctatgttttt	aggaggttca	atctctatat	ttgccttttg	taagttcaaa	300
ccatcatcag	cttttttggg	gacagtttcc	cactcttggt	cctctcctgc	tcagacacct	360
acataatgaa	ttctttgttc	tttttcactg	ggtgcttcat	ttggatgagc	tcttgaccag	420
tcatccttgt	ctcccacatg	ttcatcattg	tcactttctt	gaggatcttc	tcagttgtag	480
ttgaatctaa	agggttttctt	gctttttctt	cacatctaac	tgctatcatt	ctcttctatg	540
gggacattat	atttatatat	gtgacattct	tccaactatt	ttctgaacca	agaccagact	600
gtatccattt	tctacatggt	aagaattctt	ttgttaagcc	ccattatcta	ttgtttaata	660
aaaatgcaag	tgatttgttt	tcttgaaaat				690

<210> 253

<211> 647

<212> DNA

<213> Unknown (H38g102 nucleotide)

<220>

<223> Synthetic construct

<400> 253

cttttttttt	ttgtctgaca	cagcatcctg	acctgatagg	aaggagtaaa	agaaatttgg	60
tactttcagg	aattttctgac	atatccaaga	catagaaact	cctgtttgtc	tcttcctgca	120
tgtattattc	ctcaagaatt	ttcctaagga	ggacagtaaa	cattctattt	ctgcttaagg	180
ttatctcatt	gctttgttat	gggtcaaaac	tcagtttgtt	catttttgtt	gttactgcag	240
aatttttagct	tttggcctcc	aggatctgcc	attgctatat	tattatttgt	aaccttctct	300
ctacccaatt	ctcacattaa	aagcttttaa	tttcaattct	gacggctcat	tacaataaga	360
gagtatgtat	ttcaataaca	acatcaaaca	ctatgtctta	gctcttcttt	ggcagatcca	420
atgtggtgaa	caacttctct	gatcttctct	tgctcttaga	tttatcctgc	acatttgtga	480
gtttctgac	tccatctcag	cttctctgac	atagtcctgg	tcccataat	tttatcattg	540
tggtcaatat	aaagatttag	ttagctgaag	ggaagcaca	agacttctct	atctgtccat	600
tataatttgc	tactgtcagc	aattttttta	tggcacacat	acatatt		647

<210> 254

<211> 936

<212> DNA

<213> Unknown (H38g103 nucleotide)

<220>

<223> Synthetic construct

<400> 254

ttcatggaaa	ataggaatat	tgctactgtc	tttattctcc	tgggactttc	tcaaaacaag	60
aacattgaag	ttttttggtt	tgtattattt	gtattttgct	acattgctat	ttggatggaa	120
aacttcatca	taatgatttc	tatcatgtac	athtagctaa	ttgaccaacc	catgtatttc	180
ttccttaatt	acctcgact	ctcagatctt	tgctacatat	ccactgtggc	ccccaagcta	240
atgattgacc	tactaacaga	aaggaagatc	gtttcctata	ataactgcat	gatacagcta	300
tttatcactc	acttccttgg	agacattgag	atcttcatac	tcaaagcaat	ggcctatgac	360
cactacatag	ccatctgcaa	gcacctgcac	tacaccatca	tcacgaccaa	gcaaagctgt	420
aacaccatca	tcatagcttg	ttgtactggg	ggatttatac	actctgccag	tcagtttctt	480
cttaccatct	tcttaccgtt	ctgtggtctt	aatgagatag	atcagtactt	ctgctatgtg	540
tatcctctgc	tgaagttggc	tcgcattgat	atatacagaa	ttggtttctt	ggtaattgtt	600
aattcaggcc	tgatttcttt	gttggctttt	gtgattttga	tgggtgtctta	ttatttgata	660
ttatccacca	tcagggttta	ctctgctgag	agtcatacca	aagctctttc	aacctgtagc	720
tctcacataa	tagttgtggg	cctattcttt	gtgctgccc	tcttcattta	catcagacca	780
gccataactt	ttccagaaga	taaagtgttt	gttctcttct	gtgccatcat	tgctcccatg	840
ttcagtcctc	ttatctacat	gctgagaaag	gtggagatga	agaacgctgt	aaggaaaatg	900
tggtgtcatc	aattgcttct	ggcaaggaag	taactt			936

<210> 255

<211> 924

<212> DNA

<213> Unknown (H38g104 nucleotide)

<220>

<223> Synthetic construct

<400> 255

atggccatgg	acaatgtcac	agcagtgttt	cagtttctcc	ttattggcat	ttctaactat	60
cctcaatgga	gagacacgtt	tttcacatta	gtgctgataa	tttacctcag	cacattgttg	120
gggaatggat	ttatgatctt	tcttattcac	tttgacccca	acctccacac	tccaatctac	180
ttcttcctta	gtaacctgtc	tttcttagac	ctttgttatg	gaacagcttc	catgccccag	240
gctttggtgc	attgtttctc	tacccatccc	tacctctctt	atccccgatg	tttggtctaa	300
acgagtgtct	ccttggtctt	ggccacagca	gagtgcctcc	tactggctgc	catggcctat	360
gaccgtgtgg	ttgctatcag	caatcccctg	cgttattcag	tggttatgaa	tggcccagtg	420
tgtgtctgct	tggttgctac	ctcatggggg	acatcacttg	tgctcactgc	catgctcatc	480
ctatccctga	ggcttcactt	ctgtggggct	aatgtcatca	accattttgc	ctgtgagatt	540
ctctccctca	ttaagctgac	ctgttctgat	accagcctca	atgaatttat	gatcctcatc	600
accagtatct	tcaccctgct	gctaccattt	gggtttgttc	tcctctccta	catacgaatt	660
gctatggcta	tcataaggat	tcgctcactc	cagggcaggc	tcaaggcctt	taccacatgt	720
ggctctcacc	tgaccgtggt	gacaatcttc	tatgggtcag	ccatctccat	gtatatgaaa	780
actcagtcga	agtcttacct	tgaccaggac	aagtttatct	cagtgtttta	tggagctttg	840
acaccatgt	tgaaccccct	gatatatagc	ctgagaaaaa	aagatgttaa	acggggcaata	900
aggaaagtta	tgttgaaaag	gaca				924

<210> 256

<211> 971

<212> DNA

<213> Unknown (H38g105 nucleotide)

<220>

<223> Synthetic construct

<400> 256

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cctgaactgc	agcccgtcct	ctttgggctg	ttcctgtcca	tgtacctggt	catgggtgctg	120
gggaacctac	tcatactcct	ggcgcgcagc	tctgactccc	acctccacag	ccccatgtaa	180
ttcttctctt	ccaacttgte	ctttgtggac	acctgtttca	tctgcaccac	agtccccaag	240
atgctagtga	acatccaggc	acggagcaaa	gacatctcct	acatgggggtg	cctcactcag	300
gtgtattttt	aaatgatgtt	tgctggaatg	gatactttcc	tactggctgt	gatagcctat	360
gaccggtttg	tggccatctg	ccacccactg	cagtacatgg	tcatacataa	cccccatctc	420
tgtggccctc	tggttctggc	atcttggttc	atcattttct	ggttctccct	ggttcattat	480
ctactgatga	agaggctgac	cttctccaca	ggcactgaga	ttccgcattt	cttctgtgaa	540
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attgtctcct	ccttaatgag	aatgtcctcc	accgagggca	agtacaaagc	cttttccacc	720
tgtggatctc	acctctgtgt	ggtctccttg	ttctatggaa	caggacttgg	ggtctatctg	780
agttctgctg	tgacccatcc	ttcccagagc	agctccatgg	cctcagtgat	gtacgccatg	840
gtcaccccca	tgtgaaccc	cttcatctac	agcctgagga	acaaggatgt	gaagggggcc	900
ctggggagac	tccttagcag	ggcagcctct	tgtctcttac	ggtacacaac	ctcagaacta	960
agaggatgct	a					971

<210> 257

<211> 873

<212> DNA

<213> Unknown (H38g106 nucleotide)

<220>

<223> Synthetic construct

<400> 257

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cctgaactcc	agatattctt	ttctgtggtg	ttttctgtct	tctatttaat	gaccatgttg	120
ggcaactgcc	tgattttgct	cactgtccta	ttcacctcac	accttcactc	tcgcatgtac	180

ttcctgctca	gcaacatgtc	tcattgacat	gtgcctgtcc	tcctttgcca	caccaaagat	240
gattatggac	ttttttgctc	tgcgtaacac	catctctttt	gaaggctgca	tttctcagat	300
ctttttttta	cacctcttca	atgggactga	gattgtgctg	ttgatctcca	tgtcttttga	360
caggatatatt	gccatatgta	aaacctctcca	ctattcaaca	attatgagcc	aaagagtgtg	420
tgttgagctt	gtggcagttt	cttggtggac	agtgggcttt	ctacatacaa	tgagccaatt	480
agtttttccc	tctatttgcc	cttctgtgtt	cccaatgttg	tagacagttt	tttctgtgat	540
cttcccttgg	tcattccagtt	agcttgtata	gataattatg	ttcttgggac	ctccatgatt	600
tcaaccagtg	gtgtgattgc	tcttataagt	tttctgcttt	tgctcacctc	ctacatcatt	660
gttcttaata	ttgtcaggga	ctactcctcc	acaggatcct	ccaaggctct	ttctacctgt	720
acagcgcat	ttattgttgt	gttaatgttc	tttgggccc	gtattttcat	ttatgtgtgg	780
ccttcacaaa	acttccctgg	agacaaaatt	ctctccggtt	tctataccat	cttcactccc	840
tttctgaatc	cacttatcta	tactttgaga	aac			873

<210> 258

<211> 985

<212> DNA

<213> Unknown (H38g107 nucleotide)

<220>

<223> Synthetic construct

<400> 258

tacacagagc	cacagaatct	cacaggtgtc	tcagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggt	cctcgctggg	ctgttcctgt	ccatgtacct	ggtcacgggtg	120
ctggggaacc	tgctcatcat	cctggctgtc	agctctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttggct	gacatcggtt	tcacctccac	cacggtcccc	240
aagatgattg	tggacatgca	aactcacagc	agagtcattc	cctatgaagg	ctgcctgact	300
cagatgtctt	tttttgcctt	ttttgcatgt	atggatgaca	tgctcctgag	tgtgatggcc	360
tatgaccggg	ttgtggccat	ctgtcaccac	ctgcactacc	gaatcatcat	gaaccacgc	420
ctctgtggct	tcttaatctt	gttgtctttt	tttattagtc	ttttggactc	ccagttgcac	480
aatttgatta	tgttacagct	cacctgcttc	aaggatgtgg	acatttctaa	tttcttctgt	540
gacccttctc	aactcctcca	ccttaggtgt	tccgacacct	tcatcaatga	aatggtcata	600
tatttcatgg	tggtcatatt	tggtgtcttc	cctatctcag	ggatcctttt	ctcttactat	660
aaaattgttt	ccccattctc	gagagtcca	acatcagatg	ggaagtataa	agccttctcc	720
acctgtggct	ctcacctggc	agttgtttgc	ttattttatg	gaacagggct	tgtagggtac	780
ctcagttcag	ctgtgttacc	atcccccagg	aagagtatgg	tggcttcagt	gatgtacact	840
gtggtcaccc	ccatgctgaa	ccccttcac	tacagcctga	ggaacaagga	cattcaaagt	900
gccctgtgca	ggctgcatgg	cagaatcatc	aaatctcatc	atctccatcc	ttttgttat	960
atgggataga	aatggcagca	aaatt				985

<210> 259

<211> 976

<212> DNA

<213> Unknown (H38g108 nucleotide)

<220>

<223> Synthetic construct

<400> 259

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ttccctgggc	tggaggcctt	ccacatctgg	atctcaattc	ccttcttctt	tctgagcaca	120
gttgcctctc	tagggaacag	catgatccta	ttggttggtta	ttctggagcc	aaacctccat	180
gaaccatggt	actgttttct	cttcatgctg	tctgccgctg	acctggggct	gacctctctc	240
acaatgcccc	cgacctcag	tgtcctctgg	ttcagtgcac	gtgaaatcat	cctcaatgca	300
tgtatcatcc	agctcttttt	cctccacagc	tctggcttta	tggaaatctc	agtactgatg	360
gccatggctt	ttgaccgctt	tggtgcat	tgcagacccc	tcagatatgc	taccatcctg	420
acagactcca	gaattctaaa	gattggtgta	gcaatagtc	taagaacatt	gatcagcctc	480
tctccatccc	tctttctcat	taagagactg	tcattttgca	aagtcaatgt	cctttcccat	540
tcttactgct	tccaccctga	tgcgcttaaa	gttgcatggt	ctgattcaag	gatgaacagc	600
tatggaggct	tagctgttct	cattctgggt	accgggggtg	gtacaccatg	tgttgcgctt	660
tctacatcc	tgataatcca	ctctgtacta	aacatcatct	cttcagaggg	acggaggaag	720

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gccttcgaca cttgtggatc tcacattggg gcagttgcag tcttctacat tccctgggtt 780
gttcttttcag ttgtccacag atttttccac aaggcttcac caatatgtcc acccactatt 840
gtccaacatc tatttccttg gcccctctcg gctgaacccc atcatatata gtgtgaagac 900
taaacaaatc cgcagggcta tcttcaaact ctttcaaaca aaatcaaaag aaatgtaatg 960
ggggcttttc tctctg

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<210> 260

<211> 884

<212> DNA

<213> Unknown (H38g109 nucleotide)

<220>

<223> Synthetic construct

<400> 260

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atccaatgca agggctaata gaagtgaatt aagacattct ctgtaactcc aatattaaat 60
ggaaaccggg aaatagccag attcctctcc aacctgtcct tggctggcat cggtttcccc 120
tccaccatag tctccaagat gattgtggac atccagtctc acagcagagt catctcctat 180
gcgggctgcc tgactcaggt atctcttttt gccgtttttg gatgcatgga agacatgctt 240
ctgagtgtga tggccttatga ccggtttgtg gacatctgtc accctctgga ttatccagtc 300
atcatgaacc catgtttctg tggcttcccta gttttgttgt ctttttttct cagtctttta 360
gactcccagc tgcacaattg gattgcctta caaattacct gcttcaagga tgtggaaatt 420
cccaatttct tctgtgaccc ttctcaacac cccacccttg cctgttgtga caccttcacc 480
aatgacatag tcatgtattt ccttgctgcc atatttggtt ttcttcccat ttcggggacc 540
ttttcatctt actataaaat tgtttcctcc attctgaggg tttcatcatc aagtgggaag 600
tataaagcct tctccacctg tggctctcac ctgtcagttg tttgcttatt ttatggaaca 660
ggctttggag gggacctcag ttcagacatg tctcttatac ccagaaaagg tgcagtggcc 720
tcagtgatgt acacggtggt tactcccagc ctgaaccctt tcatctacag cctaacaggg 780
aaattaaaag tgccctgcgg cagctgcact gcagaatagt ctaatctcat tttcttatta 840
tctgttccat tcttccgta gtgtgagtta gaaaaggcag caag 884

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<210> 261

<211> 959

<212> DNA

<213> Unknown (H38g110 nucleotide)

<220>

<223> Synthetic construct

<400> 261

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gatccagaac tgcagcccggt cctcgctggg ctgttcctgt ccatgtacct gatcacggtg 120
ctggggaacc tgctcatcat cctggccggt agctgtgact cccacctcca caccctcatg 180
tacttcttcc tctccaactt gtccttgggt gacatcggac tcacctctgc caccatccct 240
aagatgattg ttgatatgca atctcacagc agaatcatct cctatgaggg ctgcctgatg 300
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accagtttgt ggccatttgt caccctctac gctaccagct catcatgaat ccccatctct 420
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agattgtgtt acaattcacc tgcttcaaga atgtggaaat ctttaatttt ttctgtgagc 540
catctcaact tctcaacctt gcctgttctg acagtgtcat caataacata ttcatgtatt 600
tagatagttg tatatttggg tttcttccca tctcagggat ccttttgtct tactataaaa 660
ttgtctcttc cattctaaga attccatcat cagatgggaa gtataaagcc ttctccacat 720
gtggctctca cctggcagtt gtttgcctat ttatggaaac aggacttgga gcctacctca 780
gttcagctgc gtcctcttcc cccaggaagg gtgcggtcac ctgagtgtg tactactgtg 840
tcatccctat gctgaacccc ttcatctaca gcctgagaaa cagggacatt aaaagtgcgc 900
tgtggagggt gcacagcaga acagtctaata ctcattatct gtccatcct ttctgtagt 959

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<210> 262

<211> 955

<212> DNA

<213> Unknown (H38g111 nucleotide)

<220>

<223> Synthetic construct

<400> 262

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gatccagaac	tgcagccact	ccttgctggg	ctgttcctat	ccatgtgcct	ggtcacgatg	120
ctggggaacc	tgtcatcat	cctggccgct	agccctgact	cccacctcca	catccccatg	180
tactttcttc	tctccaacct	gtccttgcc	gacattggtt	tcaccttggc	cacgggtcccc	240
aagatgattg	tagacatgca	atcacatagc	agagtcact	cccatgcagg	ctgtctgaca	300
cagatacctt	tctttgtcct	ttttgtatgt	atagatgaca	tgtcctgac	tgtgatggcc	360
tatgactgat	ttgtggccat	ctgtcacc	ctgcactacc	cagtcacat	gaatcctcac	420
ctctgtgtct	ctttagtgtt	gatgtctttt	tccttagcct	gttggattcc	tagctgcaca	480
actggattgt	tacaattcac	ctgcttcaag	aatgtggaaa	tctctaattt	tttctgtgac	540
tgatctcaac	ttctcaacct	tgcctgttct	gactgtcatc	agtaacatat	tcatacattt	600
agatagtact	atatttggtt	ttcttcccat	ttcagggatc	cttttgtctt	actataaaat	660
tgtgccctcc	attctaagaa	ttccattgtc	agatgggaag	tataaagcct	tctccacctg	720
tggtctctac	ctggcaattg	tttgcttatt	ttatggaaca	ggcattggca	tgtacctgac	780
ttcagctgtg	tcaccagccc	ccaggaatgg	tgtggtggca	tcagtgttgt	acgctatggt	840
cacccccatg	ctgaaccctt	tcactctgcg	cctgagaaac	aggggcattc	aaagtgcctt	900
gtggaggctg	tgcaggagga	aagtctaadc	tcattgatctg	tttcatcctt	tttct	955

<210> 263

<211> 1049

<212> DNA

<213> Unknown (H38g112 nucleotide)

<220>

<223> Synthetic construct

<400> 263

atgtcccaac	tggaagggga	caacataacc	tgggtgagtg	agttcatcct	aatgggtctc	60
tccagtgaac	ggcagaccca	ggctggactc	tttatcttat	ttggggctgc	ctacctgctg	120
accctgctgg	gcaatgggct	catcctgctc	ctgatctggc	tggacgtgag	actccacctg	180
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caaggctctg	catggcactg	gcagctgtct	cttggctagt	gggcctggct	aattctgcta	480
tggagacggc	actgaccatg	cacctgccca	cctgtgggca	caacgtgctg	aacctgtgg	540
cctgtgagac	actggcactg	gtcaggtcgg	cctgcgtgga	catcaccttc	aatcaggtgg	600
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aggcagctct	gagtcgagct	ctgatgagga	gctctgaatt	aaaacattag	agagtgtgtt	960
gagtaacaag	aaggcctcac	tctgaaaaca	gtgggcattg	gactgtgctc	tccagtataa	1020
cgtgtgtacg	catgtgtgtg	tatgtgtgt				1049

<210> 264

<211> 955

<212> DNA

<213> Unknown (H38g113 nucleotide)

<220>

<223> Synthetic construct

<400> 264

atggacagtc	ccagcaatgc	caccgtgccc	tgtggctttc	tccttcaagg	cttctccgaa	60
ttccccgacc	tgagaccctg	gctcttctt	ttgtctgtgg	gggtgcacct	ggccaccctg	120

ggcggaacc	tgctcactct	ggtggccgtg	gcctcgatgc	caagccggca	gcccattgctg	180
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tccctggctg	acctgagcac	gccggggcca	ccgcaggggc	agccctatct	ccttcctgag	300
ctgcgccctt	cagatgcaga	tggttggtgc	tctgggccc	gccgagtgtc	tccctgctggc	360
cgccatggct	aatgaccgct	acgtggccat	ctgccaccgc	ttgcgctacg	cgccgtgggtg	420
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gtacgtgcgg	cccagggcc	gctactcccc	gcgcctggac	cgaccctgg	cgctggtcta	840
caccaacgtc	acgcgctgc	tgtgcccact	catctacagc	ctgcgcaacc	gcgagatcac	900
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<210> 265

<211> 945

<212> DNA

<213> Unknown (H38g114 nucleotide)

<220>

<223> Synthetic construct

<400> 265

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ggactggagt	atgttcattc	ttggctctcc	atcctcttct	gtcttgcata	tttggttagca	120
tttatgggta	atgttaccat	cctgtctgtc	atgttgtag	aatcctctct	ccatcagccc	180
atgtattact	ttatttccat	cttagcagt	aatgacctgg	ggatgtccct	gtctacactt	240
cccaccatgc	ttgctgtgtt	atggttggat	gctccagaga	tccaggcaag	tgcttgctat	300
gctcagctgt	tcttcattcca	cacattcaca	ttcctggagt	cctcagtgtt	gctggccatg	360
gcctttgacc	gttttggtgc	tatctgccat	ccactgcact	acccaccat	cctcaccaac	420
agtgttaattg	gcaaaattgg	tttgccctgt	ttgctacgaa	gcttgggagt	tgtacttccc	480
acacctttgc	tactgagaca	ctatcactac	tgccatggca	atgccctctc	tcacgccttc	540
tgtttgacc	aggatgttct	aagattatcc	tgtacagatg	ccaggaccaa	cagtatttat	600
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gttctgattc	ttaatactgt	gctggatatt	gcattctcgt	aagagcagct	aaaggcactc	720
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atctaccttc	ttcttcccc	agtccttaac	cctattgtct	atagtgtcag	aacaaagcag	900
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<210> 266

<211> 869

<212> DNA

<213> Unknown (H38g115 nucleotide)

<220>

<223> Synthetic construct

<400> 266

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ctagccatct	tatcagccat	agacctagcc	ctctcaacat	cctcagtggc	tcgtatgttg	180
ggtatcttct	ggtttgatgc	acataaaatt	ggctttggag	cctgggtagc	ccagatgttt	240
ctgatacaca	ctttcacagg	aatggagtcc	actgtgctgc	tggcaatggc	ctttgaccgc	300
tatgtggcca	tctgtacatc	actccactat	acctctactc	tgacaccccg	agtattggca	360
ggcattgggtg	tgagcattat	aatgcgcccc	gtctgtctca	tgttgcccat	tctctacctc	420
accatcgctc	tgcccttctg	tgaggctcgg	attattgccc	actcctactg	tgagcacatg	480
ggtattgcta	agttggcctg	tgctagcatt	cacatcaatg	ctatttatgg	gctttttgtg	540
gcttcttatt	ttggatgtcg	cacttgttgg	aatctcctat	acctacattc	tccgagctgt	600
tttccacctc	ccatctcaag	acgctcgtca	caaagcactg	agaacgtgtg	gctcacatgt	660

tggggtcatg tgtgttttct atacaccctc cctcttctcc ttctcacct accgatttcg	720
caaaaaaaaaat tccccgttat gtccacattc ttgttgccaa cctctatgtg gtcattccac	780
ctgccctcaa tcctattatc tatggtgtga gaaccaaaca gattcatgag catgtgggtcc	840
atactttcac ctcaaagtaa ggtctctta	869

<210> 267

<211> 520

<212> DNA

<213> Unknown (H38g116 nucleotide)

<220>

<223> Synthetic construct

<400> 267

acatgctggg ttttgatggg gaacgtggg aatgcctaca cctgaggact atcaggagcc	60
actttcaaca ccatctgcac atttgccgc ttcttctgtg atgacaatta gatcaaatc	120
tgacacatcc tgccctgct gaagctcatt tgaataactt caggaaacag caagataatt	180
attgtgatct ttgacagctt ttatgattat agctggcact agggatcatcc tgatctctta	240
cctgctaate atcaggggctt tgaggatgaa atcatcgagt ggcaaagcca ataattttat	300
ccatccactt gtgcctccca cctaactgct atgaccttcc tttgggatcc ccatcttcag	360
acatgtgaag tacctcagat aaatcactga cagaagacaa gttggcatca tgacttgcac	420
catctttatt cctatgctag aacttttgat ccaaagtcta aagaaggata tacaagttgc	480
cttcaaaaag gccataggta acttctgggt ttttgagagg	520

<210> 268

<211> 952

<212> DNA

<213> Unknown (H38g117 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(952)

<223> n = A,T,C or G

<400> 268

attagcacia tgtctgtctt caaaagttct gcataaaacc ctgcttctc ccaaacgggc	60
ctctcaggcc ttgaaagcag atatgacttg atttccctgc ccatcttctt ggtttatgcc	120
acctcaattg ccgggaacat tagcatcctc ttcatatca gaactgagtc ttccctccac	180
caaccgatgt attactttct gtcaatgctg gcattcactg acctgggcct atctaact	240
accttaccta ccatgttcag tgtcttctgg ttccatgcc gggagatctc cttcaatgct	300
tgtctgggtcc aaatgtactt cattcatgtt ttctcgatta ttgagtcagc tgtactcctg	360
gctatggcct ttgactgctt tatagcaatc tgagaacctt tgcgctatgc agccatccta	420
accaatgatg taatcattgg gattggggtg gcaattgctg gaagggcctt ggctctggtc	480
tttccagctt ctttctctt gaagaggctt caatatcatg atgtcaatat tctgtcctac	540
ctcttctgcc tgcaccagga cctcataaag acgactgtat ccaactgtcg agtcagcagc	600
atctatggcc tcatgggtgg catctgttcc atgggacttg attcagtgtc tctcctcctc	660
tcctatgtcc tcatcctggg cacagcgttg agtatagcct ccaaggcaga gagagtgaga	720
gccctcaata cttgcatctc ccacatctgt gctgtactca ccttctatac accaatgatt	780
gggctatcta tgatccatcg ctatggacag aatgctcctc aattgtccat gtgctgatgg	840
ccaatgtcta cttgntgggt ccacctctca tgaaccccg gttctacagt gttagaccag	900
ncagattcgt gacagaatct ttcaataaaa attcagaaac atgaagtgtga ga	952

<210> 269

<211> 944

<212> DNA

<213> Unknown (H38g118 nucleotide)

<220>

<223> Synthetic construct

<400> 269

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atggaagagg aaaatgcaac attactgaca gaatttggtc tcacaggatt tttatgtcaa      60
caaggatttt tatgggaaat acccctgttc ctggcattct tggtaataga tctcatcacc      120
atcatgggga atcttgggtct gatttttctc atctggaaag accctcacct tcatatttca      180
atgtacttat tccttgggag tttagctttt gtggatactt gggtatcatc cacagtgact      240
ccgaagatgc tgatcaactt cttagctaag agtaagatga tatctctctc tgaatgcatg      300
gtacaatttt tttcccttg caatcagtgt aaccacagaa tgttttatct cggcatcaat      360
ggcatatgat cgctatgcag acatatgcaa acctttactt tatccagtca ttatgaccaa      420
tgaactatgc atctggctat ttgtcttgtc atttctaggt ggccttttct atgctttaat      480
ccatgaaggt tttttattca gactaacctt ctgtaactcc aacatgatac aacattttta      540
ctgtgacatt atccattgt taaagatttc atgtactgat tcttgattta attttctaata      600
gttttttatt ttctcagggt caattcaagt ttttaaccatt gggattgttt ttgtatctta      660
tatgtttgtt ctctttacaa tcttaaaaaa gaagtctaac aaaggcataa gggaagcctt      720
ttccacctgt ggagcccatc acataacctc ctctttatgt tatggcctcc ttctcttcat      780
gtatgtgggc cctgcagctc cacaagcaga taatcaagat atgatggagt atctatttta      840
ccctatcatt gtgcgtttgt taaaccatat tactacagcc tgagaaataa gcaataatag      900
gttcactcac aaaaatgtta aaataaaaata tttgcattgc atac                      944

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<210> 270

<211> 939

<212> DNA

<213> Unknown (H38g119 nucleotide)

<220>

<223> Synthetic construct

<400> 270

```

atgtccatta tcaacacatc atatgttgaa atcaccacct tcttcttggt tgggatgcca      60
gggctagaat atgcacacat ctggatctct atccccatct gcagcatgta tcttattgct      120
attctaggaa atggcaccat tctttttatc atcaagacag agccctcctt gcattggccc      180
atgtactatt ttctttccat gttggctatg tcagacttgg gtttgccttt atcatctctg      240
cccactgtgt taagcatctt cctgttcaat gccctgaaa cttcttctag tgcctgcttt      300
gcccaggaat tcttcattca tggattctca gtactggagt cctcagtcct cctgatcatg      360
tcatttgata gattcctagc catccacaat cctctgagat acacctcaat cctgacaact      420
gtcagagtgt cccaaatagg gatagtattc tcctttaaga gcatgctcct ggttcttccc      480
ttccctttca ctttaagaag cttgagatat tgcaagaaaa accaattatc ccattcctac      540
tgtctccacc aggatgtcat gaagttggcc tgttctgaca acagaattga tgttatctat      600
ggcttttttg gagcactctg ccttatggta gactttatc tcattgctgt gtcttacacc      660
ctgatcctca agactgtacc gggaattgca tccaaaaagg aggagcttaa ggctctcaat      720
acttgtgttt cacacatctg tgcagtgatc atcttctacc tgcccatcat caacctggcc      780
gttgtccacc gctttgccgg gcatgtctct cccctcatta atgttctcat ggcaaatgtt      840
ctcctacttg tacctccgct gatgaaacca attgtttatt gtgtaaaaaa taaacagatt      900
agagtggagag ttgtagcaaa attgtgtcaa tgggaagatt                      939

```

<210> 271

<211> 940

<212> DNA

<213> Unknown (H38g120 nucleotide)

<220>

<223> Synthetic construct

<400> 271

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atggaagaga aaaatgcaac attgctgaca gagtttggtc tcacattatt tttatatcaa      60
cctcactgga aaatacccct gttcctggca ttcttggtaa tatatctcat caccatcttt      120
gggaatcttg gtctgattgc tgcgtatgg aaagaccctc accttcatat cccaatatac      180
ttattccttg agaatttagc ttttgtggat gatttggtaa catccacatg actctgaaga      240
tgctgatcaa cttcttcact aagagtaagt tgatttctct ctgaatgctg gatacatttt      300
tttccctttg caattgggtg aaccacagaa tggttttatct tggcaacaat ggcatatgat      360
cgctatgtag ccatatgcaa acctttactt tatccagtca ttatgaccaa tggactgtgc      420

```

atctggctat	taatcttgtc	atttctaggt	ggccttcttc	atgctttaat	tcataaggt	480
tttttataga	ttaaccttct	gtaattccaa	cacaatacat	cacttttaat	gtgacattat	540
cccattgtta	aaaattttct	gtactgattc	ttctattaac	tttccaatgg	tttttatttt	600
ctcatgttca	attcaagttt	tcaccattgg	gactgttctt	gtatcttata	catttgcctt	660
ctctacaatc	ttgaaaaaga	agtctgtcaa	aggcataaga	aaagacttct	ccacctgtgg	720
agctcatatc	ttacctgtat	ctttatacta	tgggccccctc	gccttcattgt	atgtgggctc	780
tgcaccccaa	cgggctgatg	accaagatat	gatggagtct	ctattttaca	ctgtcatagt	840
tcctttatta	aatcccatga	tctacagcct	gagaaataag	caagtaatat	attcattcac	900
aaaaatgttc	aaaggaaata	atgttttagat	ctcttactca			940

<210> 272

<211> 512

<212> DNA

<213> Unknown (H38g121 nucleotide)

<220>

<223> Synthetic construct

<400> 272

tgtctagctc	aagtttctctg	agtagcagaa	aagtattgat	aaattttatt	tgttgcaactt	60
tttaacaaaa	caaaaagcat	ctgccaaaca	cagaacattg	caacacctag	gccctgggct	120
ttccccagc	attcattcac	tagcacctca	tgttttgggg	gcacaagcac	agggctttct	180
taggctgtaa	aatcacctat	atcatctgtc	tgtccactgc	ttcaactcct	tctgcagtat	240
ccctgcaaca	atattacatg	cttatgaaat	gctgcagaca	gggaattcct	gtccttctag	300
gacctctctc	tggctgtggg	cagctttacc	ataagttctt	gtcttcttat	gctgaaattg	360
atttcatttt	catcttcacg	tattattgct	tctttgctct	ctcgggtgctc	aactgagctc	420
catcgtctct	ccttctaata	ctccttctgt	catctatttt	gtcttttctt	cttcagactg	480
aaaatccctg	gtagtacctg	tagtttctt	cc			512

<210> 273

<211> 924

<212> DNA

<213> Unknown (H38g122 nucleotide)

<220>

<223> Synthetic construct

<400> 273

atgaatacca	ctctatttca	tccttactct	ttccttcttc	tgggaattcc	tgggctggaa	60
agtagcctc	tctgggttgg	ttttccttct	tttgctgtgt	tcctgacagc	tgtccttggg	120
aatatcacca	tcctttttgt	gattcagact	gacagtagtc	tccatcatcc	catgttctac	180
ttcttgccca	ttctgtcatc	tattgaccgg	ggcctgtcta	catccacat	ccctaaaatg	240
cttggcacct	tctggtttac	cctgagagaa	atctcctttg	aaggatgcct	taccagatg	300
ttcttcatcc	acctgtgcac	tggcatggaa	tcagctgtgc	ttgtggccat	ggcctatgat	360
tgtatgtgg	ccatctgtga	ccctctttgc	tacacgttgg	tgctgacaaa	caagggtggg	420
tcagttatgg	cactggccat	ctttctgaga	cccttagtct	ttgtcatacc	ctttgttcta	480
tttatcctaa	ggcttccatt	ttgtggacac	caaattatc	ctcatactta	tggtagacac	540
atgggcattg	ccgcctgtc	ttgtgccagc	atcagggtta	acatcatcta	tggcttatgt	600
gccatctcta	tcctggtctt	tgacatcata	gcaattgtca	tttcttatgt	acagatcctt	660
tgtgctgtat	ttctactctc	ttcacatgat	gcacgactca	aggcattcag	cacctgtggc	720
tctcatgtgt	gtgtcatgtt	gactttctat	atgcctgcac	ttttctcatt	catgacccat	780
aggtttgggc	ggaatatacc	tcactttatc	cacattcttc	tggctaattt	ctatgtagtc	840
attccacctg	ctctcaactc	tgtaatattt	ggtgtcagaa	ccaaacagat	tagagcacaa	900
gtgctgaaaa	tgtttttcaa	taaa				924

<210> 274

<211> 927

<212> DNA

<213> Unknown (H38g123 nucleotide)

<220>

<223> Synthetic construct

<400> 274

atggaagagg	aaaatgcaac	attgctgaca	gagtttggtc	tcacaggatt	ttacatcaa	60
cctgactgta	aaataccgct	cttcctggca	ttcttggtaa	tatatctcat	caccatcatg	120
gggaatcttg	gtctaattgt	tctcatctgg	aaagaccctc	accttcatat	cccaatgtac	180
ttattccttg	ggagtttagc	ctttgtggat	gcttcgttat	catccacagt	gactccgaag	240
atgctgatca	acttccttagc	taagagtaag	atgatatctc	tctctgaatg	catggtacaa	300
tttttttccc	ttgtaaccac	tgtaaccaca	gaatgttttc	tcttggcaac	aatggcatat	360
gatcgctatg	tagccatttg	caaagcttta	ctttatccag	tcattatgac	caatgaacta	420
tgcatcagc	tattagtctt	gtcatttata	ggtggccttc	ttcatgcttt	aatccatgaa	480
gctttttcat	tcagattaac	cttctgtaat	tccaacataa	tacaacactt	ttactgtgac	540
attatcccat	tgtaaagat	ttcctgtact	gattcctcta	ttaactttct	aatgggtttt	600
attttcgcag	gttctgttca	agtttttacc	attggaacta	ttcttatatc	ttatacaatt	660
atcctcttta	caatcttaga	aaagaagtct	atcaaaggga	tacgaaaagc	tgtctccacc	720
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ggctctgcct	ctccgcaagc	agatgaccaa	gatatgatgg	agtctctatt	ttacactgtc	840
atagttcctt	tattaaatcc	catgatctac	agcctgagaa	acaagcaagt	aatagcttca	900
ttcacaaaaa	tgttcaaaag	caatggtt				927

<210> 275

<211> 924

<212> DNA

<213> Unknown (H38g124 nucleotide)

<220>

<223> Synthetic construct

<400> 275

atggcgaaata	gaaacaacgt	gacagagttt	attctatttg	ggcttacaga	gaatccaaaa	60
atgcagaaaa	tcataattgt	tgtgttttgt	catctacatc	accaccatga	taggaaatgt	120
gctcattgtg	gtcaccatca	ctgccagccc	atcattgagg	tccccatgt	aatttttcct	180
ggcctatctg	tcctttattg	atgcctgcta	ttcctctgtc	aatgtctcta	agctgatcac	240
agattcactc	tatgaaaaca	agactatctt	actcaatgga	tgtatgactc	aagtcttttg	300
agaacatttt	ttcagagggt	ttgagggtcat	cctacttact	gtaatggcct	atgactgcta	360
tgtgggtcatc	tgcaagccct	tgcgctatac	caccatcatg	aagcagcatg	tttgtagcct	420
gctagtgagg	gtgtcacggg	tgggaggcct	tcttcattgca	accatacaga	tcctcttcat	480
cttccaatta	cctttctgta	gttctaattg	catagatcac	tttactgtga	tctcaaccct	540
ttgtctaatc	ttgcctgcac	taatacccac	actctaggac	tcttcgttgc	tgccaacagt	600
gggttcatat	gcctgttaaa	ctttctcttg	ctcctggtct	cctatgtggt	catactgtac	660
tccttaagga	cccacagctt	agaggcaagg	cacaaaggcc	tctccacctg	tgtctcccac	720
aacacagttg	tcattcttatt	ctttataccc	tgcataattg	tgtacatgag	acctccagct	780
actttaccca	ttgataaagc	agttgctgta	ttctacacta	tgataactcc	tatgttaaac	840
cccttaatct	acaccttgag	gaatgctcag	atgaaaaatg	ccattaggaa	attgtgtagt	900
aggaaagcta	tttcaagtgt	caaa				924

<210> 276

<211> 963

<212> DNA

<213> Unknown (H38g125 nucleotide)

<220>

<223> Synthetic construct

<400> 276

atgttccttc	ccaatgacac	ccagtttcac	ccctcctcct	tcctgttgct	ggggatccca	60
ggactagaaa	cacttcacat	ctggatcggc	tttccttctt	gtgctgtgta	catgatcgca	120
ctcatagggg	acttcactat	tctacttggt	atcaagactg	acagcagcct	acaccagccc	180
atgttctact	tcctggccat	gttggccacc	actgatgtgg	gtctctcaac	agctaccatc	240
cctaagatgc	ttggaatctt	ctggatcaac	ctcagagggg	tcattctttga	agcctgcctc	300
accagatgt	tttttatcca	caacttcaca	cttatggagt	cagcagtcct	tgtggcaatg	360

gcttatgaca	gctatgtggc	catctgcaat	ccactccaat	atagcgccat	cctcaccaac	420
aagggttgtt	ctgtgattgg	tcttggtgtg	tttgtgaggg	ctttaatttt	cgtcattccc	480
tctatacttc	ttatattgcg	gttgcccttc	tgtgggaatc	atgtaattcc	ccacacctac	540
tgtgagcaca	tgggtcttgc	tcattctatct	tgtgccagca	tcaaaatcaa	tattatttat	600
ggtttatgtg	ccatttgtaa	tctggtgttt	gacatcacag	tcattgccct	ctcttatgtg	660
catattcttt	gtgctgtttt	ccgtcttcct	actcatgagc	cccgaactca	gtccctcagc	720
acatgtggtt	cacatgtgtg	tgtaatcctt	gccttctata	caccagccct	cttttctttt	780
atgactcatt	gctttggccg	aaatgtgccc	cgctatatcc	atatactcct	agccaatctc	840
tatgttgtgg	tgccaccaat	gctcaatcct	gtcatatatg	gagtcagaac	caagcagatc	900
tataaatgtg	taaagaaaat	attattgcag	gaacaaggaa	tggaaaagga	agagtaccta	960
ata						963

<210> 277

<211> 894

<212> DNA

<213> Unknown (H38g126 nucleotide)

<220>

<223> Synthetic construct

<400> 277

atgagaaatc	acacaatggt	gactgaattc	atccttcttg	gaatccctga	gacagagggc	60
ctagagacag	cccttttatt	cctgttctcc	tcattttatt	tatgcaccct	cttgggaaac	120
gtgcttatcc	ttacagctat	catctcctcc	actcgacttc	acactcctat	gtattttttc	180
ttgggaaacc	tctccatctt	tgacctgggt	ttctcttcaa	cgactgttcc	caagatgttg	240
ttctaccttt	cggggaacag	ccatgctatc	tcgtatgcag	gctgcgtgtc	ccagcttttc	300
ttctaccatt	tcctaggctg	tactgagtgt	ttcctctaca	cagtgatggc	ctgtgaccgc	360
tttgttgcca	tatgttttcc	tttgagatac	acggtcatca	tgaaccacag	ggtgtgcttt	420
atgttggcca	cggggacctg	gatgattggc	tgtgtccatg	ccatgatcct	aactccccctc	480
accttccagt	taccttactg	tggccctaac	aagggtgggt	attacttctg	tgatattcct	540
gcagtgttac	ctctagctg	taaggacaca	tccttagccc	agagggtagg	ttttacaaat	600
gttgggtctt	tgtctctcat	ttgctttttt	ctcatccttg	tttctataac	ttgcattggg	660
atttccatat	caaaaatccg	ctcagcagag	ggcaggcagc	gggccttctc	cacctgcagc	720
gctcacctca	ctgcaatcct	ttgtgcttat	gggccagtca	tcgttatcta	tctacaaccc	780
aatcccagtg	ccttgcttgg	ttccataatt	cagatattga	ataatctggt	aaccccaatg	840
ttgaatccac	taatctatag	ccttaggaat	aaggatgtaa	aatcagatca	gccc	894

<210> 278

<211> 972

<212> DNA

<213> Unknown (H38g127 nucleotide)

<220>

<223> Synthetic construct

<400> 278

atggaggagg	aaaatacaac	attgctgaca	gagtttgttc	tcacaggatt	tttatatcaa	60
ccacagtggg	aaatacccct	gttccctggc	ttcttggtta	tatagctcat	caccatcatg	120
gggaatcttg	gtctaattgt	tctcatctgg	aaagaccctc	accttcatat	cccaatgtat	180
ttattccgtg	ggagtttggc	ctttgtggat	gcttggttat	catccacagt	gactccaaag	240
atgctgatca	acttcttagc	taagagtaag	atgatatctc	tctctgaatg	catggtacaa	300
tttttttctt	ttgtaatcag	tgtaaccaca	gaatgtttta	tctcggcata	aatggcatat	360
gatcgctatg	tagccatttg	caaagcttta	ctttatccag	tcattatgac	caacggacta	420
tgcattccagc	tattagtctt	gtcattttata	ggtggccttc	ttcatgcttt	aatccatgaa	480
atttttttat	tcagattaac	cttctgtaat	tccaacataa	tacaacactt	ttactgtgac	540
attatcccat	tgtaaagat	ttcctgtact	gattctttta	ttacttttct	aatggttttt	600
atttttcgag	attcaattca	agttttttacc	attggaacta	ttcttatatc	ttatacactt	660
gtcctcctta	taattcttaa	aaataagtct	gtcaaaagga	tacaaaaagc	tgtctccacc	720
tgtggagctc	atctcttata	tgtatcttta	tactatgggc	cccttgtctt	catgtatgtg	780
ggctctgcat	ccccgcaagc	agatgaccaa	gatatgatgg	agtctctatt	ttacactgtc	840
atcgttcctt	tattaaattc	catgatctac	agcctgagaa	acaagcaagt	aatagcttca	900

ttcacaaaaa tgttcaaaag aaatgttttag atctcataca atctctgttc tctgtttact 960
 aaaattttcc ca 972

<210> 279

<211> 924

<212> DNA

<213> Unknown (H38g128 nucleotide)

<220>

<223> Synthetic construct

<400> 279

atgatgagta accagacgtt ggtaaccgag ttcacctcgc agggccttttc ggagcaccca	60
gaataccggg tgttcttatt cagctgtttc ctcttctctt actctggggc cctcacaggt	120
aatgtcctca tcaccttggc catcacgttc aacctggggc tccacgtcc tatgtacttt	180
ttcttactca acttggttac tatggacatt atctgcacct ctcccatcat gcccaaggcg	240
ctggccagtc tgggtgcgga agagagctcc atctcctacg ggggctgcat ggcccagctc	300
tatttctctca cgtgggctgc atctcagag ctgctgctcc tcacgggcat ggccatgac	360
cggtagcgag ccactcgcca cccgctgcat tacagcagca tgatgagcaa ggtgttctgc	420
agcgggcttg ccacagccgt gtggctgctc tgcgcgctca acacggccat ccacacgggg	480
ctgatgctgc gcttggattt ctgtggcccc aatgtcatta tccatttctt ctgcgaggctc	540
cctccccctgc tgcttctctc ctgcagctcc acctacgtca acgggtgcat gattgtcctg	600
gcggatgctt tctacggcat agtgaacttc ctgatgacca tcgcgtccta tggcttcac	660
gtctccagca tcctgaaggt gaagactgcc tgggggaggc agaaagcctt ctccacctgc	720
tcttcccacc tcaccgtggt gtgcatgtat tacaccgctg tcttctacgc ctacataagc	780
ccgttctctg gctacagcgc aggggaagagc aagttggctg gcctgctgta cactgtgctg	840
agtctaccc tcaacccct catctatact ttgagaaaca aggaggtcaa agcagccctc	900
aggaagcttt tccctttctt caga	924

<210> 280

<211> 958

<212> DNA

<213> Unknown (H38g129 nucleotide)

<220>

<223> Synthetic construct

<400> 280

atggatgacg aaaatgcaac attgctgaca gagtttgctc tcacaggact tacatatcaa	60
tcagagtggg aaataccctt gttcctggca ttcttggtta tatatctcat caccatcatg	120
gcaaatcttg gtctgattgc tgtcatctgg aaagactcac accttcacat tccaatgtac	180
ttattccttg ggagtttagc ctttgtggat gcttggttat catcctcagt gaccctaaag	240
atgctgatca gcttttttagc taagagtatg attatttctg tctctgaatg caagatacaa	300
tttttttctt ttggaatcag tgggaaccaca gaatgttttc tcttggaac aatggcatat	360
gatcgctatg tagccatatg caaaccttta ctttatccag tcattatgac caatggactg	420
tgtatctggc tattagtctt gtcatttata ggtggcttcc ttcattgcctt aattcatgaa	480
ggtattttat tcagattaac cttctgtaat tccaacataa tacatcactt ttactgtgac	540
attatcccat tgttaaagat ttctgttact gacccttcta ttaatttttt aatgcttttt	600
attttgtctg gttcaataca ggtattcact attttgactg ttcttgtctc ttatacattt	660
gtcctcttta caatcttaaa aaaaaaagtc tgccaaagac ataaggaaag ccttttccac	720
ctgtggagcc catctcttat ctgtttcttt atactatggc ccccttctct tcatgtatgt	780
gcaccctgca tctccacaag cagatgatca agatatggg gagtctctat tttacactgt	840
cataattcct ttcttaaatc ccattatcta cagcctgaga aataagcaag tcatagattc	900
actgacaaaa acattaaaag gaaatgttta gatctcatc tggaatgtat tctctatt	958

<210> 281

<211> 933

<212> DNA

<213> Unknown (H38g130 nucleotide)

<220>

<223> Synthetic construct

<400> 281

atggttgaag	aaaatcatatc	catgaaaaat	gagtttatcc	tcacaggatt	tacagatcac	60
cctgagctga	agactctgct	gtttgtggtg	ttctttgcca	tctatctgat	caccgtggtg	120
gggaatatata	gtttgggtggc	actgatattt	acacaccgtc	ggcttcacac	accaatgtac	180
atctttcttg	gaaatctggc	tcttgtggat	tcttgtgtg	cctgtgctat	tacccccaaa	240
atgttagaga	acttcttttc	tgagggcaaa	aggatttccc	tctatgaatg	tgagtagacg	300
ttttattttc	tttgactgtg	ggaaactgca	gactgctttc	ttctggcagc	agtggcctat	360
gaccgctatg	tggccatctg	caaccactg	cagtaccaca	tcatgatgtc	caagaaactc	420
tgcatccaga	tgaccacagg	cgcttcata	gctggaaatc	tgcatccat	gattcatgta	480
gggttggtat	ttaggttagt	ttctgtgga	ttgaatcaca	tcaaccactt	ttactgtgat	540
actcttccct	tgtatagact	ctcctgtgtt	gaccctttca	tcaatgaact	ggttctattc	600
atcttctcag	gttcagttca	agtctttacc	ataggtagt	tcttaatatc	ttatctctat	660
attcttctta	ctattttcag	aatgaaatcc	aaggaggga	gggcaaagc	cttttctact	720
tggtcatccc	acttttcatc	agtttcatta	ttctatggat	ctattttttt	cctatacatt	780
agaccaaatt	tgcttgaaga	aggaggtaat	gatataccag	ctgctatttt	atttacaata	840
gtagtccct	tactaaatcc	tttcatttat	agtctgagaa	acaaggaagt	aataagtgtc	900
ttaagaaaaa	ttctgctgaa	aataaaatct	caa			933

<210> 282

<211> 979

<212> DNA

<213> Unknown (H38g131 nucleotide)

<220>

<223> Synthetic construct

<400> 282

tatacagacc	cacagaatct	aacagatgtc	tttatattcc	tcctcctaga	actctcagag	60
gatccagcac	tgcagctggg	cgtcactggg	ctgtgcctgt	gtgcctgggc	acggtgctgt	120
ggaacctgtc	cagcatcctg	gccgtcagcc	ctgactccca	cctccacacc	cccatgcact	180
tcttccctctg	caacctgtcc	ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	240
tgatcgtgga	catccaatct	cacagcagag	tcatctccta	tgcaggctgc	ctgactcaga	300
tgtctctctc	tgccattttt	ggaggcatgg	aagagagaca	tgctcctgag	tgtgatggcc	360
tatgaccagt	ttgtagccat	ctgtcaccct	ctgtatcatt	cagccatcat	gaacctcgtg	420
ttctgtggct	tcctgggttt	gttgtctttt	ttttctcagt	cttttagact	cccagctgca	480
aaactgatcg	ccttacaaat	cacctgctca	aaggatgtgg	aaattcctaa	ttttttctgt	540
gaccttcttc	aactccccca	tcttgcattg	tgtgacacct	tcaccaataa	cattatcatg	600
tatttccctg	ctgccatatt	tgggttttct	cccatctcgg	ggacctttt	ctcttactat	660
aaaattgttt	cctccattct	gagggtttca	tcatcagggt	ggagctataa	agccttcgcc	720
acctgtggat	ctcacctgtc	agttgtttgc	tgattttatg	gaacaggcgt	tggagggtac	780
ctcagttcag	atgtgtcgtc	ttccctgaga	aagcgtgcag	tggcctcagt	gatgtacacg	840
gtggtcaccc	ccatgctgaa	tcccttgatc	tacagcctga	gaaacaggga	tattaaaggt	900
gtcctgtggc	agccgtgcag	ccgcacggca	gcacagtctc	atctcaatat	cttatctgtt	960
ccattccttt	tgcaggatg					979

<210> 283

<211> 987

<212> DNA

<213> Unknown (H38g132 nucleotide)

<220>

<223> Synthetic construct

<400> 283

atggaaccac	agttcaccac	ccagggatca	atgtttgtcc	tgtagggta	gtcacagacc	60
caagagctcc	agagagtcac	gttcattctg	ttcctgttag	tctatgttac	caccattgtg	120
ggaaaccttc	ttatcatggg	cacagtgaat	tttgactgcc	ggctccacac	ccatgtattt	180
tctgtctcga	aatctagctc	tcatagacgt	ctgctattcc	acagtcacct	ctccaaagat	240
gctgggtggac	ttcctccatg	agaccaagac	gatctcctac	cagggtgca	tggcccagat	300

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cttcttcttc caccttttgg gaggtgggac tgtctttttt ctctcagtca tggcctatga 360
ccgctacata gccatctccc agcccctccg gtatgtcacc atcatgaaca ctcaattgtg 420
tgtgggcctg gtagtagccg cctggcgtgg ggggctttgt ccactccatt gtccaactgg 480
ctgtgatacg tccacagcct ctatgtggcc ccaatacct agataacttc tactgtgatg 540
ttccccaagt actgagactt gctgcaactg atacctccct cctggagtgc ctcatgatct 600
ccaacagtgg gctgctagtt atcatctggt tcctcctcag tctgatgtct tatactgtca 660
tcctgggtgat gctgaggtcc cactcgggaa aggcaaggag taaggcagct tccacttgca 720
ccaccacat catcgtggtg tccatgatct tcattccatg tatctatata tatacctggc 780
cctttcaccc cattcatcat ggacaaggct gtgtccatca gctacacagt catgaccccc 840
atgctcaacc ccatgatcta caccctgaga aaccaggaca tgaaagcagc catgaggaga 900
ttaggcaagt gcctagtaat ttgcaggag ttaaacttta agtaagttga ctttaaata 960
caaattgctc tggattttta ttttccc 987

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<210> 284

<211> 387

<212> DNA

<213> Unknown (H38g133 nucleotide)

<220>

<223> Synthetic construct

<400> 284

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atgcaaggag aaaacttcac catttgagc atttttttct tggagggatt ttcccagtac 60
ccagggttag aagtggttct ctctgtcttc agccttgtaa tgtatctgac aacgctcttg 120
ggcaacagca ctcttatttt gatcactatc ctgattcac gccttaaac ccccatgtac 180
ttattccttg gaaatctctc tttcatggat atttggtaca catctgcctc tgttcctact 240
ttgctggtga acttgctgtc atcccagaaa accattatct tttctgggtg tgctgtacag 300
atgtatctgt cccttgccat gggctccaca gagtgtgtgc tcctggccgt gatggcatat 360
gaccgttatg tggccatttg taacccg 387

```

<210> 285

<211> 1005

<212> DNA

<213> Unknown (H38g134 nucleotide)

<220>

<223> Synthetic construct

<400> 285

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tctacagacc cacagaatct aacagatgtc tctatatctc tcctcctaga acctcagagg 60
atccagaacg gcagctgggc ctgctgggc tgttctctgc catgtgcctg gtcacggtgc 120
tggggaacct gatcatcatc ctggacgtca gccctgactc ccacctcccc acccccatgt 180
acttcttctc ctccaacctg tccttgccctg acatcggttt cacctccacc acgggtccca 240
agatgattgt ggacatccaa tctcacagca gagtcatctt ctatgcaggc tgctgactc 300
agatgtctct ctttgccatt tttggaggca tgggaagagag acacgctcct gagtgtgatg 360
gcctatgacc ggtttgtagc catctgtcac cctctatgtc attcagccag catgaacccg 420
tgtttctgtg gctttctagt tttgttgtct ttttttttct tcagtctttt agacacccag 480
ctgcacaact tgattgcctt acaaatgacc tgcttcaagg atgtggacat tcctaatttc 540
ttctgtgacc ctttccaact ccccatctt gcatgttgtg acaccttcac caataacata 600
atcatgtatt tccctgctgc catatttggg tttcttcaga tctcggggac ctttttctct 660
tactataaaa ttgtttctct cattctgagg gtttcttcat cagggtggga ctataaagcc 720
ttctccacct gtgggtctca cctgtcagtt gtttctgtat tttatggaac aggcgttgga 780
gggtacctca gttcagatgt gtcattctcc ccgagaaagg gtgcagtggc ctcaagtatg 840
tacacgggtg tcacccccat gctgaacccc ttcatctaca gcctgagaaa cggggatatt 900
aaaagtgtcc tgcggcggcc gcaaggcagc aaggtctaata atcaatatct tcttatctgt 960
tccattcctt ttgtagggtg ggttaaaaaa ggcagcaagg tcaaa 1005

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<210> 286

<211> 958

<212> DNA

<213> Unknown (H38g135 nucleotide)

<220>

<223> Synthetic construct

<400> 286

atgaagaata	aaaggaatgt	gactgaattc	gttttaacag	gtcttacaca	gaaccctaaa	60
atggagaaag	tcatgtttgc	agtatttttg	gttctttaca	tgataacact	ttcaggcaac	120
ctgctccttg	tggttacaat	taccaccagc	caggctctta	gtcccccat	gtacttcttc	180
ctgagccacc	tttctttgat	agacacagtt	tattcttctt	cttcagctcc	taagttgatt	240
gtcgattccc	ttcatgagaa	gaaaatcatc	tcctttaatg	gggtgatggc	tcaagcctat	300
gaagaacaca	tttttgggtg	tactgagatc	atcctgctga	cagtgatggc	ctgtgacaac	360
tatgtggcca	tctgcaaacc	tctgcactac	acaaccatca	tgagccacag	cctgtgcatt	420
ctcctagtgg	tagtggcctg	gataggagga	tttctccatg	caaataattca	gattctattt	480
acagtatggc	tgcccttctg	tggtcccaat	gtcatagacc	acttcatgtg	tgacttgtgc	540
cctttgttaa	aacttgtttg	cctggacact	catacccttg	gtctctttgt	tgctgccaac	600
agtgggttca	tctgcttatt	aaacttcctt	ctctaggtgg	tatcctatgt	gatcatcttg	660
agatgtttaa	agaactatat	cttggagggg	aggggtaaag	ccctctccac	ctgtatttct	720
cacatcataa	tagtgttctt	attctttgtg	ccttgtatat	ttgtgtatct	gcaccagtg	780
acaaactctg	cccattgata	aagctgctgc	tgtattttat	actatggtgg	tccaatggt	840
aaatcctttg	atctacacac	tcagaaatgc	tgaggtaaaa	agtgaataa	ggaagctttg	900
gagaaaaaaa	gttatttcag	ataatgacta	aataagacca	ttgagcactc	atcataga	958

<210> 287

<211> 937

<212> DNA

<213> Unknown (H38g136 nucleotide)

<220>

<223> Synthetic construct

<400> 287

atggagattg	gaaaccatac	cacagtgaca	gagtttatta	ttttgggggt	aactgaggat	60
cctacacttt	gtgacatctt	ctttgtgata	tttctaggaa	tctacattgt	caccttaata	120
ggcaatatca	gcataataaa	gaagctgttc	ccaacttcac	actcccatgt	acctgttctt	180
cagccacttg	gcttttgtgg	acatagggct	tgccacagta	gtcacaccta	taatgcttat	240
gggattccta	agacgtggaa	cagccctccc	tgtcactagc	tgtgaagccc	agctctgttc	300
tgtagtcatg	tttgggacgt	ctgaatgctt	cctactggcg	accatggcct	atgatcgcta	360
tgtggccatc	tgctcaccce	tggtgaacte	caccacttg	tccccataa	tctgcatact	420
cttagtgggg	gtttgctacc	tggttggatg	tgtgaatgcc	tcaacattta	ctagttgttt	480
attgagtctg	tctttctgtg	gaccaaatac	gatagatcat	tttttctgtg	atttctctcc	540
tttgttgaaa	ctttcctgct	caaataatct	cattcctgaa	attatccctt	ccatctcttc	600
tggatctatc	attgtgggtca	cagtatttgc	catagccatc	tcctacatct	acatcctcat	660
caccatcctg	aagatgcgct	ccgcccagg	gcgccacaag	gccttctcca	cctgtacctc	720
ccacctcgct	gcggttactc	tctactatgg	aacgattacc	ttcatattat	tgatgccccaa	780
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catactgaac	ccctttatct	atagtctgag	gaacagagat	gtaaaggagg	cactaagaaa	900
ggcaactgtc	agaatatatt	cttaggatca	atttghta			937

<210> 288

<211> 971

<212> DNA

<213> Unknown (H38g137 nucleotide)

<220>

<223> Synthetic construct

<400> 288

cacacagagc	cacggaatct	cacagggtgc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tcagccgggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctgggtc	120
acgggtgctga	ggaacctgct	gagcatcccc	gctgtcagct	ctgactcccc	gctccacacc	180
cccacgtact	tcttctcttc	catcctgtgc	tggtgtgaca	tcgggtttcac	ctcggccacg	240

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gtttccaaga cgattgtgga catgcagtc catagcagag tcatctctca tgcgggctgc 300
ctgacacaga tgtctttctt ggtccttttt gcatgtatag aaggcatgct cctgactgtg 360
atggcctatg actgctttgt aggcattctgt cgccctctgc actaccagct catcgtgaat 420
cctcatctct gtgtcttctt tgttttggtg tectttttcc ttagcctgtt ggattcccag 480
ctgcacagtt ggattgtggt acaattcacc atcatcaaga atgtggaaat ctctaatttt 540
gtctgtgacc cctctcaact tctcaaaact gcctgttctg acagcgtcat caatagcatc 600
ttcatatatt ttggtagtac tatgtttggt tttcttccca tttcagggat ccttttgtct 660
tactataaaa tcgtcccttc cattctaagg atttcacgt cagatgggaa gtataaagcc 720
ttctccacct atggctctca cctagcagtt ttttgctgat ttgatggaa aggcatggc 780
gtgtacctga cttcagctgt ggcaccaccc ctcaggaatg gtgtgggtgt gtcagtgatg 840
taagctgtgg tcaccccat gctgaacctt tcatctaca gcctgagaaa cagggaacata 900
caaagtgcc tgcggaggct gcgcagcaga acagtcgaat ctcatgatct gtccatcct 960
ttttctggtg t 971

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<210> 289

<211> 954

<212> DNA

<213> Unknown (H38g138 nucleotide)

<220>

<223> Synthetic construct

<400> 289

```

atgattcagc ctatggcgtc acccagcaac agctccactg tcccagtctc tgaattcctc 60
ctcacctgct tcccactt ccagagttgg cagcactggc tctccctgcc cctcagcctt 120
ctcttctctc tggccatggg agctaaccac accctcctga tcaccatcca gctggaggcc 180
tctctgcacc agccctgta ctacctgtc agcctcctct ccctgctgga catcgtgtc 240
tgcctcacgc tcatcccaa ggtcctggcc atcttctggt atgatcttag gtcgatcagc 300
ttccctgctt gcttccctca gatgttcac atgaacagtt tccctcccat ggagtcctgc 360
acgtttatgg tcatggccta tgaccgttat gtggccatct gccaccact gcggtacca 420
tccatcatca ctaatcaatt tgtggccaaa gctagtgtct tcattgtggt gcggaatgcg 480
cttcttactg caccattcc tatcctcact tccctgctcc attactgtgg ggaaaatgtc 540
attgagaact gcatctgtgc caacttgtct gtgtccaggc tctcctgtga taatttcacc 600
cttaacagaa tctaccaatt tgtggctggt tggacctgct tgggctcaga tttattcctc 660
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gcagtgaagg ccctgagcac atgtggctcc cacttcatcc tcattctttt cttcagcacc 780
atactgctgg ttgtggtgtt gacaaacgtg gccagaaaga aggtcccat ggacatcctg 840
atcctgctga acgtccttca tcaccttatt cctcctgcgt tgaaccctat tgtgtatggg 900
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<210> 290

<211> 713

<212> DNA

<213> Unknown (H38g139 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(713)

<223> n = A,T,C or G

<400> 290

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ctccaaaagt acattaagaa ttgtttccaa gccaggagtt ttggccattc aaggtcaggg 120
ccataggatc gttaaggaa ccttctgcc ccccttgaa atatccctcc attcatcacg 180
gatccctttg gagtcaaggc tgccaggttt attttgccca gnaatggtgt taatgactct 240
gcccatcccc catcctttca gcacaactcc gttattgtgg aagaaatgtc attgagaact 300
gcactgtgac caatatgtct gttccagac tctcctgca tgatgtcacc atcaatcacc 360
tttaccatt tgctggaggc tggactctgc taggatctga cctcatcctt atcttctct 420
cctacacctt cattctgca gctgtgctga gactcaaggc agaggggtgc gtggcaaagg 480

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ccctaagcac	atgtggctcc	cacttcatgc	tcatectctt	cttcagcacc	atccttctgg	540
tttttgcct	cacacatgtg	gctaagaaga	aagtctcccc	tgatgtgcca	gtcttgctca	600
atgttctcca	ccatgtcatt	cctgcagccc	ttaaccccat	catttacggg	gtgagaaccc	660
aagaaattaa	gcaggggaatg	cagaggttgt	tgaagaaagg	gtgctaacaa	gga	713

<210> 291

<211> 924

<212> DNA

<213> Unknown (H38g140 nucleotide)

<220>

<223> Synthetic construct

<400> 291

atgaattccc	tgaaggacgg	gaatcacacc	gctctgacgg	ggttcatcct	attgggctta	60
acagatgatc	caatccttcg	agtcacctc	ttcatgatca	tcctatctgg	taatctcagc	120
ataattattc	ttatcagaat	ttcttctcag	ctccatcacc	ctatgtattt	ctttctgagc	180
cacttggtct	ttgctgacat	ggcctattca	tcttctgtca	caccaacat	gcttgtaaac	240
ttcctgggtg	agagaaatac	agtctcctac	cttggatgtg	ccatccagct	tggttcagcg	300
gctttctttg	caacagtcga	atgcgtcctt	ctggctgcca	tggcctatga	ccgctttgtg	360
gcaatttgca	gtccactgct	ttattcaacc	aaaatgtcca	cacaagtcag	tgccagctta	420
ctcttagtag	ttacatagc	tggttttctc	attgctgtct	cctatactac	ttccttctat	480
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cttgaactct	cctgttctga	tatcagtgct	tccacagttg	ttctctcatt	ttcttctgga	600
tccatcattg	tggtcactgt	gtgtgtcata	gccgtctgct	acatctatat	cctcatcacc	660
atcctgaaga	tgcgctccac	tgaggggcac	cacaaggcct	tctccacctg	cacttccacc	720
ctcactgtgg	ttaccctggt	ctatgggacc	attaccttca	tttatgtgat	gcccaatttt	780
agctactcaa	ctgaccagaa	caaggtgggtg	tctgtgttgt	acacagtggg	gattcccatg	840
ttgaaccccc	tgatctacag	cctcaggaac	aaggagatta	agggggctct	gaagagagag	900
cttgtagaa	aaatactttc	tcat				924

<210> 292

<211> 1006

<212> DNA

<213> Unknown (H38g141 nucleotide)

<220>

<223> Synthetic construct

<400> 292

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gatccagaac	tgcaaccggg	cgctcgctggg	ctgttcctgt	ccatgtgcct	cgatcatggg	120
ctggagaacc	tgctcatcat	cctggacgtc	agccctgact	cccacctccc	cacccccatg	180
tactttcttc	tctccaacct	gtccttgctt	gacatcggtt	tcacctccac	cacgggtcccc	240
aagatgattg	tggaatccca	gtctcacagc	agagtcatct	atgcaggctg	cctgactgtg	300
atgtctctct	ttgccatttt	tgaggcatg	gaagagagac	atgctcctga	gtgtgatggc	360
ctatgaccgg	tttgtagcca	tctgtcaccc	tctatatcgc	tcagccatct	tgaaccctgt	420
tttctgtggc	ttcctagatt	tggtgtcttt	tttttttttc	cctcagtctt	ttagactccc	480
agctgcacaa	cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
tcttctggga	accttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	accaggaaca	600
tcagcatgta	tttccctgct	gccgtatttg	gttttctttc	catctcgggg	acccttttct	660
cttactgtaa	aatgggtttc	tccattctga	gggtttctac	atcagggtggg	aagtataaac	720
cttctccacc	tgagggtccc	acctgtcagt	tgtttctcga	ttttatggaa	caggcggttg	780
agagtacctc	gggttcagatg	tgcatctctc	cccgagaaag	gggtcagtg	cctcagtgat	840
gtacacgggtg	gtcaccccca	tgctgaaccc	cttcatctac	agcctgagaa	acggggatat	900
taaaagtgtc	ctgcccgggc	cgcaaggcag	cacagtctca	tctcaatacc	ttcttatctg	960
ttccattcct	tttgtagggt	gggttaacaa	agacagcaag	gtcaaaa		1006

<210> 293

<211> 933

<212> DNA

<213> Unknown (H38g142 nucleotide)

<220>

<223> Synthetic construct

<400> 293

atggggactg	gaaatgacac	caactgtggta	gagtttactc	ttttgggggt	atctgaggat	60
actacagttt	gtgctatttt	atttcttggt	tttctaggaa	tttatgttgt	caccttaatg	120
ggtaatatca	gcataattgt	attgatcaga	agaagtcac	atcttcatac	acccatgtac	180
attttcctct	gccatttggc	ctttgtagac	attgggtact	cctcatcagt	cacacctgtc	240
atgctcatga	gcttcctaag	gaaagaaacc	tctctccctg	ttgctgggtg	tgtggcccag	300
ctctgttctg	tagtgacgtt	tggtacggcc	gagtgccttc	tgctggctgc	catggcctat	360
gatcgctatg	tggccatctg	ctcaccctg	ctctactcta	cctgcatgtc	ccctggagtc	420
tgcacatctt	tagtgggcat	gtcctacctg	gggtggatgtg	tgaatgcttg	gacattcatt	480
ggctgcttat	taagactgtc	cttctgtggg	ccaaataaag	tcaatcactt	tttctgtgac	540
tattcaccac	ttttgaagct	tgcttgcttc	catgatttta	cttttgaaat	aattccagct	600
atctcttctg	gatctatcat	tgtggccact	gtgtgtgtca	tagccataac	ctacatctat	660
atcctcatca	ccatcctgaa	gatgcactcc	accaagggcc	gccacaaggc	cttctccacc	720
tgcacctccc	acctcactgc	agtcactctg	ttctatggga	ccattacctt	catttatgtg	780
atgcccaagt	ccagctactc	aactgaccag	aacaagggtg	tgtctgtgtt	ctacaccgtg	840
gtgattccca	tgttgaaccc	cctgatctac	agcctcagga	acaaggagat	taagggggct	900
ctgaagagag	agcttagaat	aaaaatattt	tct			933

<210> 294

<211> 942

<212> DNA

<213> Unknown (H38g143 nucleotide)

<220>

<223> Synthetic construct

<400> 294

atgctcctta	gcaattcaag	ctggaggcta	tcccagcctt	cttttctcct	ggtagggatt	60
ccagggttag	aggaaagcca	gcaactggatt	gcaactgccc	tgggcaccc	ttacctcctt	120
gcttttagtg	gcaatgttac	cattctcttc	atcatctgga	tggaccacac	cttgccacca	180
tctatgtacc	tcttccctgc	catgctagct	gccatcgacc	tgggtctggc	ctcctccact	240
gcacccaaag	cccttgacgt	gtccttggtt	catgcccacg	agattgggta	catcgtctgc	300
ctgatccaga	tgttcttcat	ccatgcattc	tcctccatgg	agtcaggggt	acttggtggc	360
atggctctgg	atcgctatgt	agccatttgt	cacccttgc	accattccac	aatcctgcac	420
ccaggggtca	tagggcgcat	cggaatgggt	gtgctgggtg	ggggattact	actccttacc	480
cccttcccca	ttttgttggg	aacacttacc	ttctgccaa	ccaccatcat	aggccatgcc	540
tattgtgaac	atatggctgt	tgtgaaactt	gcctgctcag	aaaccacagt	caatcgagct	600
tatgggtgta	ctatggcctt	gcttgtgatt	gggctggatg	ttctggccat	tgggtgttcc	660
tatgccaca	tcctccaggc	agtgtgaag	gtaccaggga	gtgaggcccg	acttaaggcg	720
tttagacat	gtggctctca	tatttgtgtc	atcctggctc	tctatgtccc	tggaaatttc	780
tccttctca	ctcaccgctt	tggtcatcat	gtaccccatc	atgtccatgt	tcttctggcc	840
acacggatc	tcctcatgcc	acctgcgtc	aatcctcttg	tctatggagt	gaagactcag	900
cagatccgcc	agcgagtgtc	cagagtgttt	acacaaaagg	at		942

<210> 295

<211> 945

<212> DNA

<213> Unknown (H38g144 nucleotide)

<220>

<223> Synthetic construct

<400> 295

atgacaaaag	gcaatcgtag	cacagtgacc	gaatttgtcc	tcattgggatt	cacagaccgt	60
cctgagctgc	agctccccct	ctttgtgggt	ttccttgta	tttatctcat	cacctgggtg	120
ggaaaccttg	gcatgatcct	gctgatcaga	gcagactcgc	ggctccacac	ccccatgtac	180

tacttctca	gtcacctggc	attcattgat	ctgtgttact	catcttctat	tgggcccag	240
atgctgcaaa	atgtattggg	gaagaaaaaa	accatctcct	tttcaggctg	ttttgctcag	300
ctgtacttct	cgggtgcttt	tgccactaca	gaatgattcc	tcttggccac	aatgccctac	360
gaccgctacg	tggccatctg	caacccccctg	atttacacag	ctattatgac	gcagcgggctc	420
tgcagggaggt	tagtgatagg	ggtctatacc	tatggcttcc	gaaactctgt	gatacacaga	480
gctctgacgt	ttcagctgtc	tttctgcaac	tccgacgtca	tccaccactt	ctactgtgct	540
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atcctctttt	ccattataaa	aatccagctc	tccgagggca	agtgcagagc	attttccacc	720
cgtgcctccc	acctcactgt	cgtcaccatc	ttttatggca	cactattttt	catgtacctg	780
cagcaaccaa	aagcggggaa	ttcatgggaag	ccaaacaaag	tagtctctgt	gttttatagt	840
cttgtaattc	ccatgcttaa	ccctcttata	tatgcctga	gaaacacaga	agtaaaggat	900
gccctgaaaa	aaatgctaga	gggcaaagag	ttatagttag	tgagt		945

<210> 296

<211> 605

<212> DNA

<213> Unknown (H38g145 nucleotide)

<220>

<223> Synthetic construct

<400> 296

atgacaacac	accgaaatga	caccctctcc	actgaagctt	cagacttcct	cttgaattgt	60
tttgtcagat	ccccagctg	gcagcactgg	ctgtccctgc	ccctcagcct	ccttttctc	120
ttggccgtag	gggccaacac	caccctcctg	atgaccatct	ggctggaggc	ctctctgcac	180
cagccccgtg	actacctgct	cagcctctc	tccaaactgg	acatcgctgt	ctgcctcact	240
gtcatcccca	aggctcctgac	catcttctgg	tttgacctca	ggcccatcag	cttccctgcc	300
tgcttctctc	agatgtacat	catgaattgt	ttcctagcca	tggagtcttg	cacattcatg	360
gtcatggcct	atgatcgcta	tgtagccatc	tgccaccac	tgagatatcc	atcaatcatc	420
actgatcact	ttgtagtcaa	ggctgccatg	tttattttga	ccagaaatgt	gcttatgact	480
ctggccatcc	ccatccttcc	agcacaaact	ttattgggaa	caatgttttt	aaaaccattc	540
ttggcaaatg	ttttgttcac	aatttctgcg	gagatgcacc	ttaataacct	tacacatttc	600
tgaag						605

<210> 297

<211> 609

<212> DNA

<213> Unknown (H38g146 nucleotide)

<220>

<223> Synthetic construct

<400> 297

atgaatgaga	caaatcattc	ttgggtgaca	gaatttgtgt	tgctgggact	gtctagtcca	60
agggagctcc	aacctttctt	gtttcttata	ttttcactac	tttatctagc	aattctgttg	120
ggcaactttc	tcatcatcct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	caaacctgtc	atttatagac	gtatgtgttg	cctcttctgc	tacccctaaa	240
atgattgcag	acttttctgg	tgagcacaag	actatttctt	ttgatgcca	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatgggtg	tcctagtttc	catggcctat	360
gaccgttatg	ttgctatatg	caaacctccc	cactacatga	caatcatgag	ctgctgtgta	420
tgtgtgtgac	tcgtcctcat	ttcctgggtt	gtgggcttca	tccataccac	cagccagttg	480
gcattcacgt	taatctgcca	ttttgtggtc	ctaataagg	agatagtttt	tttctgtgac	540
cttctcttag	cgtcgaagtt	agcctgcata	gacacttatg	ttgtcagcct	actaatagtt	600
gcagatagt						609

<210> 298

<211> 912

<212> DNA

<213> Unknown (H38g147 nucleotide)

<220>

<223> Synthetic construct

<400> 298

atggcactta	gcaattccag	ctggaggcta	ccccagcctt	cttttttcct	ggtaggaatt	60
ccgggttttag	aggaaagcca	gcactggatc	gcactgcccc	tgggcatcct	ttacctcctt	120
gctctagtg	gcaatgttac	cattctcttc	atcatctgga	tggaccatc	cttgacacaa	180
tctatgtacc	tcttctgtc	catgctagct	gccatcgacc	tggttgtggc	ctcctccact	240
gcacccaaag	cccttgagc	gctcctggt	cgtgcccagg	agattgggta	caactgtctgc	300
ctgatccaga	tggtcttcac	ccatgcattc	tcctccatgg	agtcaggggt	acttgtggcc	360
atggctctgg	atcgctatgt	agccatttgt	caccccttgc	accattccac	aatcctgcat	420
ccaggggtca	tagggcacat	cggaaatggg	gtgctgggtg	ggggattact	actcctcatc	480
cccttcctca	ttctgttgcg	aaaacttatc	ttctgccaag	ccaccatcat	aggccatgcc	540
tattgtgaac	atatggctgt	tgtgaaactt	gcctgctcag	aaaccacagt	caatcgagct	600
tatgggctga	ctgtggcctt	gcttgtgggt	gggctggatg	tcctggccat	tgggtgttcc	660
tatgccacac	ttctccaggc	agtgtggaag	gtaccaggaa	atgaggcccg	acttaaggcc	720
tttagcacat	gtggctctca	tggttgtgtc	atcctgggtc	tctatatccc	gggaatgttc	780
tccttctca	ctcaccgctt	tggtcatcat	gtaccccatc	acgtccatgt	tcttctggcc	840
atactgtatc	gccttgtgcc	acctgcactc	aatcctcttg	tctatagggt	gaagaccag	900
aagatccacc	ag					912

<210> 299

<211> 330

<212> DNA

<213> Unknown (H38g148 nucleotide)

<220>

<223> Synthetic construct

<400> 299

agtcacacag	aaccacagaa	tctcacaggt	gtctcagaat	tccttctcct	gggactctca	60
gaggatccag	aactgcagcc	tgctctcgct	tggctgtcct	tgctccattta	cctgggcaca	120
gtgctgggga	acctgctcat	catcctggct	gtcagctctg	actcccacct	ccacaccccc	180
atatacttct	tcctcttcaa	cctgtccttg	gctgacattg	gtttcacctc	ggccatgggt	240
cccaagatga	ttgtggacat	gcaatcgcat	agcagagtca	tctcttatgc	gggctgcctg	300
acatagatgt	ctttctttgt	cctttttttt				330

<210> 300

<211> 980

<212> DNA

<213> Unknown (H38g149 nucleotide)

<220>

<223> Synthetic construct

<400> 300

tttttttcca	ataattctgt	tctcttccca	catactttct	tcctggctgg	catcccagga	60
ttgactgcca	cccacatttg	gattttactt	cccttttgct	ttatgttttt	cctgtcattg	120
actgggaatg	gtgtcctgct	ttttctcatc	cggacagaat	gcagccttcg	ccagcccatg	180
tttctttttc	ttgccatgct	ctcctttgtc	gacttgggtc	tctctctctc	cacactgcct	240
aagatgctgg	ccattttctg	gtttgggtgt	acagccatca	gctcgcatte	ctgtctttcc	300
cagatgttct	tcatccatgc	attctctgcc	atggagtcag	gggtgctagt	ggccatggcc	360
ctggaccgct	ctgtggccat	ctgcaaccca	ctgcgttatg	caaccatcct	tccacctgtt	420
gttgttgcca	agattggagg	cctgggtggg	ttgtgagggg	tgggattgac	catctccttt	480
ccaagcttgg	cccataggct	gcactaccat	ggctcacaca	tgattgccta	taccttctgt	540
gagcatatgg	cagtggtgaa	gcttgccctg	gaggccacca	ctgtggacaa	cctctatgcc	600
tttgtgggtg	caatctttct	tggtgggggg	gatgtgggtc	tattgcctat	tcttatgggc	660
tgattgtgag	gactgtaatg	cattttcctt	cacctgagga	acgtgcgaaa	gcaggcagca	720
catgtacagc	ccatgtctgt	gtcatcctct	tcttctatgg	actgggcttt	ctttctgtgg	780
tcatgcagcg	ctttggagca	cccacagctt	ctactgccaa	ggtcatcctt	gccaatctct	840
acttgcctct	tccccagca	ctggatccca	ttgtctatgg	catggagacc	aagcagatct	900

aggagcggct attgatgatt ctaagcccca agcagattga gcttacctga gtatagttat 960
caccagctgg acttcagggt 980

<210> 301
<211> 721
<212> DNA
<213> Unknown (H38g150 nucleotide)

<220>
<223> Synthetic construct

<400> 301
cttagacaac ttcacaacct ttttcttctt gttggatttt ttctttcttt tactcctttt 60
aagttatatg cataatctaa attctgtgac taaattttcc agtaaaacag atgaatcaaa 120
gctcaaaagc taatgtaaag tcaaatctct tttctttacc tatgctggat gctgtgagaa 180
actactgctt gctgtagaaa agagagatct tcctttttgt tcattcattt cctccttcac 240
tagtcaactg ctgtttctga ccatgccaaag gtggaacctg gagtaggaag gagagagaga 300
gggtaaggga agtctcattg actgacgcta aaataagatg gcttcacatt ttctggctct 360
ggccaatggt tactatttct tactcatatt aaacctctct gaatgcattt aaccatggga 420
gcaagtcttc tccccgaggt gcgtcccca gatttcttcc agttcccagt ggtcccat 480
aatctctcac agctggacgt tcaactcagta tgtaagacta ccatcttggg tacaatccct 540
ttcaaagcaa ctaaccact ttagtttcca tggccagtc ttcaaactg catatatctg 600
actagctata agtggagctg taactcccat tttgctgcaa agaccacggg gccagagttc 660
ggttgacgtc tgacatatcc ctgatgacag gatacacaca ttaaaacctc tgagtggccc 720
c 721

<210> 302
<211> 939
<212> DNA
<213> Unknown (H38g151 nucleotide)

<220>
<223> Synthetic construct

<400> 302
atggcatctc ccaacaatga ctccactgcc ccagtctctg aattcctcct catctgcttc 60
cccaacttcc agagctggca gcaactggtg tctctgcccc tcagccttct ctctcctctg 120
gccatgggag ctaacaccac cctcctgac accatccagc tggaggcctc tctgcaccag 180
ccccgtact acctgctcag cctcctctcc ctgctggaca tcgtgctctg cctcacctgc 240
atccccaagg tcttgcccat cttctggttt gacctcaggt cgatcagctt cccagcctgc 300
ttcctccaga tgttcatcat gaacagtttt ttgaccatgg agtcctgcac gttcatggtc 360
atggcctatg accgttatgt ggccatctgc catccattga gatacccgtc tatcatcact 420
gaccagtttg tggctagggc cgtggtcttt gttatagccc ggaatgcctt tgtttctctt 480
cctgttccca tgctttctgc caggctcaga tactgtgcag gaaacataat caagaactgc 540
atctgcagta acctgtctgt gtccaaactc tcttgtagt acatcacttt caatcagctc 600
taccagtttg tggcaggctg gactctgttg ggctctgac ttatccttat tgttatctcc 660
tattctttta tattgaaagt tgtgcttagg atcaaggccg aggggtgctg ggccaaggcc 720
ttgagcacgt gtggttccca cttcatctc atcctcttct tcagcacagt cctgctggtt 780
ctggtcatca ctaacctggc caggaagaga attcctccag atgtcccat cctgctcaac 840
atcctgcacc acctcattcc cccagctctg aacccattg tttatggtgt gagaaccaag 900
gagatcaagc agggaaatcca aaacctgctg aagaggttg 939

<210> 303
<211> 405
<212> DNA
<213> Unknown (H38g152 nucleotide)

<220>
<223> Synthetic construct

<221> misc_feature

<222> (1)...(405)

<223> n = A,T,C or G

<400> 303

aaagatttgt gaaggagaag taatattaac tttagaatag aaagtattat atttttttat	60
ataggggtgg gagagangat gggtttatga aattaattgt taatgttttg tgaaagtttt	120
taatgataaa aaactgtgtt aaggattaag ggtgagggag atatggccaa agctctaggt	180
acttgtggtt cccacttcat cctcatcctc ttcttcacca cagtctgtgt ggttctggtc	240
atcactaacc tggccaggaa gagaattcct ccagatgtcc ccatcctgtc caacatcctg	300
caccacctta ttccccagc tctgaacccc attgtttatg gtgtgagaac caaggagatc	360
aagcagggaa tccagaacct gctgaggagg ttgtaaaaaa taaaa	405

<210> 304

<211> 960

<212> DNA

<213> Unknown (H38g153 nucleotide)

<220>

<223> Synthetic construct

<400> 304

atggctccga ccaacctcac atctgcccc gtgttcctcc tcctcgccct ggtggacgga	60
acagacagac gccacccgc tgctgttcc gctctgcctt ggcattctatc tgctcaacgc	120
cctgagcaac ctgagcatgg tggcgctggg gagatctgac ggggccctcc gctcccccat	180
gtattacttc ttgggtcacc tgagcctcgt ggacgtctgc ttaccaccg tcacgggtccc	240
caggctgctg gccggcctgc tccaccggg ccaggccata tcctccagg cgtgctttgc	300
cgagatgtac ttcttcgtgg ctctgggcat caccgagagc tacctccgg cggccatgtc	360
ctacgaccgc gcgacggcg cgtgccggcc cctgcgtac ggcgcgtgg tgacgccatg	420
ggcgctgcgc ctgcgtggg cgtgcgtcgt gggccgtgac gcacctgcac tcgtgctgc	480
acacgtgct cctctccgc ctctcctacc cctacccac ccccgctgc cccttctttt	540
gcgacatgac ggtgatgctg agcttggcga cctcggacac gtccgcgcg gagacggcca	600
ttttctccga gggcctggc gtggtgttg ccccgctgct cctcgtgttc cttttcctac	660
gcgcgcatec ttgggtcggg gctcggcttg ccgcggccgg cgcgcgcct tctccacctg	720
cggggcccac ctagtggcgg tggcggtggc ggtggcgctt ttctttggct ctgtcctctc	780
cgtgtatttc ccgcgtcgt ctgcctactc agcccgctac gaccgcctgg ccagcgtggg	840
ctacgtgtc atcacgccga ccttgaaccc ttcatcaac agccttcgca acaaagaggt	900
caagggcgcc ctgaaaagg ggctcagatg gagggctgca cccaagagg cgtgagggca	960

<210> 305

<211> 975

<212> DNA

<213> Unknown (H38g154 nucleotide)

<220>

<223> Synthetic construct

<400> 305

atgttccttc ccaataacac ccagtttcac cctcctcct tcctgttgct ggggatccca	60
gggctagaaa cacttcacat ctggatcggc ttccctttt gtgctgtgta cataattgca	120
ctcatagggc gcttcactat tctacttggt atcaagactg acagcagcct ataccagecc	180
atgtttact tcctggccat gttggccacc attgacttgg gcctttcaac agctaccatc	240
cctaagatgc ttgggatcct ctggtttagc ctcagggaga ttatctgtga tgccctgcctc	300
atccagatgt ttttcatcca caactttact ggcattggagt cagcagccct cgtgggaatg	360
gcttatgacc actttgtggc catctgcaac ccgctacgat atagcatcat cctcaccaa	420
aaggctgttt ctgtgattgg tcttggtgtg ttagtgaggt catttatgtc tgttattcca	480
tttgtttttc tcatttttgc gttgcccttc tgtggggatc atgtcattcc ccacaccaac	540
tgtgagcaca tgggtcttgc tcatctgtct tgttcagta tcaagatcaa tataatctat	600
ggcttgggtg ctatttcaat cctagtatc gacatcatag ccattgccct ttcttatgtg	660
caaatacttc acgctgtttt ccattctcct tctgtaaag cctgactcaa gtcctcagc	720
acatgtggtt cacatgtgtg tgtaatcctt gccttctata caccagccct cttttccttt	780
gtgactcatc gctttggcca aaatgtgccc cgctatatcc atatactcct agccaatctc	840

tatgttgtgg	tgccaccaat	gctcaatcct	gtcatatatg	gagtcagaac	caagcagatc	900
tatgtctgtg	tgaagaatat	attctttacaa	aaataagaaa	ttgaaaagaa	atcgcatcta	960
atacatataa	gaagg					975

<210> 306

<211> 957

<212> DNA

<213> Unknown (H38g155 nucleotide)

<220>

<223> Synthetic construct

<400> 306

atgtctcctc	ttaatgacac	aaaaatggaa	gtccttagat	tcttccttat	cgggatcact	60
ggactggaga	aaagtcgcac	ctggatatcc	attcctttct	tatctgtgta	ccttctttct	120
tggatgggta	attttaccgt	cctctttttt	atcaagacag	agcaaagcct	ccatgaacct	180
atgtattatt	tgctttccat	gctctccatc	tctgacctag	ggctgtctct	gtcttcctta	240
ccctacactt	tgggactatt	cctatttgat	gtccatgaaa	ttcatgcagc	tccatgcttt	300
gcctaggaaat	tttttatcca	tctgtttaca	gtcagtgaag	cctctgtact	gtctgtaatg	360
gcatttgact	ggatgtggc	aatccacagt	cctttgagat	acagcactat	cttaactagt	420
cccagagcca	tcaaaacagg	ggttctctcg	acttccaaga	atgttctttt	gaccttcca	480
ctgccctttc	tcttgcaaag	gctgagatat	tgcatcaaaa	acctgctctc	ccactcctat	540
tgtctccacc	aggatgtcat	gaagctgatg	tgttctgaca	acacagtcaa	tgttgtctac	600
ggactctgtg	caggactttc	tactatgctg	gacttgggtg	tgattacctt	ctcctaaatt	660
atgattttaa	gggctgtact	gggaattgct	accccagac	agcagttcaa	ggccctcaac	720
acgtgcatct	ctcacatctg	tgctgtgctt	atcttctatg	tgcccacgct	gagtgtgcc	780
atgtccacc	agtttgccag	ggatgtgtct	cctatgatcc	acgtcctcat	ggctgatatt	840
tttctgctgg	tgccaccctt	gttgaatccc	atcgtgtact	gtgtgaagac	ccaccaaact	900
cgagaaaagg	ttgtggggaa	actttgtcca	aaagtaagtt	gatcaaagga	atgagaa	957

<210> 307

<211> 939

<212> DNA

<213> Unknown (H38g156 nucleotide)

<220>

<223> Synthetic construct

<400> 307

atgtccatta	tcaacacatc	atatgttgaa	atcaccacct	tcttcttggg	tgggatgcca	60
gggctagaat	atgcacacat	ctggatctct	atccccatct	gcagcatgta	tcttattgct	120
attctaggaa	atggcaccat	tctttttatc	atcaagacag	agccctcctt	gcatgagccc	180
atgtactatt	ttctttccat	gttggctatg	tcagacttgg	gtttgtcttt	atcatctctg	240
cccactgtgt	taagcatctt	cctgttcaat	gtcctgaaa	tttcatccaa	tgctgtcttt	300
gcccaggaat	tcttcattca	tggattctca	gtactggagt	cctcagtcct	cctgatcatg	360
tcatttgata	gattcctagc	catccacaac	cctctgagat	acacctcaat	cctgacaact	420
gtcagagtgg	cccaaataag	gatagtattc	tcctttaaga	gcatgctcct	ggttcttccc	480
ttccctttca	ctttaagaaa	cttgagatat	tgcaagaaaa	accaattatc	ccattcctac	540
tgctccacc	aggatgtcat	gaagttggcc	tgttctgaca	acagaattga	tgttatctat	600
ggcttttttg	gagcactctg	ccttatggta	gactttattc	tcattgctgt	gtcttacacc	660
ctgatcctca	agactgtacc	gggaattgca	tccaaaaagg	agcagcttaa	ggctctcaat	720
acttgtgttt	cacacatctg	tgcatgtatc	atcttctacc	tgcccatcat	caacctggcc	780
gttgtccacc	gctttgcccg	gcatgtctct	ccccctatta	atgttctcat	ggcaaatgtt	840
ctcctacttg	tacctccact	gacgaaccca	attgtttatt	gtgtaaaaac	taaacagatt	900
agagtgaag	ttgtagcaaa	attgtgtcaa	cggaagatt			939

<210> 308

<211> 925

<212> DNA

<213> Unknown (H38g157 nucleotide)

<220>

<223> Synthetic construct

<400> 308

atgggtgaata gaaacaatgt gacagagttt attctactgg ggcttataga gaatccaaaa	60
atgcagaaaa tcatatttgt tgtgttttgt catctacatc accaccatga taggaaatgt	120
gctcattgtg gtcaccgtca ctgccagccc atcattgagg tcccccatgt actttttacct	180
ggcctatctg tcctttattg atgcctgcta ttcctccgtc aatgcccta agctgatcac	240
agattcactc tatgaaaaa agactatctt actcaatgga tgtatgactc aagtcttttg	300
agaacatttt ttcgagggtg ttgagggtcat cctacttact gtaatggcct atgaccgcta	360
cgtgggtcatc tgcaagccct tgcactatac caccatcatg aagcagcatg tttgtagcct	420
gctagtggga gtgtcatggg taggaggctt tcttcatgca accgtacaga tcctcttcat	480
cttccaatta cttttctgtg gtcctaattg catagatcac tttatgtggg atctcaaccc	540
tttgcctaat cttgtctgca ctaataccca cactctagga ctcttcgttg ctgccaacag	600
tgggttcata tgcctgttaa actttctctt gctcctgggc tcctatatgg tcatactgta	660
ctccttaagg acccacagct tagaggcaag gtgcaagcc ctctccacct gtgtctccca	720
catcacagtt gtcactttat tctttatacc ctgcatattt gtgtacatga gacctccagc	780
tactttaccc attgataaag cagttgctgt attctacact atgatagctc ctatgtttaa	840
ccccttaatc tacaccttga ggaatgctca gatgaaaaat gccattagga aattgtgtag	900
taggaaagct atttcaagtg tcaaa	925

<210> 309

<211> 963

<212> DNA

<213> Unknown (H38g158 nucleotide)

<220>

<223> Synthetic construct

<400> 309

atggcatacc atggcaacag gggcactttt caccagcca cattttttct cattggaatc	60
ccaggctctgg aagacgtcca tatgtgaatc tccctgcact tctgctctgt ttaccttttg	120
gctttgctgg gaaatgctac cattctgcta gtcatcaagg cagaacagac cctccgggag	180
cccattgtct actttctggc catcctttcc acaattgatt tggccctttc tacaacctct	240
gtgcctcgta cgctgggtat cttctggtt gatgctcatg agattaactt tggagcatgt	300
gtggcccaga tgtttctgat ccatgccttc actggcatgg aggtgagggt ctgggtggcca	360
tggcctttga cgttacgtg gccatctgca atccacttca ctacacaaac atcttgacat	420
ccgggtgtct ggtgggcac actatgtgca ttgtaattcg tccagttctg tttacactcc	480
cgataatcta tctcatctac cgtttaccat tttggtcagg gtcataataa tagcccatc	540
ctactatgag cacatgggca ttgcaaaatt gtctgtgga aacatccgtg tcaatgctat	600
ctatgggctc tttgtggtct cctctatctc ctgaacctgg tccttattgt tatctcatat	660
gtgtacattc tctgtgctgt cttctgcctc gcatcacatg atgctcggct aaaagcccta	720
agcaacatgt ggctctcatg ttgggtcat ctgtgttttc tatatcccggt cggacttctc	780
tttcctactc attgatttgg acacaacatt ccacattaca tgacattct tgttgctact	840
ctctatttgg ttatcccacc ctctctcaac cccatcattt gtgggtgag gaccaaattg	900
aaacgagagc gagtgtctta tgtacttact aaaaaataag attctgacca tgttctttta	960
cta	963

<210> 310

<211> 483

<212> DNA

<213> Unknown (H38g159 nucleotide)

<220>

<223> Synthetic construct

<400> 310

ggcacagttt agatcctctc ccaggtctga cttcctttct atgatcccaa tgtcatagct	60
cattcatgtg tgacttaaac actttgttga aactcctctg catgggtact actaatacac	120
ttggtttctt tgttgctgcc aatgggtgggt tcaactacct attaaacatc attttcttga	180
tggtttctta agtggccatc ctatgtactt tgaaaactca cagcttgagg gaaagatgct	240

aaagccctct	ctacctgcat	ctctcacacc	accgtgggtca	tcttatcttt	gggttctgta	300
tatctgtgta	tctgtgccca	gtgacccttc	cccaatcaat	aaagcagtg	ctgtgtttta	360
taccatgata	aatcctatgt	taaaaccttt	agtctaacc	tcagaaatgc	agagggtgaaa	420
agtgtcttga	gaaagctctg	ggtcaaaaga	tgaactgaag	agagaaataa	tccaaacata	480
aga						483

<210> 311

<211> 933

<212> DNA

<213> Unknown (H38g160 nucleotide)

<220>

<223> Synthetic construct

<400> 311

atgtttttatc	acaacaagag	catattttcac	ccagtcacat	ttttcctcat	tggaatccca	60
gggtctggaag	acttccacat	gtggatctcc	gggcctttct	gctctgttta	ccttgtggct	120
ttgctgggca	atgccacat	tctgctagtc	atcaaggtag	aacagactct	ccgggagccc	180
atgttctact	tcctggccat	tctttccact	attgatttg	ccctttctgc	aacctctgtg	240
cctcgcatgc	tgggtatctt	ctggtttgat	gctcacgaga	ttaactatgg	agcttgtgtg	300
gcccagatgt	ttctgatcca	tgccttccact	ggcatggagg	ctgagggtctt	actggctatg	360
gcttttgacc	gttatgtggc	catctgtgct	ccactacatt	acgcaaccat	cttgacatcc	420
ctagtgttgg	tgggcattag	catgtgcatt	gtaattcgtc	ccgttttact	tacacttccc	480
atggtctatc	ttatctaccg	cctacccttt	tgtcagggtc	acataatagc	ccattccctac	540
tgtgagcaca	tgggcattgc	aaaattgtcc	tgtggaaaca	ttcgtatcaa	tggtatctat	600
gggctttttg	tagtttcttt	ctttgttctg	aacctgggtc	tcattggcat	ctcgtatgtt	660
tacattctcc	gtgctgtctt	ccgcctccca	tcacatgatg	ctcagctaaa	agccctaagc	720
acgtgtggcg	ctcatgttgg	agtcattctgt	gttttctata	tccttccagt	cttctctttc	780
cttactcatc	gatttggaca	ccaaatacca	ggttacattc	acattcttgt	tgccaatctc	840
tatttgatta	tcccaccctc	tctcaacccc	atcatttatg	gggtgaggac	caaacagatt	900
cgagagcgag	tgtcttatgt	ttttactaaa	aaa			933

<210> 312

<211> 946

<212> DNA

<213> Unknown (H38g161 nucleotide)

<220>

<223> Synthetic construct

<400> 312

atggagaata	ggaataacgt	gacagagttt	gttttactag	ggcttacaga	gaatccaaag	60
atgcagaaaa	tcatatttgt	tgtgtttttt	tgtcatctat	atcatcactg	tggtgggaaa	120
tgcgtcatt	gtggtcacca	tcactgccag	cccatcactg	gggtccccc	tgtacctttt	180
cctggcctat	ctctccttta	tagatgcctg	ctattcttct	gtcaataccc	ctaagctgat	240
cacagattca	ctctatggaa	agaacaccat	cctattcaat	ggatgcatga	ctcaagtctt	300
tggagaacat	ttcttcggag	gtgcagaggg	tatcctactt	actgtgatgg	cctatgaccg	360
ctatgtggcc	atctgcaagc	ccttgcaacta	tatgactatc	atgaaccagt	gtgtgtatgc	420
cctgctaata	ggagtgggtg	ggatgggagg	ctttcttcat	gcaaccatac	agatcctctt	480
catcttccaa	ttacctttct	gtggtcctaa	tgtcatagat	cacttttatg	gtgatctgaa	540
ccctttgtc	aacctgcct	gcaactgacac	ccatagtctg	ggactcttca	ttgttgccaa	600
cagtggatc	atctgcttgt	taaactttgt	cctcctgctg	gtctcctatg	tggtcatctt	660
gcgctcccta	aggactcaca	gcttggaggc	aaggcacaaa	gccctctcca	cctgtgtctc	720
ccacatcaca	gttgctcatct	tattctttgt	gccctgcata	tttgtgtaca	tgagacctgc	780
agctacttta	cctattgata	aagcagttgc	tatattctac	actatgataa	ctcctatgtt	840
aaacccttta	atctatacct	tgagggaatgc	ccagatgaaa	aatgccatca	ggaaattgtg	900
tagtagaaag	gacatttcag	gtaacaaata	aatgtaacta	gagctc		946

<210> 313

<211> 966

<212> DNA

<213> Unknown (H38g162 nucleotide)

<220>

<223> Synthetic construct

<400> 313

tcaaatactg	ggatgtccat	tctcaatacc	tctgaaatgg	aaatctctat	tttctacttg	60
ggtgggatcc	caggttttga	gcatgccaat	atttggatct	ctatccccat	atgtctcatg	120
tacactgttg	ctatcctagg	gaattgtacc	attctgtttt	tcataaaaaac	agagccttct	180
ttgcctgagc	ccatgtacta	ttttctctcc	atgttggtct	tctctgacct	gggactatcc	240
ctctcctctc	tccctaccat	gttaaggatt	tccctgttca	atgctccagg	aatttccctt	300
gatgcctgta	ttgctcaaga	gtttttcatc	catggattct	cagctatgga	gtcatctgta	360
cttcttataa	tgtcctttga	tcgctttatt	gccatctgca	accccttgag	atacacttcc	420
atcctcacca	gtgccagagt	cattcaaatt	gggcttgctt	tttctctcaa	aaatgttttg	480
ttgatcctcc	catttccttt	caactctaaa	catctaaaat	attgtaagaa	gaacctcctg	540
tcccaatcct	actgcctcca	tcaagatgtc	atgaaactgg	cctgcactga	caacaaggtc	600
aacatcatct	atggcttatt	tgtggctctc	acaggcatcc	tagacttgac	atttattttc	660
atgtcctaca	tggtgatact	gaaagcagtg	ttgagcatag	catcatgaaa	gaaaaggctc	720
aaggctctca	atacatgtgt	ttcccacatc	tgtgctgtgc	tcactctcta	tgtgcccatt	780
atctccctag	ctgtcatcta	ccggtttgcc	aaacacagtt	tcccaatcac	taggatcctc	840
atagctgatg	ctttcttgct	ggtgcctcca	ttgatgaacc	ccattgtata	ctgtgtgaag	900
agccagcaga	taagaaatct	tgtcttagaa	aaactgtgcc	agaagcaaag	ctgaagcgga	960
tgctta						966

<210> 314

<211> 961

<212> DNA

<213> Unknown (H38g163 nucleotide)

<220>

<223> Synthetic construct

<400> 314

agtcacacag	agccacagaa	tctcacaggt	gtctcagaat	tcctcctcct	gggactctca	60
gaggatccag	aactgcagcc	actccttgct	gggctgttcc	tatccatgtg	cctggtcacg	120
atgtctggga	actgctcatc	atcctggccg	tcacctgac	tcccacctcc	acatcccat	180
gtactttctc	ctctccaacc	tggtccttgg	ccatgacatt	gcgtttcacc	ttaggccacg	240
gtccccaaga	tgattgtaga	catgcaatca	catagcagag	tcactctcca	tgcaggctgt	300
ctgacacaga	tacctttctt	tgtccttttt	gtatgtatag	atgacatgct	cctgactgtg	360
atggcctatg	actgatttgt	ggccatctgt	cacccctgc	actaccaggt	catcatgaat	420
cctcacctct	gctgtcttct	tagtgttgat	gtcttttctt	tagcctgttg	gattcctagc	480
tgcacaactg	gattgttaca	attcacctgc	ttcaagaatg	tggaaatctc	taattttttc	540
tgtgactgat	ctcaacttct	caaccttgcc	tgttctgact	gtcatcagta	acatattcat	600
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taaaattgtg	ccctccattc	taagaattcc	attgtcagat	gggaagtata	aagccttctc	720
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cctgacttca	gctgtgtcac	cagccccag	gaatggtgtg	gtggcatcag	tgttgtacgc	840
tatgtcaccc	ccatgctgaa	ccccttcac	tgcagcctga	gaaacagggg	gcattcaaag	900
tgccctgtgg	aggctgtgca	ggaggaaagt	ctaactctcat	gatctgtttc	atcctttttc	960
t						961

<210> 315

<211> 960

<212> DNA

<213> Unknown (H38g164 nucleotide)

<220>

<223> Synthetic construct

<400> 315

atgcgtctca	tatgagatga	agaaatgtcc	agaagaaact	atactgaact	gacagaattt	60
------------	------------	------------	------------	------------	------------	----

gttctcttgg	gtctaacaag	cgtccagag	ctgagagttg	ctttcttggc	actgttcctt	120
tttgtctaca	tagccactgt	ggtaggaaac	ttggggatga	ttattttaat	caaagttgat	180
tctcgacttc	acactcccat	gtaatttttt	ctctccagtt	tgtccattct	agatctgtgt	240
ttctccacaa	atttcactcc	caaaatgcta	gaaaatttct	tatcagagaa	gaagaccatt	300
tcctatgcag	gttggttggat	gcagtgtctat	gttggtcattg	ctgtggtcct	tgcagagcac	360
tgcattgttg	cagtcattggc	atatgaccgc	tatatggcca	tctgtaatcc	attgtcttac	420
agtagcaaaa	tgtcccaagg	tggttgtgtc	cacctgggtca	ttgtccctta	tgtctatggc	480
tttcttctca	gtgtgatgga	aaccttaagg	acctacaacc	tctccttctg	tggaacaaat	540
gaaatcaacc	atttctactg	tgctgatcct	cctcttatca	aactggcatg	ctctgacacg	600
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ggaacctctt	tctgcatgca	tttgagacgt	cccacagacg	agtcctgtga	gcaggggaaa	840
atggtggctg	tgttttacac	cacagtgtga	ctcatgtctg	actccatgat	ctatggcctc	900
aggaacaagg	atgtgaaaga	ggcgttgaaa	aaagcaatag	gaaaacaaac	attgggaaaa	960

<210> 316

<211> 947

<212> DNA

<213> Unknown (H38g165 nucleotide)

<220>

<223> Synthetic construct

<400> 316

aggaggatgg	gcaatcacac	tgcagtgtgc	ctattccttc	tgtggggatt	ttccagtttt	60
tcagacctgc	agagtctact	ttttgtgtg	attctcttct	acatgtgacc	atcctagctg	120
caaacgtgtc	cataatgggg	gccatcaagc	tcagccacaa	ccttcacact	cctatgtact	180
ttttcctctg	tggectgtcc	ttttcagaaa	cttggtaccac	tgtggttagta	atccctcgca	240
tggtggtgga	ctttctatca	gagagcaaga	ccatttctct	tcctgagtgt	gccacacaga	300
tgtttttctt	tctgggcttt	gcacccaaca	actgtttcat	catggccgct	atgtcctacg	360
accgctacac	ggccatccac	aacctactgc	agtaccacac	ccttatgaca	agaaagatct	420
gcttgagatg	gatgatggct	tcttggtatg	ttgggttcct	gttttctctg	tgcattcatg	480
tcactgtatt	caacttgtct	ctttgcgact	tgaacactat	ccagcactat	ttctgtgata	540
tctcaccagt	ggtctccctt	gcttgtaatt	acactttcta	tcataaaatg	gctatttttg	600
tgctctctgc	ctttgtgttg	gtgggcagct	gtattttaat	tatgatttcc	tatgtcttca	660
ttgtgttcat	agtcataaag	atgccctctg	caaaggggag	gtctaaggcc	ttctcaactt	720
gtcctcctca	cctcactgtt	gtgtccatac	actatggatt	tgcttgcttt	gtctatttga	780
ggcccaagaa	cagcaactcc	ttcgatgaag	acatgctgac	ggccatgata	tatacaatc	840
tgatgcctct	gcttaacccc	atcgtgtaca	gtctgagaaa	caaagaaatg	cagatagccc	900
taagaaaaac	actaggcagt	gtatttgggg	ttttccttca	gaagaca		947

<210> 317

<211> 955

<212> DNA

<213> Unknown (H38g166 nucleotide)

<220>

<223> Synthetic construct

<400> 317

atgtcagcat	acaataacac	caatgcccg	ccatcaacct	ttatttctat	tggcattcct	60
gggttggaag	ctgtcacat	ctggatctcc	atcccccttt	gtgtggtcta	cctgttgccc	120
ctactgggaa	acggctctct	tctgtttatc	atcaagacag	agcccagcct	ccatgagcca	180
atgtacctct	tcctatgcat	gctggctgta	gttgatcttg	ttgtgtgttc	tacagctgtg	240
cccaaacttc	tcagtctctt	ctggttccat	gatggagaga	ttcgctttga	aacctgcctc	300
actcgtgttc	ctgattcact	cttgctccac	catggaatct	ggcttcttcc	tggccatggc	360
ttttgaccga	tatgtggcca	tttgcaatcc	attaagacat	tcagctattc	tgacacgcgc	420
tgtaattggg	agagtggggc	tagctattgt	tctcaggggc	atagcacttc	tcagtcctca	480
ctctttccta	ctacgctggc	ttccctactg	cagaacccat	atcatttctc	acacctactg	540
tgagttcatg	gccctcatca	ggattgcctg	tgctgagaca	aaattccgca	gagcctacag	600

cctcattgtt	gccttcctta	ctgggggtgt	agactttata	ttgatcattt	attcttatgt	660
cctcatactc	cacactgtct	tccagctccc	atccaaagat	gcccgggtca	aatctttggg	720
cacctgtggc	tcccatgtct	gtgtcatctt	agtatcctat	actccagcct	tcttctcggt	780
tctcaccac	agggttgggc	accatgtggc	tccccatttt	cacatatttg	tggccaacat	840
ctatcttctt	gtcccacca	tggatgaacc	cattatctat	ggggtaaagaa	ccaaaaggat	900
ttgggacagg	ttccttaaag	ttttcagttt	ttcaaagcct	ctaagtaa	cattt	955

<210> 318

<211> 921

<212> DNA

<213> Unknown (H38g167 nucleotide)

<220>

<223> Synthetic construct

<400> 318

atgctcaatt	tcaccgatgt	gacagagttc	attcttttgg	ggctaacgag	ccgtcgagaa	60
tggcaagttc	tcttcttcat	catctttctt	gtggtctaca	tcataccat	ggtgggcaat	120
atcggcatga	tgggtgta	caaggtcagt	cctcagctta	acaaccccat	gtacttttct	180
ctcagtcact	tgtcatttgt	tgatgtgtgg	ttttcttcca	atgtcacccc	taaaatgttg	240
gaaaacctgt	tatcagataa	aaaaacaatt	acttatgctg	gttggttagt	acagtgtttc	300
ttcttcattg	ctcttgtcca	tgtggaaatt	tttattcttg	ctgcgatggc	ctttgataga	360
tacatggcaa	ttgggaatcc	tctgctttat	ggcagtaaaa	tgtcaagggt	tgtctgtatt	420
cgactgatta	ctttccctta	catttatgg	tttctgacga	gtctggcagc	aacattatgg	480
acttacggct	tgtacttctg	tggaaaaatt	gagatcaacc	atttctactg	tgcagatcca	540
cctctcatca	aaatggcctg	tgccgggacc	tttgtaaaag	aatatacaat	gatcatactt	600
gccggcatta	acttcacata	ttccctgact	gtaattatca	tctcttactt	attcatcctc	660
attgccattc	tgcgaatg	ctcagcagaa	ggaaggcaga	aggccttttc	cacatgtggg	720
tcccatctga	cagctgtcat	tatattctat	ggtactctga	tcttcatgta	tctcagacgt	780
cccacagagg	agtctgtgga	gcaggggaag	atgggtgctg	tgttctatac	cacagtgatc	840
cccattgtga	atcccatgat	ctacagtctg	aggaacaagg	atgtgaaaaa	ggccatgatg	900
aaagtgatca	gcagatcatg	t				921

<210> 319

<211> 966

<212> DNA

<213> Unknown (H38g168 nucleotide)

<220>

<223> Synthetic construct

<400> 319

atgaccatga	caacggagaa	ccccaaccag	actgtggtga	gccacttctt	cctggagggt	60
ttgaggatca	ccgctaaaca	ttctagcctc	ttcttctctc	tcttctcctc	catctacagc	120
atcactgtgg	ctgggaatct	cctcatcctc	ctaactgtgg	gctctgactc	tcacctcagc	180
ttacctatgt	accaattcct	ggggcacctc	tccttctctg	atgectgttt	gtctacagt	240
acagtgccca	aggatcatgg	aggcctgctg	actctggatg	ggaagggtgat	ctcctttgag	300
ggctgtgccg	tacagcttta	ttgcttccac	tttctggcca	gactgagtg	cttctgtac	360
acagtcatgg	cctatgaccg	ctatctggct	atctgtcaac	ccctgcaacta	cccagtggcc	420
atgaacagaa	ggatgtgtgc	agaaatggct	ggaatcacct	gggccatagg	tgccacgcac	480
gctgcaatcc	acacctccct	caacctccgc	ctgctctact	gtgggccttg	ccacattgcc	540
tacttcttct	gcgacatacc	ccctgtccta	aagctcgctc	gtacagacac	caccattaat	600
gagctagtca	tgttggccag	cattggcatc	gtggctgcag	gctgcctcat	cctcatcggt	660
atttcttaca	tcttcatcgt	ggcagctgtg	ttgctcatcc	gcacagccca	gggccggcag	720
cgggccttct	ccccctgcac	tgccagctc	actgggtg	tcctgtacta	cggtgccact	780
gtctgtatct	acctgcagcc	tcgtctcagt	gaggcaggag	ctggggcccc	tgtgtcttct	840
tacacaatcg	taactccaat	gctcaaccca	ttcatttaca	ctttgcggaa	caaggagggtg	900
aagcatgctc	tgcgaaggct	tttgtgcagc	agcttccgag	agtctacagc	aggcagccca	960
ccccca						966

<210> 320

<211> 967
 <212> DNA
 <213> Unknown (H38g169 nucleotide)

<220>
 <223> Synthetic construct

<400> 320
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 gaatggcaag ttctcttctt catcggtttt cttgtgggtc acattatcac cgtgggtgggc 120
 aatatcgga tgatgttggt aatcaagggtc agtcctcagc ttaacagccc catgtacttt 180
 ttctctcagc acttgtcatt tgttgatgtg tggttttctt ccaatgtcac ccctaaaatg 240
 ttggaaaatc tgttatcaga taaaaaaaaa aacaatttct tatgctggct gtttagcaca 300
 gtgtttcttc ttcattgtct ttgtccatgt ggaaattttt attcttgctg cgattgcctt 360
 tgatagatac acagtgattg gaaatccttt gctttatggc agcaaatgt caagggatgt 420
 ctgtattcga ctgattactt tcccttacat ttatggtttt ctgacgagtc tgacagcaac 480
 attatggact tatggcttgt acttctgtgg aaaaattgag atcaaccatt tctactgtgc 540
 agatccacct ctcatcaaaa tggcctgtgc cgggaccttt gtaaaagaat atacaatgct 600
 catacttgcc ggcatacaact tcacatattc cctgactgta attatcatct cttacttatt 660
 catectcatt gccattctgc gaatgcgtc agcagaaggga aggcagaagg ccttttccac 720
 atgtgggtcc catctgacag ctgtcatcat attctatggg actctgatct tcatgtatct 780
 cagacgtccc acagaggagt ctgtggagca ggggaagatg gtggctgtgt tctataccac 840
 agtgatcccc atgttgaatc ccatgatcta cagtctgagg aacaaggatg tgaaaaaggc 900
 catgatgaaa gtgatcagca gatcatgtta aacaaaataa aatcaagttt gaattaattt 960
 tgtcttc 967

<210> 321
 <211> 933
 <212> DNA
 <213> Unknown (H38g170 nucleotide)

<220>
 <223> Synthetic construct

<400> 321
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 ctggacgccc tctcttttgg aatcttctctg gtggtttacg tgctcactgt gctggggaac 120
 ctctcatcc tgctggtgat cagggtggat tctcacctcc acaccccat gtactacttc 180
 ctcaccaacc tgtccttcat tgacatgtgg ttctccactg tcacgggtgcc caaaatgctg 240
 atgaccttgg tgtccccaag cggcagggtc atctccttcc acagctgcgt ggctcagctc 300
 tattttttcc acttcttggg gagcaccgag tgtttcctct acacagtcac gtcctatgat 360
 cgctacttgg ccatcagtta cccgctcagg tacaccagca tgatgagtgg gagcaggtgt 420
 gccctcctgg ccaccggcac ttggctcagt ggctctctgc actctgctgt ccagaccata 480
 ttgactttcc atttgcccta ctgtggaccc aaccagatcc agcactactt ctgtgacgca 540
 ccgcccaccc tgaaactggc ctgtgcagac acctcagcca acgtgatggg catctttgtg 600
 gacattggga tagtggcctc aggtctgctt ttctctgatag tgctgtccta tgtgtccatc 660
 gtctgttcca tctgcggat ccgcacctca gatgggaggg gcagagcctt tcagacctgt 720
 gcctcccact gtattgtggg cctttgtctt tttgttccct gtgttgatcat ttatctgagg 780
 ccaggctcca tggatgccat ggatggagtt gtggccattt tctacactgt gctgacgccc 840
 cttctcaacc ctgttggtga caccctgaga aacaaggagg tgaagaaagc tgtgttgaag 900
 cttagagaca aagtagcaca tctcagagg aaa 933

<210> 322
 <211> 953
 <212> DNA
 <213> Unknown (H38g171 nucleotide)

<220>
 <223> Synthetic construct

<400> 322

ggagttggat	tgtaaaaact	ttgatggcaa	atttatattct	ccggagactc	tttctcaaca	60
tgggaaatgt	tttctctctc	aattttacaa	cttccttaga	tgtacactgt	ggccctctca	120
gggacatcta	ttctgatttt	cttgatttag	acagatttct	gagttcacac	atcattgtac	180
tctttctgag	ttctcattga	tatagccatt	tctgttggtt	aaattgggtat	tgagggttttc	240
tctggaaaga	taaactttct	acatactggt	tgtggaactc	agattttctt	ctttctgact	300
gctggcattt	tcaaatatgt	ccttctcact	tatatggctt	atgaccataa	cgtggctatc	360
tgtgcctgag	tgaccaacct	tcatgagtga	tcagggtctt	tagcaatggg	cagtagagtc	420
ttggattgga	ggaaaacttt	cttctttggc	tcataccatt	tatatatttc	atttattcag	480
ctataaagca	aaggagatta	gccacttatg	gccaagctc	ttttaagct	cctctgtggg	540
gatccccat	atacaaatg	atgttttttt	cacaataatt	acattcttgt	tcaccctgct	600
tctcttact	ctgaccttat	cctccaagct	tattgtgttc	actatcctac	acatgaactc	660
ctcaaattgg	ggagcaaagt	cttggccaca	tactgcttct	atctgagtgt	gctgattccc	720
tgtgtggcc	aggccacttc	gtctacatga	cttccagctc	cttctgaact	gtaaacaaat	780
accagaccat	gtctgcttga	cagcataatt	atatccacgt	tgaaaccct	gatagacatt	840
ctgaagaatg	cagaagtggc	aggagcttgg	agcaagttct	tgtaaaagaa	agcgctaaaa	900
agtcaacacc	ttattatcgt	agctgtgaaa	ataaataaac	aacagagcag	agt	953

<210> 323

<211> 960

<212> DNA

<213> Unknown (H38g172 nucleotide)

<220>

<223> Synthetic construct

<400> 323

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ttgggattaa	aggatcttcc	agagcttcag	cccacctct	ttgtactgtt	cctgctaata	120
tacctgatca	ctgtcggggg	gaaccttggg	atgttggtgt	tgatcaggat	agattcacgc	180
ctccacaccc	ccatgtattt	ctttcttgct	agtttgtcct	gcttggattt	gtattactcc	240
actaatgtga	ctcccaagat	gttgggtgaac	ttcttctcag	acaagaaagc	catttcctat	300
gctgcttggt	tagtccagtg	ctattttttc	attgctgtgg	tgattactga	atattatatg	360
ctagctgtaa	tggcctatga	taggtatgtg	gccatctgta	accctttgct	ttacagcagc	420
aagatgtcca	aagggctctg	tattcgccctg	attgctggtc	catatgtcta	tgggtttctt	480
agtggactga	tggaaacat	gtggacatac	cacttgacct	tctgtggctc	caatatcatt	540
aatcacttct	actgtgctga	cccacccctc	atccgacttt	cctgctctga	cactttcatt	600
aaggaaacat	ccatgtttgt	ggtagcatga	tttaacctct	ccagctccct	catcataatc	660
ctcatctcct	acatcttcat	tctcattgcc	atcctgagga	tgcgttctgc	tgaaagtagg	720
cgcaaagcgt	tctccacctg	cgggtcccac	ctggtggcag	tgactgtgtt	ttatggaacc	780
ctgttctgca	tgtacgttag	acctcccacg	gacaggtcag	tggaacagtc	caaagtcatt	840
gctgttttct	acacttttgt	aagccctatg	ttgaacccca	tcatctatag	tttgagggaac	900
aaggatgtga	aacaagcttt	ttggaaactg	atcagaagaa	acgtgctttt	gaagtaaaat	960

<210> 324

<211> 705

<212> DNA

<213> Unknown (H38g173 nucleotide)

<220>

<223> Synthetic construct

<400> 324

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acagcattca	tcctcatgga	ccttcccat	gtcccagctc	tggacgcccc	actctttgga	120
gtcttctctg	tggtttatgt	gcttactgtg	ctggggaacc	tcctcatcct	gctggtgatc	180
aggggtgtact	ctcacctcca	cacccccaag	tactacttcc	tcaccaatct	gtccttcatt	240
gacttgtggt	tcttctactgt	catggtgccc	aaaatgccga	ggaccttgtt	gtccctgtgt	300
ggcaaggctg	tgctcttcca	cagttgtatg	acccaactct	atttcttcta	cttctctggg	360
agcaccgagt	gtttgtctcta	cacgggtcatg	tcctatgatc	gctatagagg	aaatactcag	420
cacttcccag	gtagtgaaaa	cactccccc	gaagtgcagc	aaatgctagt	ggcccgggg	480
gcacacgggc	tcccactcat	catcctggca	gatctgagtg	ggtaactaag	agttgatagt	540

tcttagtggg	caattcaaaa	ttagtaatat	aatttagtta	tccaagtga	atttattaca	600
tgtataggtc	tcagcattaa	acattattcc	aaacaacttg	cacagttata	attctttcac	660
agattatcta	agacattttt	aaattcacag	ctagattttt	attta		705

<210> 325

<211> 921

<212> DNA

<213> Unknown (H38g174 nucleotide)

<220>

<223> Synthetic construct

<400> 325

atgatcaccg	agttcatcct	tataggttc	tcaaacctgg	gggatctgca	gaccccttc	60
ttctttatct	tctattagt	ctacctgacc	actctgatgg	ccaacaccac	catcatgaca	120
gtcattcacc	tggacagggc	tttgacacct	cctatgtact	tcttcctctt	tgctccttca	180
tgttctgaaa	cctgctacac	cttggtcatt	gtacccaaaa	tgcttaccaa	cctgctatcc	240
gcaattccaa	ctatttcttt	ctctggatgt	gtgggtccagc	tctatttatt	tggtgggttg	300
gcttgtagca	actgttttct	cattgctgtg	atgggtacg	atcgctatgt	tgccatctgc	360
aacccctta	actacacact	cattgtcagc	tgagccacct	gcatgcagct	ggttctagcc	420
tccagctttt	gtggcttctt	gacttctgtg	attgtcaata	tcctgggtgt	cagtgtgtct	480
ctctgtgcct	ccaatcggat	caaccacttt	ttctgtgaca	tttcccctgt	cataaaactg	540
ggctgcacag	acaccaacct	gaaggagatg	gtcatctttt	tcctcagcat	tctgggtattg	600
ctgggtcccc	ttgtgttgat	attcatctcc	tacatcttca	tagtttccac	catcctcaag	660
atctcctcag	tggaaggaca	gtgcaaagcc	ttcgccacct	gtgcttccca	cctcacagt	720
gtcgctgtcc	actatggctg	tgcttctttt	atctacttga	ggcccacatc	cctgtactct	780
tcagataagg	accggctcgt	ggcagtgact	tatactgtga	ttactccact	actcaacccc	840
cttgtctata	cactgagaaa	taaagaagta	aagatggctc	tgagaaaggt	tctgggtaga	900
tgcttaaatt	ccaaaactgt	a				921

<210> 326

<211> 470

<212> DNA

<213> Unknown (H38g175 nucleotide)

<220>

<223> Synthetic construct

<400> 326

atttgccaca	atagaaaagt	catccctgca	tctatgtgaa	atatgtttta	tttctcttga	60
aagttgccta	agacaatttt	ctgcatgtac	tgttcatact	agctaaaact	gctccccact	120
cttattcctc	taggaaattc	ctagttattt	ttcaagcccc	agtttagatta	ttgtcctttg	180
atgcttacc	tgattcctga	aacaattagt	tattttgttt	gtatttttat	tattgaacta	240
atcatattta	actttaattt	tcagtctcct	taccatgaaa	atcaaccagc	tctttcaagg	300
caagcactgt	gatcagttgt	cttcaattcc	ccagaaagc	aacttgcag	catggagtgt	360
tcagtgtgt	ttgtgcacaa	atgtaaccat	attacaatgg	ttaaattcatt	tagcatcctg	420
aaagcatcac	agagtcaaag	tagctaactt	gtgtgaaccc	ttaattcaat		470

<210> 327

<211> 959

<212> DNA

<213> Unknown (H38g176 nucleotide)

<220>

<223> Synthetic construct

<400> 327

gggaccaagt	caatcaagct	aacttctctg	tcagagttcc	tgcttcttga	gttctccagc	60
cttgaagaaa	tccagcagat	cctttttctg	tctgcttggt	gctatatctg	attgttctga	120
gtggaaatat	caccactgtc	actgtcatcc	gcctggatca	aagcctccac	atacctgtat	180
acttattcct	agggatcctc	tccatttctg	ggacatgcta	tacctttgtc	attctgcccc	240

agatgctcat	agatctgttg	tctttgctca	gaacaatctc	at ttattaac	tgccactcca	300
gtgttcttct	ttctgggttt	tgtgtcact	aatttcatgt	tcctgggcat	gacagtttat	360
gattcctatg	ttgccatctg	ccatccactt	cactaccctg	tccttacgag	ctggcagata	420
tgtaaacaac	tggcagcaac	gtgtgctgtg	attgtttttt	ttgtttgtt	tgttttcact	480
gataggctcc	ttcttagatt	ttcagctgct	tttctgtggc	ccaaacaaga	tcaaccacta	540
cttctgtgac	atctcactgc	ttattcagct	tgctgtact	gatacctaca	tcagggagct	600
agtcactctt	attgggtgaa	ttctagcact	tacggttcct	ctgattttat	ttgcatctcc	660
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tctctacttg	tgccctccat	cttattatgg	tcgttgtcca	ttatggctgt	gcctcctttg	780
tcaacctgtg	accatcagcc	aaataatcat	ccagcaaata	accatctagc	aagaacaggc	840
tggtgacagt	gaccttacac	agttgtgact	ccgttgttga	atccatggta	tatagcttca	900
agaataagaa	cgttcagatg	gccatttggg	aagtgatttg	ccaaggagga	tttcctcct	959

<210> 328

<211> 952

<212> DNA

<213> Unknown (H38g177 nucleotide)

<220>

<223> Synthetic construct

<400> 328

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gaattacaga	ttttcctctt	cacgctgttt	ctcaccattt	acatggtcac	ggtggcagga	120
aatcttggca	tgattgcctt	catccaggcc	aacgccccgg	ctccacacgc	ccatgtactt	180
tttcttgagc	aacttatcct	ttgtggatct	gtgcttctct	tccaatgtga	ctccaaggat	240
gctggagatt	ttcctttcag	agaagaaaag	catttctctat	cctgccccgc	ttgtgcagtg	300
ttaccttttt	atcaccttgg	tcacggttga	gctctacatc	ctggctgtga	tggcctttga	360
ccggtacatg	gccatctgca	accctctgct	ttatggcagc	agaatgtcca	agagcgtgtg	420
ctctttcctc	atcacagtgc	tttatgtgta	tggagcactc	actggcctga	tgagacttat	480
gtggacctac	aacctagcct	tctgtggccc	cagtgaatt	aatcacttct	actgtgtgga	540
cccaccactg	attaagctgg	cttgttctga	cacctacaac	aaggagggtg	caatgtttgt	600
tgtggtgggt	ttcaacttca	cttatcctct	ccttatcatc	ctcatttctc	atctctacat	660
atttctctgc	accctaagga	tctgctctac	agaaggcagg	cacaaagctt	tttctacctg	720
tggtctccat	ctgacagccg	ttactatttt	ctattcagct	cttttcttca	tgtatctcag	780
acgtccatca	gaagagtcca	tggagcaggg	gaaaatggta	gctgtatttt	ataccactgt	840
aatccccatg	ttgaatccca	tgatctacag	tctgaggaa	aaagatgtga	aagaggcatt	900
atgcaaagaa	ctgttcaaaa	gaaaattggt	ttctaaataa	acattactac	tg	952

<210> 329

<211> 949

<212> DNA

<213> Unknown (H38g178 nucleotide)

<220>

<223> Synthetic construct

<400> 329

acagatgtct	gagaattcct	cctcctggga	ctctcagagg	atccagaact	gcagccggtc	60
ctcgttttgc	tgctccctgc	cctgtccatg	tatctgttca	cgggtgctgag	gaacctgtc	120
agcatectgg	ctgtcagctc	tgactcccc	ctccacaccc	ccatgtactt	cttctctcc	180
aacctgtgct	ggcctgacat	cggtttcacc	tcggccatgg	ttcccaagat	gattgtggac	240
acgcagtcgc	atagcagagt	catctctcat	gcgggctgcc	tgacacagat	gtctttcctg	300
ctccttgttg	catgtataga	aggcatgtct	ctgactgtga	tgccctatga	ctgctttgta	360
gccatctgtc	gccctctgca	ctacccaatc	atcgtgaatc	ctcacctctg	tgtcttcttc	420
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atgtttgggt	ttcttcccat	ttcagggtac	ttttgtctt	actataaaat	tgccccctcc	660
attctaagga	tttcatcgtc	agatgggaag	tataaagcct	tctccacctg	tggtgtgcat	720
ctagcagttg	tttgcctgggt	ttatgggaaca	ggcatttggt	tgtacctgac	ttcagctggg	780

tcaccacctc	ccaggaatgg	tgtgggtggct	tcagtgatgt	acgctgtggt	caccccatgc	840
tgaacctttt	catctgcagc	ctgagaaaca	gggacataca	aagtgccttg	cggaggctgc	900
gcagcagagc	agtcgaatat	catgatctgt	tccatccttt	ttcttgtgt		949

<210> 330

<211> 942

<212> DNA

<213> Unknown (H38g179 nucleotide)

<220>

<223> Synthetic construct

<400> 330

atgcgaggtt	tcaacaaaac	cactgtggtt	acacagttca	tcctgggtggg	tttctccagc	60
ctgggggagc	tccagctgct	gctttttgtc	atctttcttc	tcctatactt	gacaatcctg	120
gtggccaatg	tgaccatcat	ggccgttatt	cgcttcagct	ggactctcca	cactcccatg	180
tatggcttct	tattcatcct	ttcattttct	gagtcctgct	acacttttgt	catcatccct	240
cagctgctgg	tccacctgct	ctcagacacc	aagaccatct	ccttcattggc	ctgtgccacc	300
cagctgttct	ttttccttgg	ctttgcttgc	accaactgcc	tcctcattgc	tgtgatggga	360
tatgatcgct	atgtagcaat	ttgtcaccct	ctgaggtaca	cactcatcat	aaacaaaagg	420
ctgggggttg	agttgatttc	tctctcagga	gccacaggtt	tctttattgc	tttgggtggc	480
accaacctca	tttgtgacat	gcgtttttgt	ggccccaaca	gggttaacca	ctatttctgt	540
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tttagcctca	gcacctcgtt	aattatggtg	ccttttctgt	taattctcat	atcctatggc	660
ttcatagtta	acaccatcct	gaagatcccc	tcagctgagg	gcaagaaggc	ccttgtcacc	720
tgtgcctcac	atctcactgt	ggtccttctc	cactatggct	gtgcctctat	catctatctg	780
cggcccaagt	ccaagtctgc	ctcagacaag	gatcagttgg	tggcagtgc	ctacacagtg	840
gttactccct	tacttaatcc	tcttgtctac	agtctgagga	acaaagaggt	aaaaactgca	900
ttgaaaagag	ttcttggaat	gcctgtggca	accaagatga	gc		942

<210> 331

<211> 942

<212> DNA

<213> Unknown (H38g180 nucleotide)

<220>

<223> Synthetic construct

<400> 331

atgatgggac	aaaatcaaac	cagcatctca	gacttcctgc	tcctgggcct	gcccattcaa	60
ccagagcagc	aaaacctgtg	ctatgccctg	ttcttggcca	tgtatcttac	caccctcctg	120
gggaacctcc	tcatcattgt	cctcattcga	ctggactccc	atctccacac	gcctatgtat	180
ttgtttctca	gcaacttgct	cttctctgac	ctctgcttct	cttccgtgac	cattcccaag	240
ttgttacaga	acatgcagaa	ccaggaccca	tccatcccc	atgcggactg	cctgacccaa	300
atgtacttct	tcctgttatt	tggagacctg	gagagcttcc	tccttgtggc	catggcctat	360
gaccgctatg	tggccatctg	cttccccctg	cactacaccg	ccatcatgag	ccccatgctc	420
tgtctcgccc	tgggtggcgt	gtcctgggtg	ctgaccacct	tccatgccat	gttacacact	480
ttactcatgg	ccaggttgtg	tttttgtgca	gacaatgtga	tccccactt	tttctgtgat	540
atgtctgctc	tgctgaagct	ggccttctct	gacactcgag	ttaatgaatg	ggtgatattt	600
atcatgggag	ggctcattct	tgtcatccca	ttcctactca	tccttgggtc	ctatgcaaga	660
attgtctcct	acatcctcaa	ggcccttctt	tctaagggtg	tctgcaaggc	cttctctact	720
tgtggctccc	acctgtctgt	ggtgtcactg	ttctatggaa	ccgttattgg	tctctactta	780
tgctcatcag	ctaatagttc	tactctaaag	gacactgtca	tggctatgat	gtacactgtg	840
gtgaccccca	tgctgaaccc	cttcatctac	agcctgagga	acagagacat	gaagggagcc	900
ctgagcagag	tcattcatca	gaagaaaact	ttcttctctc	tc		942

<210> 332

<211> 822

<212> DNA

<213> Unknown (H38g181 nucleotide)

<220>

<223> Synthetic construct

<400> 332

accataataa	atgtcaatat	tagtcctgag	tttgtccttg	tgggattttc	cagtgatgca	60
gagatccaga	tcatgctctt	tgtgctaata	ctgggtgattc	atctcctgac	tttgacgggg	120
aagctgggtga	tgatcctgga	gatcagggct	gattctcacc	ttcaaagacc	catgtacttc	180
ttcctttgac	atctgtcctt	tctggatctc	agctactcct	agttactgtg	cccaggatgc	240
tacaaaattt	cctctcagaa	gaaaagcatc	tcaatgtggg	gctgcctcac	caagtttctt	300
tttcaacttc	tctgggggaa	cggaagcctg	tctgttctct	gccatggcct	atgatcacta	360
tgctaccatc	cgccaccctg	tggtctatac	catgggtcatg	aacagatctc	tctgtatggt	420
gattttgaga	attgcttggg	cagcgggatt	tctgatttcc	ttgatggaca	gtcttttcac	480
ccacaagtta	catttctgtg	ggcctgacat	catccttatt	tcaggtgtaa	gctgectcca	540
ttcttccctc	tgctctacat	tgatcccact	gtcaatgaga	ttcttctagc	tgtgtcacag	600
gcattctggg	ggctactgac	actttcccta	atcttctctc	cttactctag	aatcacatct	660
gtcatactga	gcactctgctc	ctctgagggc	caaggcaaag	ccttctccgc	atgcccttct	720
catctcgtg	tggttctctc	attctatggg	acagcttttt	tcagataccc	aggctctact	780
tcaggttcgg	tggtggggca	agtggctctc	gttcagtata	gt		822

<210> 333

<211> 935

<212> DNA

<213> Unknown (H38g182 nucleotide)

<220>

<223> Synthetic construct

<400> 333

atgagaagga	acttcacgtt	ggtgactgag	ttcattctcc	tgggactgac	gaatcaccag	60
gaattacaga	ttctcctctt	catgctgttt	ctggccattt	acatggtcac	agtggcaggg	120
aatcttagca	tgattgccct	catccaggcc	aatgcccggc	tccacacgcc	catgtacttt	180
ttcctgagcc	acttaccctt	cctggatctg	tgcttctctt	ccaatgtgac	cccaaagatg	240
ctggagattt	tcctttcaga	gaagaaaagc	atttcctatc	ctgcctgtct	tgttcagtgt	300
tacctttata	tcactcttgg	acacgttgag	atctacatcc	tggtctgtgat	ggcctttgac	360
tagtacatgg	ccatctgaaa	ccctctgctt	tatggcagca	aaatgtccaa	aagtgtgtgt	420
tccttccctc	tcacggtgcc	ttatgtgtat	ggagcgtcca	ctggcctgat	ggagaccatg	480
tggacctaca	acctagcctt	ctgtggcccc	aacgaaatta	atcacttcta	ctgtgcagac	540
ccaccactga	ttaagctggc	ttgttctgac	acctacaaca	aggagtgtgc	aatgtttgtt	600
gtggctggct	ggaatcttcc	gttttctctc	ttcatcatat	ttatttccta	cttttacatt	660
tttctgtcta	tcttaaggat	tcgctctaca	gagggcaggc	aaaaagcttt	ttctacctgt	720
ggctcccatc	tgacagctgt	tactattttc	tatgcaactc	tgttcttcat	gtgtctcaga	780
cctccatcag	aagagtccat	ggagcaagga	caaatggtag	ctgtacttta	taccactgtg	840
atccccatgt	taatcccatg	atctacagtc	tgaggaacaa	ggatgtgaaa	aaggctttat	900
ccaaagaact	gttcaaaaga	aaattgtttc	ctaaa			935

<210> 334

<211> 945

<212> DNA

<213> Unknown (H38g183 nucleotide)

<220>

<223> Synthetic construct

<400> 334

atggagccag	aagctggggac	caataggacc	gctgttgctg	agttcattct	actgggccta	60
gtgcaaacag	aagagatgca	gccagttgtc	tttgtgtccc	tcctctttgc	ctatctggtc	120
acaattgggg	gcaacctcag	catcctggca	gccgtcttgg	tggagcccaa	actccacgcc	180
cccatgtact	tcttcttggg	gaacctatca	gtgctggatg	tcggatgtat	cactgtcact	240
gttctctgaa	tgttgggtcg	tctcttgtcc	cacaagtcga	caatttccta	tgacgcctgc	300
ctctccagc	tcttcttctt	ccacctcttg	ctgggatggg	actgcttctc	gctgaccgcc	360
atggcctatg	accgactcct	ggccatctgc	cagccctcca	cctacagcac	ccgcatgagt	420

cagacagtcc	agaggatggt	ggtggctgcg	tcctgggctt	gtgccttcac	caacgcactg	480
acccacactg	tggccatgtc	cacgctcaac	ttctgtggcc	ccaatgaggt	caatcacttc	540
tactgtgacc	tcccacagct	cttccagctc	tcctgtctca	gcacccaact	caatgagctg	600
ctgctctttg	tagcagcagc	cttcatggct	gtggcaccct	tggcttctcat	cagtgtgtcc	660
tatgcccacg	tggtagctgc	tgtgctgcaa	atccgctctg	ctgagggcag	aaagaaggcc	720
ttctccacat	gtggctccca	cctcactgtg	gtgggcatct	tctatgggac	agggtgtctc	780
agctacatga	ggctgggttc	agtggaatct	tcagacaagg	ataagggggt	tgggggttttc	840
atgactgtga	tcaaccccat	gctgaaccca	cttatctaca	gcctcagaaa	tactgatgtt	900
cagggcgctc	tgtgtcagct	acttgtgggg	gagcgatcac	tgacc		945

<210> 335

<211> 950

<212> DNA

<213> Unknown (H38g184 nucleotide)

<220>

<223> Synthetic construct

<400> 335

atgctaagga	atggcagcat	agtgcaggaa	tttatcctcg	tgggctttca	gcagagctcc	60
acttccacac	gagcattgct	ctttgccctc	ttcttggccc	tctacagcct	caccatggcc	120
atgaatggcc	tcatcatctt	tatcacctcc	tggacagacc	ccaagctcaa	cagcccccag	180
tactttcttc	tggcctctg	tctctcctgg	atgtctgctt	catcaccact	accatcccac	240
agatgttgat	ccacctcgtg	gtcagggacc	acattgtctc	ctttgtatgt	tgcatgacct	300
agacgtactt	tgtcttctgt	gttgggtgtg	ccgagtgcac	cctcttggct	ttcatggcct	360
atgaccgtta	tgttgctatc	tgctaccac	ttaactatgt	cccgatcata	agccagaagg	420
tctgtgtcag	gcttgtggga	actgcctggt	tctttgggct	gatcaatggc	atctttctcg	480
agtatatattc	attccgagag	cccttccgca	gagacaacca	catagaaagc	ttcttctgtg	540
aggcccccac	agtgattggc	ctctcttgtg	gggaccctca	gtttagtctg	tgggcaatct	600
ttgccgatgc	catcggtgta	attctcagcc	ccatggtgct	cactgtcact	tcctatgtgc	660
acatcctggc	caccatcctc	agcaaagcct	cctcctcagg	tcgggggaag	actttctcta	720
cttgtgcctc	tcacctgact	gtggctcatc	ttctctacac	ttcagctatg	ttctcttaca	780
tgaaccccca	cagcacacat	gggcctgaca	aagacaaacc	ttctccctc	ctgtacacca	840
tcattacccc	catgtgcaac	cccatcattt	atagtgtccg	caacaaggaa	attaaggagg	900
ccatggtgag	ggcacttgga	agaaccaggc	tggcccagcc	acagtctgtc		950

<210> 336

<211> 972

<212> DNA

<213> Unknown (H38g185 nucleotide)

<220>

<223> Synthetic construct

<400> 336

atgttttact	tctttccccc	tttgcagatc	ttggcagaaa	acctcaccat	ggtcaccgaa	60
ttcctgttgc	tgggtttttc	cagccttggg	gaaattcagc	tggccctctt	tgtagttttt	120
ctttttctgt	atctagtcat	tcttagtggc	aatgtcacca	ttatcagtgt	catccacctg	180
gataaaaagcc	tccacacacc	aatgtacttc	ttccttggca	ttctctcaac	atctgagacc	240
ttctacacct	ttgtcattct	acccaagatg	ctcatcaatc	tactttctgt	ggccaggaca	300
atctccttca	actgttgtgc	tcttcaaatg	ttcttcttcc	ttggttttgc	cattaccaac	360
tgccctgctat	tgggtgtgat	gggttatgat	cgctatgctg	ccatttgcac	ccctctgcat	420
taccccactc	ttatgagctg	gcaggtgtgt	ggaaaactgg	cagctgcctg	tgcaattggg	480
ggcttcttgg	cctctcttac	agtagtaaat	ttagttttca	gcctcccttt	ttgtagcgcc	540
aacaaagtca	atcattactt	ctgtgacatc	tcagcagtea	ttcttctggc	ttgtaccaac	600
acagatgtta	acgaatttgt	gatattcatt	tgtggagtgc	ttgtacttgt	ggttcccttt	660
ctgtttatct	gtgtttctta	tctctgcatt	ctgaggacta	tcctgaagat	tcctcagct	720
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tatggctgtg	cttcttcat	ctacctgagg	cctacagcaa	actatgtgtc	caacaaagac	840
aggctgggtga	cggtagacata	cacgattgtc	actccattac	taaaccctat	ggtttatagc	900
ctcagaaaaca	aggatgtcca	acttgcctatc	agaaaagtgt	tgggcaagaa	aggttctcta	960

aaactatata at

972

<210> 337

<211> 982

<212> DNA

<213> Unknown (H38g186 nucleotide)

<220>

<223> Synthetic construct

<400> 337

aagcttcaat	taaacaattt	tactgaagtc	accatgttta	tattaataag	cttcacagaa	60
gaatttgatg	tgcaagtctt	cctattttta	ttatttttag	caatctatct	attcactcta	120
ataggcaatt	tagggctggg	tgtaccgatc	attggggatt	tctgggttca	cagcccaatg	180
tactattttc	ttgggtgttt	atcattcttg	gatgtctgct	attctacagt	tgtcactcca	240
aaaatgttgg	tcaatttcct	ggcaaaaaat	aaatctattt	catttcttgg	atgtgcaaca	300
cagatgtttc	ttgcttgta	ttttggaacc	acagaatgct	ttctcttggc	tgcaatggct	360
tatgatcgct	atgtagccat	ctacaaccct	ctcctgtatt	cagtgaagcat	gtcaccacaga	420
gtctatgtgc	cactcatcac	tgcttccctat	gttgctagca	ttttacatgc	tactatacat	480
acagtggcta	catttagcct	gtccttctgt	ggatccaatg	aaattaggca	tgtcttttgt	540
aataatgcct	cctctgcttg	ctatttcttg	ttctgacact	cacgtaatcc	agcttctatt	600
cttctacttt	gtgggctcta	ttgagatagt	cactatcctg	attgtcctga	tctcctatgg	660
ttttattctg	ttggccattc	tgaagatgca	gtctgctgaa	gggaggagaa	aagtcttctc	720
tacatgtgga	gtcacctaa	ctggagtgc	aatttatcat	gggacaatcc	tcttcattga	780
tgtgagacca	agttccagct	acacttcgga	caatgacatg	atagtgtcaa	tattttatac	840
cattgtgatt	cccatgctga	atcccatcat	ctacagtttg	cggaacaaag	atgtaaagga	900
ggcaatcaaa	agattgcttg	tgagaaattg	gttcataaat	aagttatagt	tttaaaattg	960
agtaaagtgg	caaataatat	tg				982

<210> 338

<211> 962

<212> DNA

<213> Unknown (H38g187 nucleotide)

<220>

<223> Synthetic construct

<400> 338

atggatagag	taaataattc	tgcggtatct	aaatttgtat	tgatttggac	tttccaagcc	60
tccttgggag	atgcatcttt	ttcttttttg	gttcttctct	gtgttctaca	tggaatttat	120
cctggaaaat	ctcttcattg	tgttcacagt	aattattgac	tctcatttaa	attccccagg	180
tactgcttac	tgcccaacat	ttatcttctt	gatctgggtc	ttctcctaca	gttctgactt	240
tttactaac	tgacagcatc	tttcttttcc	aagatgcac	atacagatat	ttttcatttg	300
tgtcatgcgt	aaaaattgag	atggtgctgc	tcataaccat	ggcatagagc	aggtacactg	360
ccaatctgta	agcctcccca	ttacctgacc	acaatgaacc	ccaaaatgtg	tgtttccttt	420
gttggaggca	tcctggatag	tcaggataat	ccatgctgta	tctcagtttg	tttttgccat	480
aaacttgcc	ttttgtggcc	ctaataagag	aggtagtgtt	cactgtgatt	ttccttatgt	540
catgaaactt	gcttggttag	acacttacaa	actagagggt	gtagtactg	ctaacagtgg	600
gcttatatcc	atagctacct	gtttcttatt	aataatatcc	tatattttca	tttcggtaac	660
cgtctagaat	ccttcttcag	gagacttata	taaagcattt	gtgtcatggt	agatcacatc	720
acagttagga	ttttgttttt	tatgccatgt	atatttctgt	atgtgtagcc	tttgccataa	780
acaacacatg	attaatat	gttcattggt	ccttttgcta	tcacctctgt	ctaggatcta	840
cacattaaga	aacaaagaca	tgaacgtctc	catggaaaga	ctgggaaaat	ggattgcagg	900
ttctagcagg	atgtcataat	aaatggtgca	tatccagagt	gcaagatgat	tcagtctcac	960
ca						962

<210> 339

<211> 972

<212> DNA

<213> Unknown (H38g188 nucleotide)

<220>

<223> Synthetic construct

<400> 339

atgaccacca	taattctgga	agtagataat	catacagtga	caacacgttt	cattcttctg	60
gggtttccaa	cacgaccagc	cttccagctt	ctctttttct	ccattttcct	ggcaacctat	120
ctgctgacac	tgctggagaa	tcttcttata	atcttagcta	tccacagtga	tgggcagctg	180
cataagccca	tgtacttctt	cttgagccac	ctctccttcc	tggagatgtg	gtatgtcaca	240
gtcatcagcc	ccaagatgct	tggtgacttc	ctcagtcag	acaagagtat	ttccttcaat	300
ggctgcatga	ctcaacttta	cttttttgtg	acctttgtct	gcactgagta	catccttctt	360
gctatcatgg	cctttgaccg	ctatgtagcc	atttghtaat	cactacgcta	cccagtcata	420
atgaccaacc	agctctgtgg	cacactggct	ggaggatgct	ggttctgtgg	actcatgact	480
gccatgatta	agatggtttt	tatagcacia	cttactact	gtggcatgcc	tcagatcaat	540
cactactttt	gtgatatact	tccactcctt	aacgtctcct	gtgaggatgc	ctcacaggct	600
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aaggcattct	ccacctgtgc	ctcccacctg	accgtctgta	ttctcttcta	ttccatgaca	780
cttttcacct	atgcccgtcc	caaactcatg	tatgcctaca	attccaacaa	agtggatatct	840
gttctctaca	ctgtcattgt	tccactcctc	aaccccatca	tttactgtct	gaggaaccat	900
gaagtaagg	cagccctcag	aaagaccata	cattgcagag	gaagtgggcc	ccagggaaat	960
ggggctttca	gt					972

<210> 340

<211> 969

<212> DNA

<213> Unknown (H38g189 nucleotide)

<220>

<223> Synthetic construct

<400> 340

atgatgggac	aaaatcaaac	cagcatctca	gacttcctgc	tcctgggcct	gcccatacaa	60
ccagagcagc	aaaacctgtg	ctatgccctg	ttcttggcca	tgtatcttac	cacctcctg	120
gggaacctcc	tcatcattgt	cctcattoga	ctggactccc	atctccacac	gcctgtgtat	180
ttgtttctca	gcaacttgct	cttctctgac	ctctgctttt	cctcagtcac	aatgccccaa	240
ttgctgcaga	acatgcagaa	ccaagaccca	tccatccctt	atgcagactg	cctgacccaa	300
atgtacttct	tcttgtattt	ttcggatcta	gagagcttcc	tccttgtggc	catggcctat	360
gaccgctatg	tggccatctg	cttccccatg	cactacaccg	ccatctgctt	cctcctgcac	420
tacaccgcca	tcatgagccc	catgctctgt	ctctccgtgg	tggcgctgtc	ctgggtgctg	480
accaccttcc	atgccatggt	acacacttta	ctcatggcca	ggttgtgttt	ttgtgcagac	540
aatgtgatcc	cccacttttt	ctgtgatatg	tctgctctgc	tgaagctggc	ctgctctgac	600
actcgagtta	atgaatgggt	gatatttata	atgggagggc	tcattcttgt	catcccatte	660
ctactcatcc	ttgggtccta	tgcaagaatt	gtctcctcca	tcctcaagg	cccttcttct	720
aagggtatct	gcaaggcctt	ctctacttgt	ggctcccacc	tctctgtgg	gtcactgttc	780
tatgggaccg	ttattgggtct	ctacttatgc	ccatcagcta	atagttctac	tctaaaggac	840
actgtcatgg	ctatgatgta	cactgtgggt	accctatgc	tgacccctt	catctacagc	900
ctgaggaaca	gagacatgaa	gggagccctg	gaaagggtca	tttgtaaaag	gaaaaatccc	960
ttccttcta						969

<210> 341

<211> 933

<212> DNA

<213> Unknown (H38g190 nucleotide)

<220>

<223> Synthetic construct

<400> 341

atgggtagaa	gaaataacac	aaatgtgcct	gacttcatcc	ttacgggact	gtcagattct	60
gaagaggctc	agatggccct	ctttatacta	tttctcctga	tataccta	tactatgctg	120
ggcaatgtgg	ggatgatatt	gataatccgc	ctggacctcc	agcttcacac	tcccatgtat	180

tttttcctta	ctcacttgtc	at ttattgac	ctcagttact	caactgtcat	cacacctaaa	240
accttagcga	acttactgac	ttccaactat	atttccttca	tgggctgctt	tgcccagatg	300
ttcttttttg	tcttcttggg	agctgctgaa	tgttttcttc	tctcatcaat	ggcctatgat	360
cgctacgtag	ctatctgcag	tcctctacgt	taccagttta	ttatgtccaa	aaggctgtgt	420
tgcgctcttg	tcactgggcc	ctatgtgatt	agctttatca	actcctttgt	caatgtgggt	480
tggatgagca	gactgcattt	ctgcgactca	aatgtagttc	gtcacttttt	ctgcgacacg	540
tctccaattt	tagctctgtc	ctgcatggac	acatacgaca	ttgaaatcat	gatacacatt	600
ttagctgggt	ccaccctgat	gggtgtccct	atcacaaat	ctgcatccta	tgtgtccatt	660
ctctctacca	tcctgaaaat	taattccact	tcaggaaagc	agaaagcttt	gtctacttgt	720
gcctctcatc	tcttgggagt	caccatcttt	tatggaacta	tgattttttac	ttatttaaaa	780
ccaagaaagt	cttattcttt	gggaagggat	caagtggctt	ctgtttttta	tactattgtg	840
attcccatgc	tgaatccact	catttatagt	cttagaaaca	aagaagttaa	aaatgctctc	900
attagagtca	tgcagagaag	acaggactcc	agg			933

<210> 342

<211> 915

<212> DNA

<213> Unknown (H38g191 nucleotide)

<220>

<223> Synthetic construct

<400> 342

atgggtgactg	aattcatttt	tctgggtctc	tctgattctc	aggaactcca	gaccttccta	60
tttatgttgt	ttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggtat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
ctcattgatc	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaag	tcattctctt	caagggtctc	cttggtcaga	tatttctcct	tcacttcttt	300
gggtgggagt	agatgggtgat	cctcatagcc	atgggctttg	acagatatat	agcaatatgc	360
aagcccctac	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
acatggggaa	ttggctttct	ccattcgggt	agccagttgg	cgtttgccgt	gcacttactc	480
ttctgtggtc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggg	aatcaaaact	540
gcctgtacag	atacctacag	gctagatatt	atggtcattg	ctaacagtgg	tgtgtctact	600
gtgtgtttct	ttgttcttct	aatcatctca	tacactatca	tcctaataac	catccagcat	660
cgcccttttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagttagt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccc	caagtcatta	780
gataaattcc	ttgtgtgatt	ttattctgtg	atcacccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 343

<211> 936

<212> DNA

<213> Unknown (H38g192 nucleotide)

<220>

<223> Synthetic construct

<400> 343

atggagcggg	tcaatgagac	tgtggtgaga	gaggtcatct	tcctcggctt	ctcatccctg	60
gccaggctgc	agcagctgct	ctttgttata	ttcctgctcc	tctacctgtt	cactctgggc	120
accaatgcaa	tcatcatttc	caccattgtc	ctggacaggg	cccttcata	ccccatgtac	180
ttcttccttg	ccatcccttc	ttgctctgag	atttgtctca	ccttcacat	tgtacccaag	240
atgctgggtg	acctgctgtc	ccagaagaag	accatttctt	tcctgggctg	tgccatccaa	300
atgttttctt	tcctcttctt	tggctgctct	cactcctttc	tgctggcagt	catgggttat	360
gatcggtaca	tagccatctg	taaccactg	cgctactcag	tgctaattgg	acatgggggtg	420
tgtatgggac	tagtggtgtc	tgctgtgccc	tgtggcttca	ctgttgacac	gatcatcaca	480
tccttggtat	ttcacctgcc	tttttattcc	tccaatcaac	tacatcactt	cttctgtgac	540
attgctcctg	tcctcaagct	ggcatctcac	cataaccact	ttagtcagat	tgtcatcttc	600
atgctctgta	cattggctct	ggctatcccc	ttattgttga	tcttgggtgtc	ctatgttcac	660
atcctctctg	ccatacttca	gtttccttcc	acactgggta	ggtgcaaagc	tttttctacc	720

tgtgtatctc	acctcattat	tgtcactgtc	cactatggct	gtgcctcctt	tatctactta	780
aggcctcagt	ccaactactc	ctcaagccag	gatgctctaa	tatcagtatc	ctacactatt	840
ataactccat	tgttcaaccc	aatgatttat	agcttgagaa	ataaagagtt	caaactcagct	900
ctttgtaaaa	ttgtgagaag	aacaatttcc	ctgttg			936

<210> 344

<211> 732

<212> DNA

<213> Unknown (H38g193 nucleotide)

<220>

<223> Synthetic construct

<400> 344

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gtcaccctgg	ttggtaatat	tctcatcatt	gttattatcc	agattgattc	ccatcttcaa	180
acccccatgt	acttctttct	catacaagta	tccttcttag	atatctgctc	cacaccacg	240
gttctgggtga	actgctagaa	ggactttcca	agtgtatcct	atagtggctg	cttattctaa	300
atgactatct	ttctttactt	aggggtgacg	gagtgtgttt	ttttttgtt	ctgttttgag	360
tgttttctta	ttgctgttat	ggcctatgac	aggtttgttg	ccatctcaaa	acccttgtgt	420
taccattca	ttatcaatag	caatgtttgc	atctggatgg	tggcaggagt	ttgggcccac	480
cctggctcgca	ccaatccaat	tctgtggcca	caatgtagtc	aacattttac	atgtgagctc	540
caagtaattt	tcaaactcac	ttgctctcct	gtactagtca	aagagatcca	gtgattcatg	600
attccaggtt	gtacattata	ggcattgtat	cagcattaag	tgtgctccta	cagttaagct	660
cgccagcaaa	cccattcccag	gagctgagag	gcatacaatt	agggcataag	gtgaggtatt	720
atcggggtac	ac					732

<210> 345

<211> 919

<212> DNA

<213> Unknown (H38g194 nucleotide)

<220>

<223> Synthetic construct

<400> 345

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ggaaacctgg	gactgatcat	gttaatcaga	atggattctc	agcttcacac	ccctatgtac	180
tttttcttca	gcaatttagc	attcattgac	atattttact	cctcttccgt	aacacctaa	240
acattggcga	atttccaatc	caatcagaga	tccatctcct	ttgttggctg	ctttgttcaa	300
atgtactttt	ctgttggtat	gggtgtgact	gagtgtttcc	tgctgggac	aatggcctat	360
gattgctatg	tagcaatctg	gaatccctca	ttcagtagtc	atttcttaga	aagcgtgcaa	420
ctggctggga	gtaatgtcat	acacgatagg	tttcacaaat	tctctgggat	ctgtctgtgt	480
gataagtggg	tttgttctgt	gattccagca	tcaatctttt	ttttctgtga	caccacagct	540
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cacctcatgg	gttaactatc	ttctatgggt	ccctgatttt	cacctatttg	caactggata	780
aaacatcatc	cctgatccac	gcacagttgg	catttgtatt	ctatatgact	gtcattccca	840
tgctgaatcc	actcatctag	agtctgagga	acaaagatgt	aaaaaatgct	ctttgagagt	900
catacataga	aaacttttt					919

<210> 346

<211> 753

<212> DNA

<213> Unknown (H38g195 nucleotide)

<220>

<223> Synthetic construct

<400> 346
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 atcatcatca tctcagtcac tcatttggat cacagcctcc acacacccat gtacttcttt 180
 ctaggtattc tttctatctc tgaaatcttc tacacaactg ttattctgcc caagatgctt 240
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 ttcttctctg gttttgctgt cactaactgt ctgcttctgg gagtgatggg ttatgatcgt 360
 tatgctgccca tctgtcagcc tttgcaatac gctgttctca tgagctggag agtatgtgga 420
 caactgatag caacttgtat tattagtggc ttcctaatat ctctgggtggg aacaactttt 480
 gtcttttagcc tccctttctg tggctccaac aaggctcaacc actacttttg tgatatttca 540
 ccagttatcc gtctcgctg tgetgacagc tacatcagtg aactgggtcat cttcatcttc 600
 ggggtcttgg tgettggtgt gcccttgata tttatctgca ttctctatgg cttcattgtc 660
 cgcaccatcc tgaagatccc atcagctgaa ggcaaacaaa aagccttctc cacctgtgct 720
 tcccatctca ttgtagtcac tgtccattat ggt 753

<210> 347

<211> 941

<212> DNA

<213> Unknown (H38g196 nucleotide)

<220>

<223> Synthetic construct

<400> 347
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 cagcgtttga gaacatcctt atcgttgctg tagtgagatg agattctcga cttcatactc 180
 ctatgggatt tttttttcct cagtacctta tccctccctg aaatgtgtta ctccatcagc 240
 tgggagctat aagtcttggc tcaatgcac aaggacttcc ccaccatctc ctataacagc 300
 tgttctgttc agatgatcac acacctcttt ctggggatga cagtgtctcc tccctgtctg 360
 catggcttac aacaggtttg ttgaaatctc ttatctcctc cattacacta ttattatgag 420
 caatcgggtc tgtatacagt tggccttggg aatctggacc catgccttct tagtagcagt 480
 cacactaatc attgcaattc ctgctagtta ttatggacac aatgtcatca accattttac 540
 cttgagatcc aggcctgct gaagctcgtc tgctcagaca cccttgctcag cctgattcag 600
 ggtctgggta tcagtgtgtt cacactgccc ctgcccttca cattcatcct catctcctaa 660
 ttttgcattt ttgttgtgct gtggaggcta ggcggtgaagc tttctccacc tgtggatctc 720
 atctgactgg agtcaccata ttttatgggg cagccatctg catgtacttg aaacctcagt 780
 caaagggaac ccaggaagag gataaagtgt tctcaaaaact ttatggagca gttactccca 840
 tgttaaattc cccaatttac attcagagaa ataaggatat aaaagggtgca cttagaaagt 900
 tagccaaagg aatatgaaaa tccataacagt tctcttttaa c 941

<210> 348

<211> 957

<212> DNA

<213> Unknown (H38g197 nucleotide)

<220>

<223> Synthetic construct

<400> 348
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 atggggatta cagacaaccc tgggctgcag gctccactgt ttggactctt cctcatcata 120
 tatctgggtca cagtgatagg caatctgggc atgggttatct tgacctactt ggactccaag 180
 ctacacaccc ccatgtactt tttccttaga catttgtcaa tcaactgatc tgggttactcc 240
 actgtcattg ccccggaagat gttagtaaac ttcatagtgc acaaaaacac aatttcttac 300
 aattggatg ccaactcagc agcattcttt gagattttca tcatctctga gctctttatt 360
 ctatcagcaa tggcctatga tcgctacgta gccatctgta aacctcttct gtacgtgatc 420
 atcatggcag agaaagtact ttgggtgctg gtaattgttc cctatctcta tagcagttt 480
 gtgtcactat ttctcacaat taagttattt aaactgtcct tctgtggctc aaacataatc 540
 agctattttt actgtgactg tatccctctg atgtccatac tctgttctga cacaatgaa 600

ttagaattaa taattttgat cttctcaggc tgtaatttgc tcttctccct ctcaattgtt	660
ctcatatcct acatgtttat tctagtggcc attctcagaa tgaactcaag gaaagggagg	720
tacaaagcct tctccacctg tagctctcat ctgacagtgg tgatcatgtt ctatgggaca	780
ttgttattta tttacttgca acccaagtcc agtcatactt tggctattga taaaatggcc	840
tcagtgtttt ataccctgtt gattcctatg ctgaatccgt tgatctacag cctaaggaac	900
aaagaagtaa aagatgctct aaagagaact ttaaccaatc gattcaaaat tcccatt	957

<210> 349

<211> 471

<212> DNA

<213> Unknown (H38g198 nucleotide)

<220>

<223> Synthetic construct

<400> 349

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gaaggtaggc acatttaggg gatgttcttg gcctttccgt ttggctgacc tatcccaaaa	120
cttttcctct gggctctctat cagagacatg gcagtaacct ggatggacca taggcacgag	180
tcctgtagcc cattcctccc gaagctgcag cctttttcat cctgccatgt atctgagtta	240
tgacagtgcc ttgacacctt cactaaatca tatataactt gaatccgggg actcaagggg	300
ttcaaccatc tttgttttct tctccattac tgtcactgtg ctagagccca agtctcctga	360
aatgcgcctt ggagccttgc tcaaagatgt caaccacaac tgctgatcag gtagctattt	420
tgtctgaagc tggtagttca tgacaggctc tgacatgtgc tgagcttgc c	471

<210> 350

<211> 951

<212> DNA

<213> Unknown (H38g199 nucleotide)

<220>

<223> Synthetic construct

<400> 350

atgggccaaa agaactaac agtgcttact gaattaattc tgatggaaat cacaaggcgg	60
cttgagctgc agctctccct tttttgggtc ttctcatca tctgcacatt cacagtgggtg	120
agcaaagagt gcataatcat tttgaacaat gtggacttgg gtctacacaa catttgtgta	180
ttttttaaat caggtacctg aattttatta atcttggtaa ttctatggtc atttatccca	240
agatactggg aaactttgtt gtggctcaaa atgccattcc ctggtatgca tgtaccatgc	300
agatggcttt cttcattatg ttcattatct gtgaactttt cgtctcatca gccatggcct	360
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tgtttctttg ttagccatgg tggactcaaa tgcatgagga atagaaatgt tgatcacact	600
attttcagta cttaatttga tattctttct tctggtagtc ctaatgtcct ccatgctgat	660
tctattaact gtttgttgaa tgcattctgc agagagcagt aaaaaacttt cttcacgtat	720
gtttcttgtc tgatagtggg ggttgtgttc tgtgggtttc tatactttat gtacttgcag	780
ctcaaattca gtcccttttt ttttgataat aataaaatga cctccatgtt ttccctctta	840
gtgattacca tgctttacca tttgggtctgt agtgtaaaga acaaagggag taaaaaaaaat	900
gccttctata gtttttttat gaagcagtga aaactttgta atttaatggt c	951

<210> 351

<211> 906

<212> DNA

<213> Unknown (H38g200 nucleotide)

<220>

<223> Synthetic construct

<400> 351

atgacgaact tgaatgcac acaggccaac caccgtaact tcattctgac aggtatccca	60
--	----

ggaacgccag	acaagaaccc	atggttggcc	tttcccctgg	gatttctcta	cacactcaca	120
ctcctgggaa	atggtaccat	cctagctgtc	atcaagggtg	agccaagtct	ccatgagccc	180
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gcctttgaca	gatttgtggc	catccgaaac	ccattacact	atgtttccat	cctcactcac	420
gatgttattc	gaaagactgg	aatatctgtc	ctcaccgggg	cagtctgtgt	ggtattccct	480
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gcctccatga	tcacagatt	ttgggagcat	ttatcaccag	tagtgcacat	ggtcatggct	840
gatatatacc	tactgtctcc	gcctgtgcta	aaccccatg	tctacagtgt	gaagaccaag	900
caaatt						906

<210> 352

<211> 971

<212> DNA

<213> Unknown (H38g201 nucleotide)

<220>

<223> Synthetic construct

<400> 352

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gatccagaac	tcagaccggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctgggc	120
acagtgtga	ggaacctgct	cagcatcccg	gctgtcagct	ctgactcca	cctccacacc	180
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gttcccaaga	tgattgtgga	catgcagtg	tatagcagag	tcattctctca	tcggggctgc	300
ctgacacaga	tgtctttctt	ggtccttttt	gcattgtatag	aaggcatgct	cctgactgta	360
atggcctatg	actgctttgt	aggcatctat	cgcctctctg	actaccaggt	catcgtgaat	420
cctcatctct	gtgtcttctt	tgttttgggt	tcctttttcc	ttagcctggt	ggattcccag	480
ctgcacagtt	ggattgtggt	acaattcacc	atcatcaaga	atgtggaaat	ctctaatttt	540
gtctgtgacc	cctctcaact	tctcaaactt	gcctcttatg	acagcgtcat	caatagcata	600
ttcatatatt	tcgatagtac	aatgtttggt	ttcttctcta	tttcagggat	cctttcatct	660
tactataaaa	ttgtcccctc	cattctaagg	atgtcatcgt	cagatgggaa	gtataaaact	720
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atgtaccttg	cttcagctat	gtcaccaacc	cccaggaaatg	gtgtgggtgt	gtcagtgatg	840
taagctgtgg	tcacccccat	gctgaacctt	ttcatctaca	gcctgagaaa	caggacata	900
caaagtgcc	tcgggaggct	gcgcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
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<210> 353

<211> 431

<212> DNA

<213> Unknown (H38g202 nucleotide)

<220>

<223> Synthetic construct

<400> 353

ttctctgtta	caggatcag	cgttgtggat	tgctgtttct	agtccacagt	tattcctgaa	60
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ttattattat	tattattatt	attattatta	acattttttt	aaaaatttct	tttcatagaa	180
tgcatttttg	tattagagat	tcctctagtg	ggaaaataac	agttttattac	ttatagttct	240
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tagaatttgt	aatattttga	tacttctaca	agggggacct	tgcccttaaa	cagaactttg	360
ctatactcag	aagcattcca	agcttttctt	cctaggattt	agaaattcat	aatgtgagat	420
atcagcattt	c					431

<210> 354
 <211> 938
 <212> DNA
 <213> Unknown (H38g203 nucleotide)

<220>

<223> Synthetic construct

<400> 354
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 agagtggaaa aatacacttt tgaacccgaa acaaagtctc attttctaag attttggcat 360
 aaaatatacc gtgtaccttt tgctcttaaa acacttcggt gttaatacat tcaattttaa 420
 ggtacttatg agtggcaggc tatgggacta gttagttcct gtctagaatc tcctctataa 480
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 aatttcttac attgatccat ttattaactc attagtattt ttgtgggttt cactgctttt 600
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 ctctctgtct ctttgttcta tagcagtgtc ttcttcatgt atgggtgccc cagggtctggc 780
 ccagattaac agtggaaatga aatgtatttt ccgttctaca tgattataat tcctctgcag 840
 actcctttat ttacagtatg aaaaacaaag aagttttagg tacacttaga acaatgataa 900
 agaaatattt ttggagaaca ctttcataat tctttcca 938

<210> 355

<211> 759

<212> DNA

<213> Unknown (H38g204 nucleotide)

<220>

<223> Synthetic construct

<400> 355
 atgtgcttgt tcctgtgtca cctctccttc ttggacatga ccatttcttg tgctattgtc 60
 cccaagatgc tggctggctt tctcttgggt agtaggatta tctcctttgg gggctgtgta 120
 atccaactat tttctttcca tttcctgggc tgtactgagt gcttccttta cacactcatg 180
 gcttatgacc gtttccttgc catttgtaag cccttacact atgctaccat catgaccac 240
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 caaacaagtt ttgtattccg gctgcccttc tgtggcccca atcggttcca ctacatcttc 360
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 tacctgcggc cttgttcaca ggagccctg gatgggttgg tagctgtctt ttacactgtc 660
 atcactccct tgcttaactc catcatctac acactgtgca acaaagaaat gaaggcagca 720
 ttacagaggc tagggggcca caaggaagtg cagcctcac 759

<210> 356

<211> 933

<212> DNA

<213> Unknown (H38g205 nucleotide)

<220>

<223> Synthetic construct

<400> 356
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 ccgcaactgg agcccatcct gtttgtcttt atttttattt tctactccct aactctcttt 120
 ggcaacacca tcatcatcgc tctctcctgg ctagaccttc ggctgcacac acctatgtac 180

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gacctctatg	ctgctgtctg	tcgtccactc	cactacatgg	ccatcatgca	ccccatctc	420
tgccagaccc	tggctatcgc	ctcctggggt	gcgggtttcg	tgaactctct	gatccagaca	480
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cctgtatttc	tgaagtggc	ttgtgcggac	acagaaggaa	cagaggccaa	gatgtttgtg	600
gccccagtc	tagtcgtggc	tgttcctgca	gcacttattc	taggctccta	tgtgcacatt	660
gctcatgcag	tgtgaggggt	gaagtcaacg	gctgggcgca	gaaaggcttt	tgggacttgt	720
gggtcccacc	tcctagtagt	tttccttttt	tatggctcag	ccatctacac	atatctccaa	780
tccatccaca	attattctga	gcgtgaggga	aaatttgttg	ccctttttta	tactataatt	840
acccccattc	tcaatcctct	catttatata	ctaagaaaca	aggacgtgaa	gggggctctg	900
tggaaagtac	tatggagggg	cagggactca	ggg			933

<210> 357

<211> 934

<212> DNA

<213> Unknown (H38g206 nucleotide)

<220>

<223> Synthetic construct

<400> 357

atgaagataa	agaatcacac	tccagtaact	gaggtccccc	tgatgggaat	ccctcatata	60
aaggggatgg	aaaatgtgct	ttttgtctta	tttctggcct	tctacctctt	caccttgctg	120
gggaacctac	tcattcttct	ggcgtcctc	actttctcca	acctccacac	ccccatgtat	180
ttcttctctg	gaaacctgtc	tgtgtttgac	atatttttcc	cttcagttag	ttcccccaaa	240
atgatgctct	gcttagtggg	acaaagctgc	accatctctt	tccagggttg	tgcctcccag	300
ctcttctttc	accatttctt	gggttgcacc	gagtgtttcc	tgtacactgt	gatggcctat	360
gaccgatatt	cagccatctg	ccaccctttg	ccatacacgg	tcacatgaa	acgcagggtg	420
tgtgccctcc	tgacgttagg	cacctggacg	gggagctgtc	tgcacatc	tgtcctcaca	480
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catcaacgta	ggtgttgttg	cgctcatgtg	ttttcttctt	atcctcacct	cttatgcttg	660
cattgttatc	tctatactga	aaatcagttc	ctcagaaggt	aggcgcagag	ccttctcaac	720
ctgcagtgcc	catctgacgt	ccatcctgct	cttctatgga	ccaatagtc	tcatttatct	780
ccgacctgcc	tccagccctt	ggctggactc	tgtggttcag	gtgttgaata	atattgttat	840
cccttccctg	aatcctttga	tatatacttt	gagaacaaa	ggtgtaaagc	tggcactgag	900
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<210> 358

<211> 892

<212> DNA

<213> Unknown (H38g207 nucleotide)

<220>

<223> Synthetic construct

<400> 358

gtgcgtgggt	ccaagcagct	gcggaatggg	accctagtgt	cccagtttct	tctgaaaggg	60
ctgaggggaca	gcaaggcttg	gaggcccctg	ctgttcacca	cctttctgct	aatctacata	120
gtggttggtg	ttgggagcca	catgttcaca	gtggactacc	gacgccacac	tcccatgtac	180
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gtgctgggtg	atttgcctgg	tccggtaggg	cccgtacttt	attgtgcttg	tctcatccag	300
atatgctttc	tccacttctt	ggcaccctag	gagtccttcc	tcctcacagc	cgtggcctat	360
gattctatgc	agctatctgc	cagccattgc	actactttgt	cctcgtgggc	cgactgaccc	420
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tccgtcactg	ctcagactct	cttgcttcag	cacacgtacc	aatgaacttg	ccctgttctt	600
cagttttctg	gtggctcttg	cacactgcgt	cctggctcgt	gtctcctatg	gacacgttgt	660
ggctgctggt	caggattcat	tccacccagg	gctgaagaaa	agccttttct	acctgtgttg	720

cccatctcgc	tatgatcggt	cttttctacg	tcacttcagt	cccctgctac	atccttccca	780
actctgcata	ctctggettg	ggcgactggg	tgctctctgt	gctatgtgtg	gtcctcactc	840
acatgctaaa	ccccatcttc	cccagcatgc	tgggatgaca	ggcatgagcc	ac	892

<210> 359

<211> 936

<212> DNA

<213> Unknown (H38g208 nucleotide)

<220>

<223> Synthetic construct

<400> 359

atgggtgtaa	aaaaccattc	cacagtgact	gagtttcttc	tttcaggatt	aactgaacaa	60
gcagagcttc	agctgcccct	cttctgcctc	ttcttaggaa	tttacacagt	tactgtgggtg	120
ggaaacctca	gcatgatctc	aattattagg	ctgaatcgtc	aacttcatac	ccccatgtac	180
tatttctctga	gtagttttgtc	tttttttagat	ttctgtctatt	cttctgtcat	taccctaaa	240
atgctatcag	ggtttttatg	cagagataga	tccatctcct	attctggatg	catgattcag	300
ctgttttttt	tctgtgtttg	tggtatttct	gaatgctaca	tgctggcagc	catggcctgc	360
gatcgctacg	tggccatctg	cagcccactg	ctctacaggg	tcacatgtc	ccctagggtc	420
tgttctctgc	tggtggctgc	tgtcttctca	gtaggtttca	ctgatgctgt	gatccatgga	480
ggttgtatac	tcaggttgtc	tttctgtgga	tcaaactca	ttaaactta	tttctgtgac	540
attgtccctc	ttattaaact	ctcctgctcc	agcacttata	ttgatgagct	tttgattttt	600
gtcattgggtg	gatttaacat	gggtggccaca	agcctaacaa	tcattatttc	atatgctttt	660
atcctcacca	gcacctcgcg	catccactct	aaaaagggca	ggtgcaaagc	gttttagcacc	720
tgtagctccc	acctgacagc	tggtcttatg	ttttatgggt	ctctgatgtc	catgtatctc	780
aaacctgctt	ctagcagttc	actcaccag	gagaaagtat	cctcagtatt	ttataccact	840
gtgattctca	tggtgaatcc	cttgatatat	agtctgagga	acaatgaagt	aagaaatgct	900
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<210> 360

<211> 753

<212> DNA

<213> Unknown (H38g209 nucleotide)

<220>

<223> Synthetic construct

<400> 360

atgtactatt	tcctcagcca	cctggccttt	gttgaccttt	gttactcctc	tgctattaca	60
ccgaagatga	tggtgaattt	tggtgtggaa	cgcaacacca	ttcctttcca	tgcttgtgca	120
acccaactgg	gttggtttct	caccttcacg	atcactgagt	gtttccttct	agcctccatg	180
gcctacgatt	gctatgtcgc	catctgtagt	cccctgcatt	attcaacact	gatgtcaaga	240
agagtctgca	ttcaactggg	ggcagttcca	tatatataca	gcttcttggt	tgccctcttc	300
cacaccgtta	tcactttccg	tctgacttac	tgtyggccaa	acttaattaa	ccattttctat	360
tgtagtgacc	tccccttctt	agctctgtcc	tgctcagaca	cacacatgaa	ggaaattctg	420
atatttgcct	ttgctggcct	tgatatgac	tcttctctct	ccattgtcct	cacctcctac	480
atctttatta	ttgccgctat	cctaaggatc	cgctctactc	aggggcaaca	caaagccatt	540
tccacctgtg	gtcccatat	gggtactgtc	actattttct	atggcacact	gatctttatg	600
tacctacagc	ccaaatcaaa	tcactccttg	gacacagaca	agatggcttc	tgtattttac	660
acagtgggtga	tccccatgtt	aaacccccta	atctatagtc	taaggaaaca	agaagtgaag	720
gatgcctcaa	agaaagcctt	ggataaagggt	tgt			753

<210> 361

<211> 933

<212> DNA

<213> Unknown (H38g210 nucleotide)

<220>

<223> Synthetic construct

<400> 361

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ctggagcccc	ccctctttgg	aatcttccctg	gtggttttacg	tgctcactgt	gctggggaac	120
ctcctcatcc	tgctggtgat	caggggtggat	tctcacctcc	acaccccat	gtactacttc	180
ctcaccaacc	tgctcttcat	tgacatgtgg	ttctccactg	tcacgggtgcc	caaaatgctg	240
atgaccttgg	tgcccccaag	cggcaggact	atctccttcc	acagctgcgt	ggctcagctc	300
tattttttcc	acttccctggg	gagcaccgag	tgtttctct	acacagtcac	gtcctatgat	360
cgctacctgg	ccatcagtta	cccgtcagg	tacaccaaca	tgatgactgg	gcgctcgtgt	420
gccctcctgg	ccaccggcac	ttggctcagt	ggctctctgc	actctgctgt	ccagaccata	480
ttgactttcc	atttgcccta	ctgtggaccc	aaccagatcc	agcactactt	ctgtgacgca	540
cgcgccatcc	tgaaactggc	ctgtgcagac	acctcagcca	acgagatggg	catctttgtg	600
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gcctcccact	gtatcgtggg	cctttgcttc	tttggccctg	gtcttttcat	ttacctgagg	780
ccaggctcca	gggacgcctt	gcattggggt	gtggccgttt	tctacaccac	gctgactcct	840
cttttcaacc	ctgttggtga	caccctgaga	aacaaggagg	taaagaaagc	tctgttgaag	900
ctgaaaaatg	ggtcagtatt	tgctcagggt	gaa			933

<210> 362

<211> 827

<212> DNA

<213> Unknown (H38g211 nucleotide)

<220>

<223> Synthetic construct

<400> 362

cactcctcac	tctcttttgc	tgtcttctctg	ctgacctact	ccgtgactct	gggtgggcaac	60
ctgggcatga	cagatctgat	ctgccaatct	gcaccagctc	tgccctccac	accccatgt	120
gcttctctct	gagcgtattc	tcttccctag	acatctgcag	ttcctccatg	tgacccccag	180
gctgctgac	cactttctca	ccactaacca	tccatctcct	ttgcagggtg	tataatccag	240
atggccctca	tgaccttcta	tgccacaggg	gaatgtctgc	tgctggccat	cgtagcctat	300
gactgagttg	tgcccatttg	ccaccctttc	ccctagcata	tcattcatgtc	caaggggact	360
gtgtgcccag	ctggtgggtg	ttacctctgc	tgtgggggtg	ctcatttcag	ctctagacag	420
gatgcattca	tctgcacctc	ccgtggccta	acatcattga	tcattactat	gttctgttac	480
attccccacc	cccatgctcc	aactggcctg	ctcagatgcc	actgtggcca	acatgatcct	540
gtttgtctct	tctgccttga	tcactatccc	taccatctca	gtcatcttgg	tctcttacac	600
ttacatcctg	gttaatcagt	gggatgaggt	ccctggatgc	ccagtgcata	gctttctcca	660
ctcgtgcctc	ccacctcact	gctcactgcc	tgttttatgg	gtttgtgttc	cttgtataca	720
ttccacccaa	ccctgaaatg	gcctcagcct	ataacaaaat	cctcttcacc	gttgtgatcc	780
ccatgctgaa	cctcctggtc	taaggcctga	gaaataaaga	tgtcaaaa		827

<210> 363

<211> 937

<212> DNA

<213> Unknown (H38g212 nucleotide)

<220>

<223> Synthetic construct

<400> 363

tcagtggcca	aaggcaatca	ttcaacagtg	tatgaattta	tctctttggg	gctcacagat	60
aatgcagagc	ttcaagtcac	tctcttttgg	atattccttg	tagtatactt	agctagcttt	120
atgggtaatt	tcgggttgat	tatgctaatt	caaatacagc	ctcagcttca	tacacccatg	180
tattttttcc	tcagccatct	ggcttttgg	gatttttctt	ttacttcac	tggtgcccc	240
aataccttgg	taaattttct	gtgtgaagtt	aaaagtataa	cattttatgc	atgtgccatt	300
caggatgct	gcttcatcac	attttagtt	tgtgaattat	atttgcctc	aatcatggca	360
tatgatcggt	atgttgccat	ctgtaaccct	ttactttatg	tcattctcat	tcctagaaaa	420
ctgtattaaa	ctgattgcta	gcacgtatgt	gtatggattc	actgtgggac	ttgtacagac	480
agtggcgaca	tcctacttgt	ctttttgtga	ttccaacgtg	atcaaccact	tctaccatga	540
tgatgttcca	ttagtggtc	tgccctgttc	tgacactcat	gtcaaagagc	tgatgttgtt	600

aatcattgct	gggttcaata	ctctctgctc	tctagtaatt	gtgctgattt	cttatggttt	660
cattttcttt	gccatcctga	ggatacattc	tgctgaaggg	agacagaaag	cattttctac	720
cagtgtctcc	catctgacct	ccatcacaaat	attttatgga	acaatcattt	ttatgtaccc	780
gcagcccaag	tcaagccatt	ccctgaatat	ggataaagtt	gcttctgtgt	ttaatgtggt	840
agtgttcct	acattaaacc	cactgatcta	tagtttaaga	aatcaggagg	taaaaaatgc	900
actaaagaga	attatagaaa	agttatgttt	ggctgtc			937

<210> 364

<211> 697

<212> DNA

<213> Unknown (H38g213 nucleotide)

<220>

<223> Synthetic construct

<400> 364

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agctttgtgt	tggactcagc	tatactgctg	gccatggcat	ttgaccgcta	tatggccatt	120
tgctcaccct	tcgagataca	ctactattct	gactcccaaa	accattgtca	aaattgctgt	180
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gcttgctgtg	gctgatatct	ccatcaatat	ctgggtgtga	ttttgtgttc	ccatcatgac	360
ggtgatgaca	gacgtgatcc	tcattgctgt	ctcctacacc	ctcatcctct	gtgctgtctt	420
ttgcctcccc	tcccaagatg	cccgctcagaa	ggccctttgc	tcctgtgggt	cccatgtctg	480
tgttatcctc	atattctata	taccagcatt	cttctccatt	cttgcccat	gctttgggca	540
taatgtccct	catacctttc	atattatgtt	tgccaacctt	tatgtaatca	ttccacctgc	600
tctcaactct	attgtctaca	gaataaagac	caagcaaatc	cagaacagaa	tccttttgct	660
ctttcccaag	gggtcccagt	gataggtgcc	tgagctc			697

<210> 365

<211> 930

<212> DNA

<213> Unknown (H38g214 nucleotide)

<220>

<223> Synthetic construct

<400> 365

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ctggacgccc	ccctcttttg	agtcttctcg	gtggtttacg	tgctcactgt	gctggggaac	120
ctcctcatcc	tgctggtgat	cagggtggat	tctcacctcc	acaccaccat	gtactacttc	180
ctcaccaacc	tgctgttcat	tgacatgtgg	ttctccactg	tcacggtgcc	caaattgctg	240
atgacttttg	tgttcccaag	tggcagggct	atctccttcc	acagctgcat	ggctcagctc	300
tattttcttc	acttcctagg	gggcaccgag	tgtttccctc	acagggtcac	gtcctgtgat	360
cgtacctg	ccatcagtta	cccgtcagg	tacaccagca	tgatgactgg	gcgctcggtg	420
actcttctg	ccaccagcac	ttggctcagt	ggctctctgc	actctgctgt	ccaggccata	480
ttgactttcc	atttgcccta	ctgtggaccc	aactggatcc	agcactattt	gtgtgatgca	540
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gtctgttcca	tcctgcggt	ccgcacctca	gaggggaagc	acagagcctt	tcagacctgt	720
gcctcccact	gtatcgtggt	cctttgcttc	tttggccctg	gtcttttcat	ttacctgagg	780
ccaggctcca	ggaaagctgt	ggatggagtt	gtggccggtt	tctacactgt	gctgacgccc	840
cttctcaacc	ctgttgtgta	cacctgagg	aacaaggagg	tgaagaaagc	tctgttgaag	900
ctgaaagaca	aagtagcaca	ttctcagagc				930

<210> 366

<211> 933

<212> DNA

<213> Unknown (H38g215 nucleotide)

<220>

<223> Synthetic construct

<400> 366

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gaattaca	aa ttctctctt	cacgctgttt	ctggccattt	acatgggtcac	ggtggcaggg	120
aaccttggca	tgattgtcct	catccaggcc	aacgcctggc	tccacatgcc	catgtacttt	180
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taccttttta	tcgccttggg	ccatgttgag	atctacatcc	tggctgtgat	ggcctttgac	360
cggtagatgg	ccatctgcaa	ccctctgctt	tatggcagca	gaatgtccaa	gagtgtgtgc	420
tccttcctca	tcacgggtgcc	ttatgtgtat	ggagcgctca	ctggcctgat	ggagaccatg	480
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gtggctggct	ggaacctttc	ttttctcttc	ttcatcatat	gtatttctta	cctttacatt	660
ttccctgcta	ttttaagat	tcgctctaca	gagggcaggg	aaaaagcttt	ttctacctgt	720
ggctcccatc	tgacagctgt	cactatatct	tatgcaaccc	ttttcttcat	gtatctcaga	780
ccccctcaa	aggaatctgt	tgaacagggt	aaaatggtag	ctgtatttta	taccacagta	840
atccctatgc	tgaaccttat	aatttatagc	cttagaaata	aaaatgtaaa	agaagcatta	900
atcaaagagc	tgtaaatgaa	gatatacttt	tct			933

<210> 367

<211> 945

<212> DNA

<213> Unknown (H38g216 nucleotide)

<220>

<223> Synthetic construct

<400> 367

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ttggaaggca	tcaaacactg	gatttttcac	ccctttttct	ttatgtacat	ggttgccatc	120
tcaggcaatt	gtttcattct	gatcattatt	aagaccaacc	ctcgtctgca	cacacccatg	180
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accactatgg	ggatcttctg	gtttaactcc	cagagtatct	actttggagc	gtgtcaaata	300
cagatgttct	gcatecactc	tttttccttc	atggagtcct	cagtgtcctc	catgatgtcc	360
tttgaccgct	ttgtggccat	ctgccaccct	ctgagggtatt	cggtcattat	cactggccag	420
caagtgggtca	gagcaggcct	aattgtcatc	ttccggggac	ctgtggccac	tatccctatt	480
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acatgcaccg	ctcatctctg	tgtgtgtgta	gtattctttg	tgcctatgat	ggggctgtcc	780
ctggtgcacc	gttttgggaa	gcatgccccca	cctgctatct	atcttcttat	ggccaatgtc	840
tacctttttg	tgcctcccat	gcttaacccta	atcatataca	gcattaagac	caaggagatc	900
caccgtgcca	ttatcaaact	cctaggtctt	aaaaaggcca	gtaaa		945

<210> 368

<211> 969

<212> DNA

<213> Unknown (H38g217 nucleotide)

<220>

<223> Synthetic construct

<400> 368

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cacctcatat	agttcctggg	gttcctgggg	ttaatgggtg	cctacattgt	aacagccaca	120
ggcaagctgc	taattattgt	gctcagctgg	atagaccaac	gcctgcacat	acagatgtac	180
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atgcttctgc	tcatactcac	gggggatcac	accatctcat	ttgtcagctg	catcatccag	300
tctacctctc	acttctttct	aggcaccact	gacttcttcc	tcttggccgt	catgtctctg	360

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gatcgttacc tggcaatctg ccgaccactc cgctatgaga cctgatgaa tggccatgtc 420
tggtcccaac tagtgctggc ctctgggcta gctggattcc tctgggtcct ttgccccact 480
gtcctcatgg ccagcctgcc tttctgtggc cccaatggta ttgaccactt ctttcgtgac 540
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atcacacccc tcttgaaccc attcatcttc actctccgca atgacaaggt gcagcaagca 900
ctgagagaag ccttgggggtg gccagggtc actgctgtga tgaaactgag ggtcacaagt 960
caaaggaaa

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<210> 369

<211> 1016

<212> DNA

<213> Unknown (H38g218 nucleotide)

<220>

<223> Synthetic construct

<400> 369

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gctgtccagc atctggggaa tgctcttttc ctgggtgcacc tgctggcata cctggcctcc 120
atcatggcaa acatgctcat aatcaccatc acctgggctg accatcacct ccagacacct 180
atgtatttct tctcaacag tttttccttc tgtgaatgct gttttatcac cacagttatt 240
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aggactagct tccacctggt cactgtctgc tttgtcgtgg gcttcactct catcactggt 480
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caggctctga gggatgctca gtccagaatg aaattgtaaa aacagaatca caacctccca 960
gtgaaggaat gcaccttctc cttgatctaa tccaatcttt ctctgtttc tggaat 1016

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<210> 370

<211> 927

<212> DNA

<213> Unknown (H38g219 nucleotide)

<220>

<223> Synthetic construct

<400> 370

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gtgcagagtg tatgctttgt ggtgtttctc cccgtgtacc ttgccacggg ggtgggcaat 120
ggcctcatcg ttctgacggg cagtatcagc aagagtctgg attctcccat gtacttcttc 180
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cctttattca agcttgctg cactgacacc ttcatggagg gggttattgt gttggccaac 600
agtggattat tctctgtctt ctcttctcct atcttgggtg cctcttatat tgtcattctg 660
gtcaacttga ggaaccattc tgcaaggggg aggcacaaag ccctctccac ctgtgcttct 720
cacatcacag tggtcattct gtttttttga cctgctatct tctctacat gcgaccttct 780

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tccactttca	ctgaagataa	acttgtggct	gtattctaca	cggtcacac	ccccatgctg	840
aaccccatca	tttacacact	caggaatgca	gagggtgaaa	tcgccataag	aagattgtgg	900
agcaaaaagg	agaatccagg	gagggag				927

<210> 371

<211> 965

<212> DNA

<213> Unknown (H38g220 nucleotide)

<220>

<223> Synthetic construct

<400> 371

atggcaaaag	gcaatcattc	atcagtgact	gagttcatcc	tcctagggct	cacagataat	60
caggaacttc	aagtcattct	ctttgggtga	ttcctactga	tttacttagt	tactgtgttg	120
ggtaatcttg	gtttgattgt	gctaatacat	atcagtcctc	agcttcacac	acctatgtat	180
tttttcctca	gccatctggc	ttttgtggat	ttttacggta	cctctgctat	cactccaaac	240
acccttgtea	actctttgca	tgaaattaaa	agcatgtcat	tttatgcatg	tgccactcaa	300
gtgtgtgtgt	tcattacact	ttcagtcctg	gaattattgt	tgctctcatg	gcataatgat	360
ggtagtgggc	catctgcaac	cctttactct	atgtagttct	catgcctagg	agactctgca	420
ttcaaatggg	cactggctta	tatatattat	gtttcaccat	gggactcata	caagcagtgg	480
ccacattoca	catgtcgttt	tgtgactcta	atgtgggtcaa	ccagttctac	tgtgatgatg	540
ttcctctgat	tgctctggct	tggtctgata	cacaagtcaa	ggaattgatg	ttgttcatca	600
ttgtctcggt	caatgttttt	tggtctctta	tcattgttct	catctcctat	gtattcatcg	660
tctttgctat	ctaaggatcc	actctgccgt	aggaagacag	aaagcctttt	ctacctgtgc	720
ttctcacatg	ttttctattt	ccatatatta	tgggaccctc	agttttatgt	acctacagcc	780
taagtcaagc	cactcactag	ataaagacaa	gtattgcctca	gtattctatg	cagtgggtgat	840
tcccatgcta	aacccattga	tctatagctt	gaggaatcaa	gaggtaaaaa	aatgctatga	900
aaaaaattat	tgaaaaaatg	tggtctagta	atcaacagta	aaatttggtg	gtactaaaag	960
aaata						965

<210> 372

<211> 951

<212> DNA

<213> Unknown (H38g221 nucleotide)

<220>

<223> Synthetic construct

<400> 372

atgtcccagg	tgactaacac	cacacaagaa	ggcatctact	tcacccctac	ggacatccct	60
ggatttgagg	cctcccacat	ctggatctcc	atcccgcgtc	gctgtctcta	caccatctcc	120
atcatgggca	ataccacat	cctcactgtc	attcgacacag	agccatctgt	ccaccagcgc	180
atgtatctgt	ttctctccat	gctggccctg	acggacctgg	gtctcaccct	caccacccta	240
cccacagtca	tcagcttct	ctggttcaac	gttcgtagaa	tcagctctga	ggcctgtttt	300
gctcagtttt	tcttccctca	tggattctcc	tttatggagt	cttctgtcct	cctggctatg	360
tccgttgact	gctatgtggc	catctgctgt	cccctccatt	atgcctccat	cctcaccaat	420
gaagtcattg	gtagaactgg	gttagccatc	atgtgctgct	gtgttctggc	ggttcttccc	480
tcccttttct	tactcaagcg	actgcctttc	tgccactccc	accttctctc	tcgctcctat	540
tgccctccacc	aggatatgat	ccgcctggtc	tgtgctgaca	tcagggtcaa	cagctgggat	600
ggatttgctc	ttgccttgct	cattattatc	gtggatcctc	tgctcattgt	gatctcctat	660
acacttatte	tgaaaaatat	cttgggcaca	gccacctggg	ctgagcgact	ccgtgccctc	720
aataactgcc	tgtcccacat	tctagctgtc	ctggctctct	acattcccat	ggttgggtga	780
tctatgactc	atcgctttgc	caagcatgcc	tctccactgg	tccatgttat	catggccaat	840
atctacctgc	tggcaccccc	ggtgatgaac	cccatcattt	acagtgtaaa	gaacaagcag	900
atccaatggg	gaatgttaaa	tttcctttcc	ctcaaaaata	tgcatccaag	a	951

<210> 373

<211> 945

<212> DNA

<213> Unknown (H38g222 nucleotide)

<220>

<223> Synthetic construct

<400> 373

atgaatccag	caaatcattc	ccaggtggca	ggatttggtc	tactggggct	ctctcagggt	60
tgggagcttc	ggtttggttt	cttcactggt	ttctctgctg	tgtattttat	gactgtagtg	120
ggaaaccttc	ttattgtggt	catagtgacc	tccgaccac	acctgcacac	aaccatgtat	180
tttctcttgg	gcaatctttc	tttcctggac	ttttgctact	cttccatcac	agcacctagg	240
atgctgggtg	acttgctctc	aggcaaccct	accatttcct	ttgggtggatg	cctgactcaa	300
ctcttcttct	tccacttcat	tggaggcatc	aagatcttcc	tgctgactgt	catggcgat	360
gaccgctaca	ttgccatttc	ccagcccctg	cactacacgc	tcattatgaa	tcagactgtc	420
tgtgcactcc	ttatggcagc	ctcctgggtg	gggggcttca	tccactccat	agtacagatt	480
gcattgacta	tccagctgcc	attctgtggg	cctgacaagc	tggacaactt	ttattgtgat	540
gtgcctcagc	tgatcaaatt	ggcctgcaca	gatacctttg	tcttagagct	tttaatgggtg	600
tctaacaatg	gcctgggtgac	cctgatgtgt	tttctgggtg	ttctgggac	gtacacagca	660
ctgctagtca	tgctccgaag	ccactcacgg	gagggccgca	gcaaggccct	gtctacctgt	720
gcctctcaca	ttgctgtggt	gaccttaatc	tttctgcctt	gcactctacg	ctatacaagg	780
ccttttcgga	cattccccat	ggacaaggcc	gtctctgtgc	tatacacaat	tgtaaccccc	840
atgctgaatc	ctgccatcta	tacctgaga	aacaaggaag	tgatcatggc	catgaagaag	900
ctgtggagga	ggaaaaagga	ccctattggt	cccctggagc	acaga		945

<210> 374

<211> 960

<212> DNA

<213> Unknown (H38g223 nucleotide)

<220>

<223> Synthetic construct

<400> 374

atgtcatttc	taaatggcac	cagcctaact	ccagcttcat	tcatacctaaa	tggcatccct	60
ggtttggaag	atgtgcattt	gtggatctcc	ttcccactgt	gtaccatgta	cagcattgct	120
attacagga	acttcggcct	tatgtacctc	atctactgtg	atgaggcctt	acacagacct	180
atgtatgtct	tccttgccct	tctttccttc	acagatgtgc	tcatgtgcac	cagcaccctt	240
cccaacactc	tcttcatatt	gtggtttaat	ctcaaggaga	ttgattttaa	agcctgcctc	300
gccagatgt	tctttgtgca	caccttcaca	gggatggagt	ctgggggtgt	catgctcatg	360
gccctggacc	actgtgtggc	catctgcttc	cctctgcgtt	atgccaccat	cctcactaat	420
tcagtcatgt	ctaaagctgg	gttcctcact	tttcttaggg	gtgtgatgct	tgttatccct	480
tccactttcc	tcaccaagcg	ccttcacatac	tgcaagggca	acgtcatacc	ccacacctac	540
tgtgaccaca	tgtctgtggc	caagatatct	tgtggtaatg	tcagggttaa	cgccatctat	600
ggtttgatag	ttgccctgct	gattgggggc	tttgatatcc	tgtgcattac	aatctcctac	660
actatgattc	ttcaagcagt	tgtgagtcta	tcatacagcag	atgctcgaca	gaaggccttc	720
agcacctgca	ctgcccactt	ctgtgccata	gtcctcacct	atgttccagc	cttctttacc	780
ttctttacac	accatttttg	gggacacacc	attctcttac	acatacatat	tattatgggt	840
aatctctacc	tactaatgcc	tcccacaatg	aaccctattg	tgtatggggg	gaaaaccagg	900
caggtacgag	aaagtgtcat	taggttcttt	cttaagggaa	aggacaattc	tcataacttt	960

<210> 375

<211> 915

<212> DNA

<213> Unknown (H38g224 nucleotide)

<220>

<223> Synthetic construct

<400> 375

atggttgcta	caaacaatgt	gactgaaata	attttcgtgg	gattttccca	gaattggagt	60
gagcagaggg	tcattttctgt	gatgtttctc	ctcatgtaca	cagctgttgt	gctgggcaat	120
ggcctcattg	tggtgaccat	cctggccagc	aaagtgtctc	cctcccccat	gtattttctt	180
ctcagctact	tatcctttgt	ggagatctgc	tactgttctg	tcatggcccc	caagcttacc	240

tttgactcct	ttatcaagag	gaaagtcatt	tctctcaagg	gctgcctcac	acagatgttt	300
tcctccatt	tctttggtg	cactgagggc	tttctcctga	tggtgatggc	ctatgaccgc	360
tatgtggcca	tctgcaagcc	cttgactac	atggccatca	tgaaccagcg	aatgtgtggt	420
ctcctcgtga	ggatagcatg	gggcgggggc	ctgctgcatt	ctgttgggca	aaccttctctg	480
attttccagc	tcccgttctg	tggccccaac	atcatggacc	actacttctg	tgatgtccac	540
ccagtgtg	agctggcctg	cgcagacacc	ttcttcatta	gcctgctgat	catcaccaat	600
ggcggctcca	tctccgtagt	cagtttcttc	gtgctgatgg	cttctacct	gatcatcctg	660
cacttctcga	gaagccacaa	cttggagggg	cagcacaagg	ccctctccac	ctgtgcctct	720
catgtcacag	ttgtcgacct	gttcttcata	ccttgctcct	tggtctatat	taggccctgt	780
gtcacccctcc	ctgcagacaa	gatagttgct	gtattttata	cagtggtcac	acctctctta	840
aacctgtga	tttactcctt	caggaatgct	gaagtgaaaa	atgccatgag	gagatttatt	900
gggggaaaag	taatt					915

<210> 376

<211> 939

<212> DNA

<213> Unknown (H38g225 nucleotide)

<220>

<223> Synthetic construct

<400> 376

atggctcctg	aaaatttcac	cagggtcact	gagtttattc	ttacaggtgt	ctctagctgt	60
ccagagctcc	agattcccct	cttcttggtc	tttctggtgc	tctatgggct	gaccatggca	120
gggaacctgg	gcatcatcac	cctcaccagt	gttgactctc	gacttcaaac	ccccatgtac	180
tttttctctg	aacatctggc	tctcattaat	cttggttaact	ctactgtcat	tgcccctaaa	240
atgctgatta	acttttttagt	aaagaagaaa	actacctcat	tctatgaatg	tgccacccaa	300
ctgggagggt	tcttgttctt	tattgtatcg	gaggtaatca	tgctggcttt	gatggcctgt	360
gaccgctatg	tggtattttg	taaccctctg	ctgtacatgg	tggtgggtgc	tcggcgggctc	420
tgcctcctgc	tggtctccct	cacatacctc	tatggctttt	ctacagctat	tgtgggtttca	480
tcttatgtat	tctctgtgtc	ttattgtctc	tctaataata	tcaatcattt	ttactgtgat	540
aatgttcctc	tgtagcatt	atcttgctct	gatacttact	taccagaaac	agttgtcttt	600
atatctgcag	caacaaatgt	ggttggttcc	ttgattatag	ttctagtatc	ttatttcaat	660
attgttttgt	ctatttttaa	aatatgttca	tcagaaggaa	ggaaaaaagc	cttttctacc	720
tgtgcttcac	atatgatggc	agtcacaatt	ttttatggga	cattgtctatt	catgtatgtg	780
cagccccgaa	gtaaccattc	actggatact	gatgataaga	tggtctctgt	gttttacacg	840
ttggtaattc	ctatgtgtaa	tcccttgatc	tacagcctga	ggaataagga	tgtgaagact	900
gctctacaga	gattcatgac	aaatctgtgc	tattccttt			939

<210> 377

<211> 979

<212> DNA

<213> Unknown (H38g226 nucleotide)

<220>

<223> Synthetic construct

<400> 377

atgaaaattt	ctaataactc	tttggggttt	ttacctacga	cattcatttt	ggttggcatc	60
ccagggtg	agtcagagca	cctctggata	tccgtcccct	tctctctgat	atacatcatc	120
attttccttg	ggaatggcat	cattcttcac	gtcatcagaa	cagatattgc	cctacatcaa	180
cccatgtacc	tcttcttg	catgttggca	ctggccgagg	ttcgtgtctc	tgcatccacc	240
ctgcctacag	tgtaggcat	attccttttt	ggaaatactg	aaattagtct	tgaagcttat	300
ctttttccag	atgttctcca	tccattcttt	atccatgatg	gagtcagctg	tgctgctggc	360
catgtctttg	gaccgcttta	tagccatcta	cagccactg	agctatacag	ctatcctgac	420
actgccagg	gtctttggca	caggagctat	tatcgtactg	aaaagcatta	tgctcatggc	480
tccgttgccc	attctcttat	ggcgtctgcc	cttctgtggc	cacaatgccc	tctcacattc	540
ctattgtctg	caccccaate	ttatctatct	atcttgtggg	aacatttctg	ttaaccaatat	600
ctatgggatt	ttcattgtta	cctctacttt	tgggctggat	tcgttctgta	ttgtgatctc	660
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cttgtctata	gtgcaccgcc	ttggacatcg	tgtgtccct	ctgctgcaag	ccatgatggc	840
caatgcctac	ctcttcttcc	cacctgttgt	caatcctatt	gtctacagca	ttaagaccaa	900
ggagatccat	ggtgccattg	tccgaatgct	attagagaaa	agacgcagag	tgtagccaaa	960
aaccatagta	ggaagaaat					979

<210> 378

<211> 933

<212> DNA

<213> Unknown (H38g227 nucleotide)

<220>

<223> Synthetic construct

<400> 378

atgtccaaga	ccagcctcgt	gacagcggtc	atcctcacgg	gccttcccca	tgccccaggg	60
ctggacgccc	cactctttgg	aatcttcctg	gtggtttacg	tgctcactgt	gctggggaac	120
ctcctcatcc	tgtgtgtgat	caggggtgat	tctcacctcc	acaccccat	gtactacttc	180
ctcaccaacc	tgtccttcat	tgacatgtgg	ttctccactg	tcacgggtgc	caaaatgctg	240
atgaccttgg	tgtccccaag	cggcagggtc	atctccttcc	acagctgcgt	ggctcagctc	300
tattttttcc	acttctctgg	gagcaccgag	tgtttctctc	acacagtcac	gtcctatgat	360
cgctacttgg	ccatcagtta	cccgtcagg	tacaccagca	tgatgagtgg	gagcagatgt	420
gccctcctgg	ccaccagcac	ttggctcagt	ggctctctgc	actctgctgt	ccagaccata	480
ttgactttcc	atttgcccta	ctgtggaccc	aaccagatcc	agcactatct	gtgtgatgca	540
ccgcccaccc	tgaaactggc	ctgtgcagac	acctcagcca	acgagatggg	catctttgtg	600
gacattgggc	tagtggcctc	gggctgcttt	ctcctgatag	tgctgtctta	tgtgtccatc	660
gtctgttcca	tcctgcggat	ccacacctca	gaggggaggg	acagagcctt	tcagacctgt	720
gcctcccact	gcctcgtggg	cctttgcttt	tttgttccct	gtgttttcat	ttacctgaga	780
ccaggctcca	gggacgtcgt	ggatggagtt	gtggccattt	tctacactgt	gctgacaccc	840
cttctcaacc	ctgttgtgta	cacctgaga	aacaaggagg	tgaagaaagc	tgtgttgaaa	900
ctgagagaca	aagtagcaca	ttctcagggg	gaa			933

<210> 379

<211> 936

<212> DNA

<213> Unknown (H38g228 nucleotide)

<220>

<223> Synthetic construct

<400> 379

atgccttcta	tcaatgacac	ccactttctat	cccccttct	tcctcctgct	aggaatacca	60
ggactggaca	ctttacatat	ctggatttct	ttccattct	gtattgtgta	cctgattgcc	120
attgtgggga	atatgaccat	tctctttgtg	atcaaaactg	aacatagtct	acaccagccc	180
atgttctact	tcctggccat	gttgtctatg	attgatctgg	gtctgtccac	atccactatc	240
cccaaaatgc	taggaatctt	ctggttcaac	ctccaagaga	tcagctttgg	gggatgcctt	300
cttcagatgt	tctttattca	catgtttaca	ggcatggaga	ctgttctggt	ggtgggtcatg	360
gcttatgacc	gctttgttgc	catctgcaac	cctctccagt	acaccatgat	cctcaccaat	420
aaaaccatca	gtatcctagc	ttctgtgggt	gttgggaagaa	atttagttct	tgtaacccca	480
tttgtgtttc	tcattctgcg	tctgccattc	tgtgggcata	acatcgtacc	tcacacatac	540
tgtgagcaca	gggtctcggc	cgggttggcc	tgtgcaccca	ttaagatcaa	cataatctat	600
gggtcatggt	tgatttctta	tattattgtg	gatgtgatct	taattgcctc	ttcctatgtg	660
cttatcctta	gagctgtttt	tcgccttccc	tctcaagatg	tccgactaaa	ggccttcaat	720
acctgtgggt	ctcatgtctg	tgttatgctg	tgtttttaca	caccagcatt	tttttctttt	780
atgacacatc	gttttggcca	aaacattccc	cactatatcc	atattctttt	ggctaacctg	840
tatgtgggtg	tcccacctgc	ccttaaccct	gtcatttatg	gagtcaggac	caagcagatc	900
cgagagcaaa	ttgtgaaaat	atttgtacag	aaagaa			936

<210> 380

<211> 909

<212> DNA

<213> Unknown (H38g229 nucleotide)

<220>

<223> Synthetic construct

<400> 380

atgactgaat	tcatttttct	ggtactttct	cccaaccag	agggtgcagag	ggtttgcttt	60
gtgatatttc	tggtcttgta	cacagcaatt	gtgctgggga	atttcctcat	tggtgctcact	120
gtcatgacca	gcagaagcct	tggttcccc	atgtacttct	tcctcagcta	cctctccttc	180
atggagatct	gctactcctc	cgctacagcc	cccaaactca	tctcagatct	gctggctgaa	240
aggaaagtca	tatcttggtg	gggctgcatg	gcacagcttt	tcttcttgca	cttctttggt	300
ggcactgaga	ttttcctgct	cactgtgatg	gcctatgacc	actatgtggc	catctgcaag	360
cccctcagct	acaccacat	catgaactgg	cagggtgtgta	ctgtccttgt	aggaatagca	420
tgggtgggag	gcttcatgca	ttcctttgca	caaatccttc	tcattctcca	cctgctcttc	480
tggtggcccca	atgtgatcaa	tcaactattc	tgtagacctag	ttccccctct	caaacttgcc	540
tgctctgaca	ccttctcat	tggtctgctg	attggtgccca	atggaggcac	cctgtctgtg	600
atcagttttg	gggtcctctt	agcatcctat	atgggtcatct	tgctccatct	gagaacctgg	660
agctctgaag	gggtggtgcaa	agccctctcc	acctgtgggt	cccatttcgc	tggtggtatc	720
ttgttctttg	ggccctgctg	cttcaactct	ctgaggcctt	ctaccactct	gcccatagac	780
aagatggtgg	ctgtgttcta	cacagtgata	accgcgatcc	tgaacctgt	catctactct	840
ctgagaaatg	ctgaaatgag	gaaggccatg	aagaggctgt	ggattaggac	attgagacta	900
aatgagaaa						909

<210> 381

<211> 947

<212> DNA

<213> Unknown (H38g230 nucleotide)

<220>

<223> Synthetic construct

<400> 381

cttatagcta	caggaaactg	gacaagaata	agtgagttaa	tcctcatgag	cttctcttcc	60
ctgcctactg	aaatacagtc	attactcttt	ctgacatttc	taaccatcta	cctggtcacc	120
ctgatgggaa	actgcctcat	cattctgggt	accctagctg	accccatgct	acacagcccc	180
atgtacttct	tcctcagaaa	cttatctttc	ctggagattg	gcttcaacct	agtcattgtg	240
cccaaaatgc	tggggaccct	gcttgcccag	gacacaacca	tctccttctt	tggctgtgcc	300
actcagatgt	atttcttctt	cttctttgga	gtggctgaat	gcttcctcca	ggctaccatg	360
gcataatgacc	gctatgtggc	catctgcagt	cccttgcaat	acccagtcac	catgaaccaa	420
aggactcgtg	ccaaactggc	tgctgcctcc	tggttcccag	gctttcctgt	agctactgtg	480
cagaccacat	ggctcttcag	ttttccattc	tgtagcacca	acaaggtaga	ccacttcttc	540
tgtagacagcc	cacctgtgct	gaggctggtc	tgtagcacca	cagcactgtt	tgagatctac	600
gccatcgctg	gaaccattct	gggtggtcatg	atccccctgt	tgctgatctt	gtgttcctat	660
actcgatttg	ctgctgccat	cctcaagatc	ccatcagcta	aagggaagaa	taaagccttt	720
tctacatgtt	cctcacacct	ccttggtgtc	tctcttttct	atatatcatt	aagcctcacc	780
tacttccggc	ctaaatcaaa	taattcacct	gagggcacga	agctgctatc	attgtcctac	840
actgttatga	ctcccatgtt	gaacccatt	atctacagcc	tgagaaataa	cgaggtgaag	900
aatgccctca	gcaggacggg	ctctaaggcc	ctagccctca	gaaactg		947

<210> 382

<211> 927

<212> DNA

<213> Unknown (H38g231 nucleotide)

<220>

<223> Synthetic construct

<400> 382

atgcctaatt	tcacggatgt	gacagaattt	actctcctgg	ggctgacctg	tcgtcaggag	60
ctacagggttc	tcttttttgt	gggtttccta	gcggtttaca	tgatcactct	gttgggaaat	120
attgggatga	tcattttgat	tagcatcagt	cctcagcttc	agagtcccat	gtactttttc	180
ctgagtcata	tgtcttttgc	ggacgtgtgc	ttctcctcca	acgttaccac	caaaatgctg	240

gaaaacttat	tatcagagac	aaaaaccatt	tcctatgtgg	gatgcttggt	gcagtgtac	300
tttttcattg	ccgttggtcca	cgtggaggtc	tatatcctgg	ctgtgatggc	ctttgacagg	360
tacatggccg	gctgcaaccc	tctgctttat	ggcagtaaaa	tgtctaggac	tgtgtgtgtt	420
cggctcatct	ctgtgcctta	tgtctatgga	ttctctgtca	gcctaataatg	cacactatgg	480
acttatggct	tatacttctg	tggaaacttt	gaaatcaatc	acttctattg	tgcagatccc	540
cctctcatcc	agattgcctg	tgggagagtg	cacatcaaag	aaatcacaat	gattgttatt	600
gctggaatta	acttcacata	ttccctctcg	gtggctcctca	tctcctacac	tctcattgta	660
gtagctgtgc	tacgcattgc	ctctgccgat	ggcaggagga	aggcgttctc	cacctgtggg	720
tcccacttga	cggctgtttc	tatgttttat	gggaccccc	tcttcattgta	tctcaggaga	780
cccactgagg	aatccgtaga	gcagggcaaa	atgggtggctg	tgttttacac	cacagtaatt	840
cctatgttga	atccccatgat	ctacagtctg	agaaataagg	atgtaaaaga	agcagtcaac	900
aaagcaatca	ccaagacata	tgtgagg				927

<210> 383

<211> 960

<212> DNA

<213> Unknown (H38g232 nucleotide)

<220>

<223> Synthetic construct

<400> 383

atgcttcata	ccaacaatac	acagtttcac	ccttcacact	tcctcgtagt	gggggtccca	60
gggctggaag	atgtgcatgt	atggattggc	ttccccctct	ttgcgggtgta	tctaacagcc	120
cttctaggga	acatcattat	cctgtttgtg	atacagactg	aacagagcct	ccaccaaccc	180
atgttttact	tcctagccat	gttggccggc	actgatctgg	gcttgtctac	agcaaccatc	240
cccaagatgc	tgggaatttt	ctggtttaat	cttgagagaga	ttgcatttgg	tgcctgcatc	300
acacagatgt	ataccattca	tatatgcact	ggcctggagt	ctgtggtact	gacagtcacg	360
ggcatagatc	gctatattgc	catctgcaac	cccctgagat	atagcatgat	ccttaccac	420
aaggtaatag	ccattctggg	catagtcatc	attgtcagga	ctttggtatt	tgtgactcca	480
ttcacatttc	tcaccctgag	attgcctttc	tgtggtgtcc	ggattatccc	tcatacctat	540
tgtgaacaca	tgggcttggc	aaagttagct	tgtgccagta	ttaatgttat	atatggattg	600
attgccttct	cagtgggata	cattgacatt	tctgtgattg	gattttccta	tgtccagatc	660
ctccgagctg	tcttccatct	cccagcctgg	gatgcccggc	ttaaggcact	cagcacatgt	720
ggctctcacg	tctgtgttat	gttggctttc	tacctgccag	ccctcttttc	cttcatgaca	780
caccgctttg	gccacaacat	ccctcattac	atccacattc	ttctggccaa	tctgtatgtg	840
gtttttcccc	ctgctcttaa	ctctgttatc	tatgggtgca	aaacaaaaca	gatacgagag	900
caggtaactta	ggataactcaa	ccctaaaagc	ttttggcatt	ttgaccccaa	gaggatcttc	960

<210> 384

<211> 936

<212> DNA

<213> Unknown (H38g233 nucleotide)

<220>

<223> Synthetic construct

<400> 384

atggaacaac	acaatctaac	aacggtgaat	gaattcattc	ttacgggaat	cacagatatac	60
gctgagctgc	aggcaccatt	atgtgcattg	ttcctcatga	tctatgtgat	ctcagtgtatg	120
ggcaatttgg	gcatgattgt	cctcaccaag	ttggactcca	ggttgcaaac	ccctatgtac	180
ttttttctca	gacatctggc	tttcatggat	cttggttatt	caacaactgt	gggacccaaa	240
atgttagtaa	attttgttgt	ggataagaat	ataatttctt	attatttttg	tgcaacacag	300
ctagctttct	ttctgtgtgt	cattggtagt	gaacttttta	ttctctcagc	catgtcctac	360
gacctctatg	tggcctctg	taaccctctg	ctatacacag	taatcatgtc	acgaagggtta	420
tgtcaggtgc	tggtagcaat	cccttacctc	tattgcacat	tcatttctct	tctagtccac	480
ataaagattt	ttactttatc	cttctgtggc	tacaacgtca	ttagtcatct	ctactgtgac	540
agtctccctt	tgttaccttt	gctttgttca	aatacacatg	aaattgaatt	gataattctg	600
atctttgcag	ctattgattt	gatttcatct	cttctgatag	ttcttttata	ttacctgtct	660
atccttgtag	ccattctcag	gatgaattct	gctggcagac	aaaaggcttt	ttctacctgt	720
ggagcccacc	tgacagtggg	catagtgttc	tatgggactt	tgcttttcat	gtacgtgcag	780

cccaagtcca	gtcattcctt	tgacactgat	aaagtggctt	ccatatttta	caccctgggt	840
atccccatgt	tgaatccctt	gatctatagt	ttacgaaaca	aagatgtaaa	atatgcccta	900
cgaaggacat	ggaataactt	atgtaatat	tttgtt			936

<210> 385

<211> 945

<212> DNA

<213> Unknown (H38g234 nucleotide)

<220>

<223> Synthetic construct

<400> 385

atgatgtggg	aaaactggac	aattgtcagt	gaatttgctt	tcgtgagctt	ctcagccctg	60
tccactgagc	ttcaggctct	actgtttctc	cttttcttga	ccattttactt	ggttacttta	120
atgggcaatg	tcctcatcat	cctgggcact	atagctgact	ctgcactaca	aagtcctatg	180
tacttcttcc	tcagaaactt	gtccttcctg	gagatagggt	tcaacttggg	cattgtgccc	240
aagatgctgg	ggaccctgat	cattcaagac	acaaccatct	ccttccttgg	atgtgccact	300
cagatgtatt	tcttcttctt	ttttggggct	gctgagtget	gcctcctggc	caccatggca	360
tatgaccgct	acgtggccat	ctgtgacccc	ttgcactacc	cagtcatcat	gggccacata	420
tcctgtgccc	agctggcagc	tgccctcttg	ttctcagggt	tttcagtggc	cactgtgcaa	480
accacatgga	ttttcagttt	ccctttttgt	ggccccaaca	gggtgaacca	cttcttctgt	540
gacagccctc	ctgttattgc	actgggtctgt	gctgacacct	ctgtgtttga	actggagggt	600
ctgacagcca	ctgtcccatt	cattctcttt	cctttcttgc	tgatcctggg	atcctatgtc	660
cgcatectct	ccactatctt	caggatgccg	tcagctgagg	ggaacatca	ggcattctcc	720
acctgttccg	cccacctctt	ggttgtctct	ctcttctata	gcactgccat	cctcacgtat	780
ttccgacccc	aatccagtgc	ctcttctgag	agcaagaagc	tgctgtcact	ctcttccaca	840
gtggtgactc	ccatgttgaa	ccccatcatc	tacagctcaa	ggaataaaga	agtgaaggct	900
gcactgaagc	ggcttatcca	caggaccctg	ggctctcaga	aacta		945

<210> 386

<211> 931

<212> DNA

<213> Unknown (H38g235 nucleotide)

<220>

<223> Synthetic construct

<400> 386

atggccaaaa	ccaataattc	agaagttact	gaattcatcc	tcttgggact	cacagacaat	60
ccagagctcc	aagccctttt	ttagggggat	ctttctagt	atcaatttaa	gtagtgtcat	120
gggtagcctt	gggttaatta	tgctaattca	tatcagtcct	cagcttcaca	cagctatgta	180
tttttttctc	agccacgtag	cttttgttta	tttttgctac	acctcctcta	tcacccctaa	240
cagcctagt	aacctcctcc	aagaaactaa	aagaatatcc	ttacctactt	gtgcctctca	300
gttgcatgtc	tttatcatgt	ttgtgggttg	tgacatgtat	gtgctctcag	ccatggcata	360
tgacaggat	gtggccatct	gcaacccttt	actctatagt	atcatcatga	acagaagggt	420
ctgtattcaa	atgggtggtaa	gtacatat	gtatggcttt	tctgtgagac	tcctacaggc	480
aattcttaca	ttccacttgt	ctttctgaga	ttcaaata	ataaataatt	cctattgtga	540
tgatgttccc	ctagcatgtc	taccctatca	taaaaacat	tacaaagatg	taaaagaact	600
gatattgttc	acacttgctg	gtttcaatac	acttttctcc	cttcttatca	tcctcatctc	660
ctacatatca	gtactgtctg	ccattctgag	aattaattca	gctgaaagta	gacaaaaggc	720
attttctact	tgtgactccc	acctgacttc	tatcatcata	ttttatggta	taattacctt	780
catgtatatg	cagtgaaaaa	caaataattc	tctggataca	gacaaaatag	cttctgtttt	840
ctgtattgtg	aaaattcctt	caatatatag	cctgaggaac	cacgaagtca	aagatgcttt	900
gaagatgatt	atggaaaatc	tatgtcttac	t			931

<210> 387

<211> 552

<212> DNA

<213> Unknown (H38g236 nucleotide)

<220>

<223> Synthetic construct

<400> 387

ttagttaagg	taaaaaaaaa	ctagaatatt	tttctctcaa	cagcatatca	ctttttcccc	60
acactttctg	taaataataa	caaatttcta	taaataataa	ataataattt	ctaggataaa	120
tttaatttac	atagtgaac	aagccattct	taggtatatt	ccttagttct	gtcttcgaaa	180
gtctgcatcc	tgtagcagc	tggcgtagtt	ggtgggatac	ttagcagaag	gattgtatgt	240
gtgtcctact	gtttcactgt	cctcctccag	gtccaatgcc	atcaatcact	ttttctgtaa	300
taaaccctta	gggcttggtc	tttcatgcta	caacatttat	atcagcacag	cagtcctgc	360
ctttgcgag	tttgagtgtc	gcattcattg	ccatatttgg	tcattcatgtt	ctcctggaca	420
tatatcctgg	ttgctatcaa	gaggatgtcc	tcagtgggga	gaaaagaatt	gtctatttgt	480
gtctcccacc	tgaaaactag	caccattttt	catacagccc	tcttttatgt	gtacttacag	540
cctgattttt	tt					552

<210> 388

<211> 963

<212> DNA

<213> Unknown (H38g237 nucleotide)

<220>

<223> Synthetic construct

<400> 388

atgtctgggg	acaacagctc	cagcctgacc	ccaggattct	ttatcttgaa	tggcgttcct	60
gggctggaag	ccacacacat	ctggatctcc	ctgccattct	gctttatgta	catcattgct	120
gtcgtgggga	actgtgggct	catctgcctc	atcagccatg	aggaggccct	gcaccggccc	180
atgtactact	tcctggccct	gctctccttc	actgatgtca	ccttgtgcac	caccatggta	240
cctaataatgc	tgtgcatatt	ctggttcaac	ctcaaggaga	ttgactttaa	cgctgcctg	300
gcccagatgt	tttttgtcca	tatgctgaca	gggatggagt	ctgggggtgct	catgctcatg	360
gccctggacc	gctatgtggc	catctgctac	cccttacgct	atgccaccat	ccttaccac	420
cctgtcatcg	ccaaggctgg	tcttgccacc	ttcttgagga	atgtgatgct	catcatccca	480
ttcaactctcc	tcaccaagcg	cctgccctat	tgcgggggga	acttcatccc	ccacacctac	540
tgtgaccata	tgtctgtggc	caaggtatcc	tgtggcaatt	tcaaggtaaa	tgctatttat	600
ggtctgatgg	ttgctctcct	gattgggtgtg	tttgatatct	gctgtatctc	tgtatcttac	660
actatgattt	tgcaggctgt	tatgagcctg	tcattcagcag	atgctcgtca	caaagccttc	720
agcacctgca	catctcacat	gtgttccatt	gtgatcacct	atgttgctgc	ttttttcact	780
tttttcactc	atcgttttgt	aggacacaat	atcccaaacc	acatacacat	catcgtggcc	840
aacctttatc	tgctactgcc	tcctaccatg	aacccaattg	tttatggagt	caagaccaag	900
cagattcagg	aagggtgaat	taaattttta	cttgagagaca	aggtagttt	tacctatgac	960
aaa						963

<210> 389

<211> 400

<212> DNA

<213> Unknown (H38g238 nucleotide)

<220>

<223> Synthetic construct

<400> 389

tgtttctgtg	gctttgctgt	tctcaccagt	tgctgtttct	gtctaacccc	ggagaggtaa	60
ataacaccct	gagaatggcc	ctaggctcac	acaggtttcc	cagttagcca	atcaagaaga	120
attacaaatg	gccacactat	cagccagagc	tgctgcctca	ctggagttcc	aaaacggaga	180
ggatctgctc	ccctgcaccc	tcaggcttgg	aaatgctgag	aaatgctaag	ccactggggg	240
ttcaattata	cctaatttaa	aacgagcaaa	gtagacttgc	cccccaagg	gttccacaaa	300
aaacttaaag	cctggcagct	cagccctgag	ttcatactgc	ttaaaagaca	ccgggggagg	360
aggtaagtga	tcagggtgaga	gaagttcgtt	ccccagagag			400

<210> 390

<211> 954

<212> DNA

<213> Unknown (H38g239 nucleotide)

<220>

<223> Synthetic construct

<400> 390

atgaagccaa caatacaaat ggcttcagga aatctcacat gggtgacgga gttcattctt	60
gtgggagtct cagatgatcc ggagctccag attccccctct tcctgggtctt cctgggtgctc	120
tatttgctga ccggtggcagg gaacctgggc atcatcaccc tcaccagtgt tgacctcaa	180
cttcaaacc ccatgtactt ttctctctga cacttgggta ttattaatct ttgcaattct	240
actgtcggtg cccctaaaat gctgggtaac ttcttgggta ccaagaaaac catatcatac	300
tatggatgtg cagcccaact ggggtggattc ttggttttca ttgtggctga gattttcacg	360
ctggctgcaa tggcctatga ccgctatgtg gctatttggg gccctctgct ctacgccgta	420
gtgggtgtctc caaagggtgtg tcgtctgctg gtgtccctca cataccttca gagtcttctc	480
acagcactga ctgtctcttc ctgtgtgttc tctgtgtcat actgttcttc caacattatc	540
aaccattttt actgtgatga tgtccctttg ctagcattgt cctgttctga tacctacatt	600
ccagaaacag cagtctttat cttttcaggg accaacttgc ttttctccat gatcggtgtt	660
ctgatatctt acttcaactt tgttattacc attttgagga tacgttcctc agaaggacga	720
caaaaagcct tttccacctg tgcttctcac atgtatagctg tgggtgtgtt ctatgggact	780
ctccttttca tgtatttgca accaaggagt aatcattcat tagatactga caaaatggct	840
tcgggtcttct acaccctggt gataccagtg ctgaaccctc taatctacag cctcaggaac	900
aagaacgtga aggatgcact aaagagggtc ctagataacc catgccgac actc	954

<210> 391

<211> 945

<212> DNA

<213> Unknown (H38g240 nucleotide)

<220>

<223> Synthetic construct

<400> 391

atgttggtccc caaaccacac catagtgcaca gaattcattc tcttaggact gacagacgac	60
ccagtgtctag agaagatcct gtttgggggtg ttcttggcga tctacctaat cacactggca	120
ggcaacctgt gcatgatcct gctgatcagg accaattccc aactgcaaac acccatgtat	180
ttcttctctg gtcacctctc cttttagagac atttgcattt cttccaatgt tactccaat	240
atgctgcaca atttctctc agaacagaag accatctcct acgctggatg cttcacacag	300
tgcttctctt tcatcgccct agtgatcact gagttttact tccttgcttc aatggcattg	360
gatcgctatg tagccatttg cagcccttta cattacagtt ccaggatgtc caagaacatt	420
tgcactctctc tggctactgt gccttacatg tatggcttcc ttaatgggct ctctcagaca	480
ctgctgacct ttcacttctc cttctgtggc tcccttgaaa tcaatcattt ctactgcgct	540
gatcctcctc ttatcatgct ggctgtctct gacaccctgt tcaaaaagat ggcaatgttt	600
gtagtgtcag gctttactct ctcaagctct ctcttcatca ttcttctgtc ctatcttttc	660
atttttgcag cgatcttcag gatccgttct gctgaaggca ggcacaaagc cttttctacg	720
tgtgcttccc acctgacaat agtcactttg ttttatggaa ccctcttctg catgtacgta	780
aggcctccat cagagaagtc tgtagaggag tccaaaataa ttgcagtctt ttatactttt	840
ttgagcccaa tgcagaacct attgatctat agcctacgga acagagatgt aatccttgcc	900
atacaacaaa tgattagggg aaaatccttt tgtaaaattg cagtt	945

<210> 392

<211> 939

<212> DNA

<213> Unknown (H38g241 nucleotide)

<220>

<223> Synthetic construct

<400> 392

atgcctatag ctaacgacac ccagttccat acttcttcat tctactgct gggtatocca	60
gggctagaag atgtgcacat ctggattgga ttcccttttt tctctgtgta tcttattgca	120

ctcctgggaa	atgctgctat	cttctttgtg	atccaaactg	agcagagtct	ccatgagccc	180
atgtactact	gcctggccat	gttggattcc	attgacctga	gcttgtctac	ggccaccatt	240
cccaaaatgc	tgggcatctt	ctggttcaat	atcaaggaaa	tatcttttgg	aggctacctt	300
tctcagatgt	tcttcatcca	tttcttcaat	gtcatggaga	gcacgtattt	ggtggccatg	360
gcctttgacc	gctacattgc	catttgcaaa	cctctttggt	acaccatgat	cctcaccagc	420
aaaatcatca	gcctcattgc	aggcattgct	gtcctgagga	gcttgtacat	ggcattcca	480
ctgggtgttc	tcctcttaag	gttgcccttc	tgtggacatc	gtatcatccc	tcatacttac	540
tgtgagcaca	tgggcattgc	ccgtctggcc	tgtgccagca	tcaaagtcaa	cattatgttt	600
ggtcttggca	gtatttctct	cttgttattg	gatgtgctcc	ttattattct	ctcccatatc	660
aggatcctct	atgctgtctt	ctgcctgccc	tcctgggaag	ctcgactcaa	agctctcaac	720
acctgtggct	ctcacattgg	tggtatctta	gccttttcta	caccagcatt	tttctcttct	780
tttacacact	gctttggcca	tgatattccc	caatatatcc	acattttctt	ggctaattcta	840
tatgtggttg	ttctccccc	cctcaatcct	gtaattctatg	gggtcagaac	caaacatatt	900
agggagacag	tgctgaggat	tttcttcaag	acagatcac			939

<210> 393

<211> 984

<212> DNA

<213> Unknown (H38g242 nucleotide)

<220>

<223> Synthetic construct

<400> 393

atgcatatct	tcaagtttgt	tctagatttc	aacatgaaga	atgtcactga	agttacctta	60
tttgtactga	agggcttcac	agacaatctt	gaactgcaga	ctatcttctt	cttcctgttt	120
ctagcaatct	acctcttcac	tctcatggga	aatttaggac	tgatttttagt	ggtcattagg	180
gattccacgc	tcacaaacc	catgtactat	tttctgagta	tgttgtcttc	tgtggatgcc	240
tgctattcct	cagttattac	cccaaatatg	ttagtagatt	ttacgacaaa	gaataaagtc	300
atttcattcc	ttggatgtgt	agcacagggtg	tttcttgctt	gtagtttttg	aaccacagaa	360
tgctttctct	tggctgcaat	ggcttatgat	cgctatgtag	ccatctacaa	ccctctctctg	420
tattcagtga	gcattgtcacc	cagagtctac	atgccactca	tcaatgcttc	ctatgtttgct	480
ggcattttac	atgctactat	acatacagtg	gctacattta	gcctatcctt	ctgtggagcc	540
aatgaaatta	ggcgtgtctt	ttgtgatata	cctcctctcc	ttgctatttc	ttattctgac	600
actcacacaa	accagcttct	actcttctac	tttgtgggct	ctatcgagct	ggtcactatc	660
ctgattgttc	tgatctccta	tggtttgatt	ctgttggcca	ttctgaagat	gtattctgct	720
gaagggagga	gaaaagtctt	ctccacatgt	ggagctcacc	taactggagt	gtcaatttat	780
tatgggacaa	tcctcttcat	gtatgtgaga	ccaagttcca	gctatgcttc	ggaccatgac	840
atgatagtgt	caatatttta	caccattgtg	attcccttgc	tgaatcccgt	catctacagt	900
ttgaggaaca	aagatgtaaa	agactcaatg	aaaaaatgt	ttgggaaaaa	tcagggttatc	960
aataaagtat	attttcatac	taaa				984

<210> 394

<211> 984

<212> DNA

<213> Unknown (H38g243 nucleotide)

<220>

<223> Synthetic construct

<400> 394

atgaatggag	ccaacagctc	cagcctgaca	ccaagatatt	tcattctcag	tggcgcttcct	60
gggctggaag	ctgcacacat	ctggatctcc	ctgcctttct	gcttcatgta	catcattgtt	120
gttttggga	actgtggact	tatatacctc	attagccatg	aggaggccct	gcaccaaccc	180
acctactact	tcctagactt	gctgtctctt	acagatgtta	ctggatgcac	ctcatttgtt	240
cccaatatgt	tatgtatttt	ttggtttggc	ctcaaggaaa	ttgactttaa	tgctgcctt	300
gtgcagatgt	ttttcatcca	catgctgaca	ggcatggagt	ctggggcgct	catgcttatg	360
gctctagacc	gctatgtggc	catttgctac	cctctacact	attccaccat	cttcaccaac	420
actgtaatta	ccaaagtggg	gcttgtcacc	ttcattcaaa	gtgtgttgct	tatgattcca	480
tttgctttcc	tgatcaagtg	tcttccctat	tgcaggggca	acctcatcca	ccacacctat	540
tttaacatat	gtctgtggcc	aaattatcct	gtggtaattg	ccagattaat	gccatctatg	600

gtctcatagc	tgccatattg	attggggggg	ttgacatgtt	ctgtatctcc	atgtcttaca	660
ccatgattat	ccgtgctgta	gtgaatttgt	catctgcaga	tgctgccaca	aagccttcag	720
tacctgtaca	gcacatatat	gtgctatttt	catcacttat	gtcccagcct	ttttcaactt	780
cttcactcac	cgctttgggg	gacacaccat	acctcatcat	gttcacattt	ttatagccaa	840
cctttacctg	atgctgcctc	ccaccttaaa	tccaattgtc	tatggagtga	agaccaagca	900
gatccgtgaa	ggagtgatca	aattgttttt	tagagagaaa	ggatatttta	gtatgacata	960
aatctatgat	atagaagtct	gaat				984

<210> 395

<211> 903

<212> DNA

<213> Unknown (H38g244 nucleotide)

<220>

<223> Synthetic construct

<400> 395

atggccagta	caaataatgt	gactgagtca	atgatcacca	gccttttcca	ggatccagca	60
gtgcagagag	tgtgctttgt	gggtgttctc	ccgtgtact	ggccatggag	gtgggcaatg	120
gcctcatcgt	tctgacggtc	agtatcagca	agagtctgca	ttcccctgtg	tacttcttcc	180
tgagctacct	gtcattgatg	gagatcagtt	acttcactgt	tgccctaaa	ttcatcacag	240
acttacttgc	caagattaaa	gccatctctc	tggagggtca	tctggctcag	atattcttgc	300
acttctttgg	catcccctgg	atctttctgc	tcccactgat	gaccaatgac	caatatatgg	360
ccaactgcaa	actttattac	tacacaacca	tcatgagctg	cctgtctgtc	accttctggg	420
ggctggttcc	tggctgaggg	gcataattca	ctcaatgggt	cagatccctg	tctctgtcca	480
attgttcttc	tgtggtccca	acatgattga	ccactcattc	tgtgacctcc	aggtcttatt	540
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agtatctgtc	ttcttcccta	tcttgggtgc	ctcttaatat	catcatccta	gtcaacttga	660
ggaaccattc	tgagagggg	aggtgcaaag	ccctctccac	ctgtgcctct	tatcttgtat	720
tttgaacttg	ccattttcct	ctacgtgtga	ctctctcca	cctttactaa	agataaactc	780
gtggctgtat	ttacgtggg	catcaccccc	atgtggaacc	ccttcatcta	cacgcttggg	840
aatgcagaga	tgaaaatcac	catgaggaga	ttgttgggca	ggacagtga	ctcaggaatg	900
gaa						903

<210> 396

<211> 972

<212> DNA

<213> Unknown (H38g245 nucleotide)

<220>

<223> Synthetic construct

<400> 396

gggagctgaa	agcaatgaaa	gtcttgacct	cctatctgtc	ttcctgactg	gcatcccagg	60
actggaggcc	caacatgggt	ggctctccat	ccctttcttc	accatgtaca	ttgtggccat	120
tgtgggaaac	atcctaatta	tggcagcagt	gcaggaagac	tctgccctac	atgagcccat	180
gtacttattt	ctctccatgt	tggctgtcac	tgagggtggc	gtctctgtgt	ctacactgct	240
actgttacag	gcattctttg	gtttgatgcc	cacagagttg	actttgatgg	ctgcctggcc	300
cagatgttct	tcattcacac	cttctcctgc	atggagtcag	gggtcctact	agccatgagc	360
tatgaccgct	ttgtagccat	ctacaacctc	ctgcgtata	cagccatcct	gacctgccc	420
cgtattatct	gcatgggtct	gggcattaca	ctgaagagt	tggcactcat	ggccccactt	480
ccaatccttt	tgaggcaact	gccctattgc	cacactaatg	tcctctcaca	ctcctactgc	540
ctccactcag	atctgatcca	gctgccttgt	gcagatacta	aactcaacag	catcctgggc	600
ttagccattg	ttctcgcaaa	tttcgggctg	gactcattgc	ttatcgtggg	ctcttatgtc	660
ttgattcttt	atacagtgat	gggcattgct	tctggagagg	gacggtgga	ggctctcaac	720
acatgtgtgt	cacatatttg	tgcagtgtct	atatattatg	tgccatgat	tgggggtgtct	780
gtgatgcac	gtgctgccaa	acatgcttct	cccattgtcc	acacacttat	gtctagcatc	840
tgccttttgg	tgccacctgt	acttaatccc	atcatctata	gtgttaagac	ccagacaata	900
agacagggaa	ttctcacctt	gttttctctg	aagagggaat	tgctctgaat	cactgcaagg	960
agtcaggaac	tg					972

<210> 397
 <211> 874
 <212> DNA
 <213> Unknown (H38g246 nucleotide)

<220>
 <223> Synthetic construct

<400> 397
 acttttgttta ttatttcaaa atttcaaggc tgctgaaagg taggtcttta tacacagtca 60
 ctttattttgc tagctgagta. ttttcatcgg gggcaactga tgaaaaatgtt gacttccact 120
 aacctaagcc tgtccgttgt tactatcgta tcttccagtt caacgtcagg gaaatagttt 180
 ttggtgcttt ccttgtttat atacagatgt ttatgactta tctatgcact ggcctggaat 240
 ctgggggtact gataatcctg gccatagacc actatgtcgt aattcgcaat ccactgagat 300
 ataccatgat tctcatgaac aatgtggttag ccaccctagg aagtcatgat aattagatct 360
 ttaatcttta tcatcccttt tgagtttctc atcttgctgt tgtcattctg tgctgcccac 420
 atcatccccc acaccaaagt tgagcacatg ggcattgccc atctttcctg tgccagtgtc 480
 agagccaata atatgttttg gatggttgcc tttttgtggg atttattgac cttattgcaa 540
 ttggtttctc ctaatgaaag aaactacaca ctgtttcact taccaccatg gaatggccag 600
 ttcgaggctc tcaatacctg tggttcccat gtgttgcatt ctcatcttct acatcccagt 660
 attttttttc tgatacactg cttggtgaaa gcacccctgc tatattcgta tattttctggc 720
 caatgtatat acggttggtc tacctgtatt caaccctgtt atctatggga tcaggaaaaa 780
 acagatccca gactagggtg tagacctaaa gacatttgat gatcagtcac ttctagtcac 840
 gatgatatat atattgggat atatatgcaa atat 874

<210> 398
 <211> 936
 <212> DNA
 <213> Unknown (H38g247 nucleotide)

<220>
 <223> Synthetic construct

<400> 398
 atggatgaag ccaatcactc tgtggtctct gagtttgtgt tcctgggact ctctgactcg 60
 cggaagatcc agctcctcct ctctcctttt ttctcagtggt tctatgtatc aagcctgatg 120
 ggaaatctcc tcatttgtgt aactgtgacc tctgaccctc gtttacagtc ccccatgtac 180
 ttctctgctgg ccaacctttc catcatcaat ttggtatttt gtctctccac agctcccaag 240
 atgatttatg accttttcag gaagcacaag accatctctt ttgggggctg tgtagttcag 300
 atcttcttta tccatgcagt tgggggaact gagatggtgc tgctcatagc catggctttt 360
 gaccgatatg tggccatatg taagcctctc cactacctga ccatcatgaa cccacaaagg 420
 tgcattttgt ttttagtcat ttcttggtat ataggtatta ttcactcagt gattcagttg 480
 gcttttggtg tagacctgct gttctgtggc cctaataaat tagatagttt cttttgtgat 540
 ctctctcgat ttatcaaact ggcttgcata gagacctaca cattgggatt catggttact 600
 gccaatagtg gatttatttc tctggcttct tttttaattc tcataatctc ttacatcttt 660
 attttggtga ctgttcagaa aaaatcttca ggtgtatat tcaaggcttt ctctatgctg 720
 tcagctcatg tcatttgtgt gggtttgtgc ttggggccat taatcttttt ctatattttt 780
 ccatttccca catcacatct tgataaattc cttgccatct ttgatgcagt tatcactccc 840
 gttttgaatc cagtcactta tacttttaga aataaagaga tgatggtggc aatgagaaga 900
 cgatgctctc agtttgtgaa ttacagtaaa atcttt 936

<210> 399
 <211> 503
 <212> DNA
 <213> Unknown (H38g248 nucleotide)

<220>
 <223> Synthetic construct

<400> 399
 aagcagtcca gtggtgacag tgggaaccag accacctggc tgatcctagt gggcttcggg 60

gagctgcaat	acctgggctt	ccttcccttc	actctcttcc	tggccatcta	tgtggtgaca	120
gttggggcaa	tgcctcctc	atgctggctg	tggcctctag	tcggacactg	cacccaccaa	180
tgtacttctt	cctctgccac	ttctccctgc	tggagattgg	ctatacctcc	aacgtcatac	240
tatggctggt	gcagagtttc	ttggagggga	aggaagtcac	ctctctagtc	agctgtctgg	300
ctcagttcta	cgtgttttcc	tcgctggctg	cagctgagtg	cctcctgcta	tctgccgtgt	360
cctatgactg	ttacttggcc	atctgctgcc	cccttcaacta	tcctgccttg	atgagcacct	420
ggttttgtca	ctgcctggcc	gctggtgctt	ggttcagtg	cttcttctcc	tctgccttca	480
ctatggccct	ggcagcacct	ctg				503

<210> 400

<211> 963

<212> DNA

<213> Unknown (H38g249 nucleotide)

<220>

<223> Synthetic construct

<400> 400

atgctaacac	tgaataaaac	agacctaata	ccagcttcat	ttattctgaa	tggagtccca	60
ggactggaag	acacacaact	ctggatttcc	ttcccattct	gctctatgta	tgttgtggct	120
atggtaggga	attgtggact	cctctacctc	attcactatg	aggatgccct	gcacaaaccc	180
atgtactact	tcttggccat	gctttccttt	actgaccttg	ttatgtgctc	tagtacaatc	240
cctaaagccc	tctgcatctt	ctggtttcat	ctcaaggaca	ttggatttga	tgaatgcctt	300
gtccagatgt	tcttcatcca	caccttcaca	gggatggagt	ctgggggtgct	tatgcttatg	360
gccctggatc	gctatgtggc	catctgctac	cccttacgct	attcaactat	cctcaccaat	420
cctgtaattg	caaagggttg	gactgccacc	ttcctgagag	gggtattact	cattattccc	480
tttacttttc	tcaccaagcg	cctgccctac	tgcagaggca	atatacttcc	ccatacctac	540
tgtgaccaca	tgctgttagc	caaattgtcc	tgttggaatg	tcaagggtcaa	tgccatctat	600
ggtctgatgg	ttgccctcct	gattgggggc	tttgacatac	tgtgtatcac	catctcctat	660
accatgatc	tcggggcagt	ggtcagcctc	tcctcagcag	atgctcggca	gaaggccttt	720
aatacctgca	ctgccacacat	ttgtgccatt	gttttctcct	atactccagc	tttcttctcc	780
ttcttttccc	accgcttttg	ggaacacata	atccccctt	cttgccacat	cattgtagcc	840
aatattttatc	tgtccttacc	acccactatg	aaccctattg	tctatgggg	gaaaaccaa	900
cagatacgag	actgtgtcat	aaggatcctt	tcaggttcta	aggataccaa	atcctacagc	960
atg						963

<210> 401

<211> 945

<212> DNA

<213> Unknown (H38g250 nucleotide)

<220>

<223> Synthetic construct

<400> 401

atgacaacac	accgaaatga	caccctctcc	actgaagctt	cagacttcct	cttgaattgt	60
tttgtcagat	ccccagctg	gcagcactgg	ctgtccctgc	ccctcagcct	ccttttcttc	120
ttggccgtag	gggccaacac	caccctcctg	atgaccatct	ggctggaggc	ctctctgcac	180
cagccccgtg	actacctgct	cagcctcctc	tcctgtctgg	acatcgtgct	ctgcctcact	240
gtcatcccca	aggctctgac	catcttctgg	tttgacctca	ggcccatcag	cttccctgcc	300
tgcttctctc	agatgtacat	catgaattgt	ttcctagcca	tggagtcttg	cacattcatg	360
gtcatggcct	atgatcgta	tgtagccatc	tgccaccac	tgagatatcc	atcaatcatc	420
actgatcact	ttgtagtcaa	ggctgccatg	tttattttga	ccagaaatgt	gcttatgact	480
ctgcccatcc	ccatccttcc	agcacaactc	cgttattgtg	gaagaaatgt	cattgagaac	540
tgcattctgtg	ccaatatgtc	tgtttccaga	ctctcctgcg	atgatgtcac	catcaatcac	600
ctttaccaat	ttgctggagg	ctggactctg	ctaggatctg	acctcatcct	tatcttcttc	660
tcctacacct	tcattctgcg	agctgtgctg	agactcaagg	cagaggggtgc	cgtggcaaag	720
gccctaagca	catgtggctc	ccacttcatg	ctcatcctct	tcttcagcac	catccttctg	780
gtttttgtcc	tcacacatgt	ggctaagaag	aaagtctccc	ctgatgtgcc	agtcttgctc	840
aatgttctcc	accatgtcat	tcctgcagcc	cttaacccca	tcatttacgg	ggtgagaacc	900
caagaaatta	agcagggaat	gcagaggttg	ttgaagaaag	ggtgc		945

<210> 402
 <211> 906
 <212> DNA
 <213> Unknown (H38g251 nucleotide)

<220>
 <223> Synthetic construct

<400> 402

ttgagctcta	tgtgtctcac	cattgtgatg	cattgtgaat	tcttcctcat	ggacttgact	60
gatgatcctc	agcttcatcc	cacettctct	gccctcttcc	tccccatcta	tgtagtcatg	120
gtgatggaaa	cctgggcctc	cttgccctca	ttgtggcag	tccccaattc	ctcaccacca	180
tgtatttctt	cctcagcaac	tggtcctctg	ttgacttctg	ttattcttca	gtaacagtcc	240
caaaaaatc	aatgggggtc	ttttctgact	gccaaagtct	ctccttctct	ggttgcatgg	300
cccagttaag	ctgcttttaa	aatatttgct	gacaccgagt	tcttcctcct	ggcctccatg	360
gtctattacc	gctaagaggc	cgtctgcaat	cctctgctct	accatatcac	catgtcccca	420
aagctctgct	tgcatgtggt	ggccaccagc	tatgaacatg	gtgctcccta	gtagcacaat	480
ctttcatctg	atcttctgta	agtcgtgcc	atcattcatt	aattctgtta	tttcctcccc	540
caccgaggct	ttaaaaaact	tcctgctctg	acatgcaagg	ccttcaactt	cttacctttg	600
cctctagtag	ctttaatgta	tcgggtgccc	ggacaatctt	ccttgctctc	atttaattat	660
gagaatgccc	tcggtttgag	gcaaacactt	gtgcttccca	cctgacagca	gtcagcctgt	720
gctatggaac	caagtggttc	cttcacctgc	acctatcctt	gaagtgttca	ccagacagag	780
atatgctggg	ctctgtttta	cacagtggct	attctcatgc	tcaaccccat	ggtccaaagt	840
ctgaggaaca	aggatgtgaa	gaaaacattt	gggacttcc	catgaagggt	tacaattcct	900
ctcctt						906

<210> 403
 <211> 972
 <212> DNA
 <213> Unknown (H38g252 nucleotide)

<220>
 <223> Synthetic construct

<400> 403

atgcctctat	ttaattcatt	atgctgggtt	ccaacaattc	atgtgactcc	tccatctttt	60
attcttaatg	gaatacctgg	tctggaaaga	gtacatgtat	ggatctccct	cccactctgc	120
acaatgtaca	tcatcttcc	tgtggggaat	cttgggtctg	tgtacctcat	ttattatgag	180
gagtccttac	atcatccgat	gtattttttt	tttggccatg	ctctctccct	cattgacctc	240
cttacctgca	ccaccactct	acccaatgca	ctctgcatct	tctggttcag	tctcaaagaa	300
attaacttca	atgcttgctt	ggcccagatg	ttctttgttc	atgggttcac	aggtgtggag	360
tctgggggtg	tcatgtcat	ggctctagac	cgctatgtag	ccatttgcta	ccctttgcgt	420
tatgctacca	cactcaccaa	ccctatcatt	gccaaggctg	agcttgccac	cttctgagg	480
ggtgtattgc	tgatgattcc	tttccattc	ttggttaagc	gtttgccttt	ctgccaaagc	540
aatattatct	cccatacgta	ctgcgaccac	atgtctgtag	ttaaagctatc	ttgtgccagc	600
atcaagggtca	atgtaatcta	tgggtctaag	gttgctctcc	tgattggagt	gtttgacatt	660
tggtgtatat	ctttgtctta	cactttgatc	ctcaaggcag	cgatcagcct	ctcttcatca	720
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tatgttccag	cattcttcac	tttctttgcc	caccgttttg	ggggacacac	aattccccct	840
tctcttcaca	tcattgtggc	taatctttat	cttcttcttc	ccccaactct	aaaccctatt	900
gtttatggag	taaagacaaa	acagatacgc	aagagtgtca	taaagttctt	ccagggtgat	960
aaggggtgcag	gt					972

<210> 404
 <211> 821
 <212> DNA
 <213> Unknown (H38g253 nucleotide)

<220>
 <223> Synthetic construct

<400> 404

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gagagaaatc ccagtgtagc agaaaagtgc cttcaaggga tgactgattc ctctcaccat      60
tatcttttagc ttaactccct ctcttcaggc tgtaatcct cttgtatact atcattacga      120
tagggaattt gggcacggtc attctcattg ggatcagtct cggtttatat gtctgtctcg      180
cctagatttc tgctattcac tttttccatg ctccagagtc tagtaaaatg tttttgaagt      240
acagtgtctg ccttctcttt ctggagtctt gaagcacaga ttaacttctt cagcatcttg      300
tgtatcacag agttctttcc cttggccaca atggcctatg atgacaatgt tgccacttgt      360
gaacctttat tccacccttt caccagtttg agactcaact ggcatttggt tgagaaaaac      420
tgtatcttag agccttcacc tcagccctcc cctcaactct tccgttccac ctccccttct      480
tcaattccca ctgtgtctca cttcagtgac attactttct gggccaagtt gtctcttgaa      540
acatgactcc caactttaaa ctccctgatt tctctaactc caatgtgaac ttagtaagcc      600
tgtgtgtgct aacctctgct tgctacccca tcattttaag gtcattatca tcccataact      660
aatctgaaaa acaaattatt gataatcatt ttttttcaga attccactca ttgtctctta      720
ttttctgttc agatgaaaat gtttattaaa ccatttgagg tatcactgac tagttcatta      780
aaagtaaaaa ttgtgtacat attcccttaa tgcagattct t                                821

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<210> 405

<211> 945

<212> DNA

<213> Unknown (H38g254 nucleotide)

<220>

<223> Synthetic construct

<400> 405

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atgtcttctc tcaatgtcac tgaacccac ctctcttctt tctgtttggt taggaattcc      60
aggattggaa gctgcacaac gctggctagg ctttcccttc tgtgttgat atctgattgc      120
tcttgttgga aatcttatca ttctatttgt tatctggact gataaaaacc ttcaccaacc      180
catgttctac tttctggcca tgctgtcagt catgacctga gtctttctac atctactatc      240
cccaagatgt tgggcatctt ctggttcagc cttcaggagt tgtgctttgg gtgctgtggt      300
gctcaagtct tttttatcca ttttttttgc agtcatggag agcattgtac ttcttgtcat      360
gggattttgat cgctatgttg ctatttgcaa ccccttcagg tagaccaaga tcctcaccaa      420
cagaattact ggtgtgattg ctatggttgt ggttcttaga agcttatgta tgattgctcc      480
catcattttt ctctcatga ggctgcctta ctgtggacat agaatcatcc cttataccta      540
ttgtgagcac atgggagtggt ctggtctggc ttgtgccagc atcagtgatca atgtctctca      600
tggctcttggg aatattttta tcttgtttct ggatatgttt cttatcatca tctcctatgc      660
tagaatttta tgcacagtct ttcacctccc ttcccaagag gccacactga aggcctctaa      720
tacctgttag tcccatatct gtgtcatctt agcatttttt ggcccagctc tcttctcctt      780
tctcactcat cgctttggtc atggcatccc acagtatata catattctcc tggctaattct      840
ctatatatag tcattccccc tgctcttaac ccagtcattt atggagttag gaccaagcaa      900
atccaggagc gggtagaaaag tctctttact aaaaattgat tgaat                                945

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<210> 406

<211> 970

<212> DNA

<213> Unknown (H38g255 nucleotide)

<220>

<223> Synthetic construct

<400> 406

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gtggaaaatt caccatggt gactgacttc atctttctcg gcatgacaga taactctcag      60
cttgaagtcc tgctatttgg agtctttctt attgcttaca tcatcactgt gttggagaat      120
ctaggccttg tggttctgat cagagtcagc tccgcctcc acaccccatg tactttttcc      180
tctctaatac gtcttctctt gatgtctggt tctcttccat tacaattcca cagaatttag      240
cacatttggt ttctaagctg cagtatgttt ctttcttttt cccgtataac ttaaagtggc      300
ttgtttgtaa tctttgcctc tgctgaatgc aattttttta acttgcatgg cctatgaccg      360
ctttactgcc atctgtcacc cactgttcta ccacattacc atgtcaagag gccattatct      420
tttcttggtg gcaggatgct accttgggtg gttagttaag atggtcactg tgacaacttc      480
catcacacaa ctatcgcttt gtcaacatg tgctctcctt gccttcttct gtgacattcc      540

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ctcattgttg	gtactgggtt	gctcagatcc	ttggatcacc	tcccgatctt	gggtggtggc	600
tgtgggggat	tcaccctgg	cacctctgtt	gtgggtgatcc	ttgtctccta	catgtcttcc	660
ctcatgacta	tcctaggaat	tcccttagct	tctggaaaac	agagagcctt	ctccacctgt	720
gcctccact	tgactgctgt	tagcctgtac	tatgaaacaa	ctatgtacac	ttacttggcc	780
gcctcgcgac	atggatccgg	ggcaggaaat	cagattgtgt	cagtatttta	tacaatgggtg	840
atccccatgt	taaatcctct	catctatagt	ttgagaaatg	aggaagtgaa	agttggcccta	900
tgaaaaacat	tgagacatag	tccttaatat	tctattgagt	gtctcaaaaa	tgcaaaatat	960
tctgtgaaga						970

<210> 407

<211> 934

<212> DNA

<213> Unknown (H38g256 nucleotide)

<220>

<223> Synthetic construct

<400> 407

tggttgatg	aaaaaaaaa	agattctaac	gtgacagAAC	ttgttcttct	gggcctatca	60
tcttcttggg	agctgcagct	atttctctta	ttactatttt	tgttttttta	cattgctatt	120
gtcttgggaa	acctcttgat	agtggtaaca	gtgcaagccc	atgctcatct	gctccaatct	180
cctatgtatt	attttttagg	tcatctctct	ttcattgacc	tatgcctaag	ctgtgttact	240
ctgccaaga	tgtagggga	tttctacag	cagggcaaga	gcatctcttt	ttcaggatgc	300
ctggcccaga	tctacttct	ccactttcta	ggagccagtg	agatgttttt	gctgacagtt	360
atggcctatg	acaggatgt	tgccatctgt	aaccctttgc	gctaccttat	aagtcagaa	420
ccccagcta	tgcttttgg	tggttcttgc	ctgctgggtg	gggggtttta	tccactctat	480
catgcaggtc	atactagtca	tccagctgcc	tttctgtggc	cccaatgaac	tggacaactt	540
ctactgtgat	gtcccacagg	tcatcaagct	ggcctgcag	gacacctatg	tggtagaggt	600
gctgatgata	gccaacagtg	gtctgctctc	tcttgtctgc	ttcttgggtc	tactattctc	660
ttatgctgtc	atcctgatca	ccctgagaac	acacttcggc	cagggccaga	acaagttcct	720
ctctacctgt	gcttctcacc	tgacagtgg	cagcctgac	ttcatgccat	gtatattcat	780
ctatttgagg	cctttctgca	gcttctctgt	ggataagata	ttctccatgt	ttacacaggt	840
gatgacacct	atggttagcc	ccctcatcta	cacactcaga	aatgctgata	tgaagacagc	900
tatgaagaag	ctgaggataa	aaccatgtga	catt			934

<210> 408

<211> 954

<212> DNA

<213> Unknown (H38g257 nucleotide)

<220>

<223> Synthetic construct

<400> 408

atgatgggtg	atcccaatgg	caatgaatcc	agtgtacat	acttcacct	aataggcctc	60
cctgggttag	aagaggctca	gttctgggtg	gccttcccat	tgtgtccct	ctaccttatt	120
gctgtgctag	gtaacttgac	aatcatctac	attgtgcgga	ctgagcacag	cctgcatgag	180
cccatgtata	tatttctttg	catgctttca	ggcattgaca	tcctcatctc	cacctcatcc	240
atgccccaaa	tgctggccat	cttctgggtc	aattccacta	ccatccagtt	tgatgcttgt	300
ctgtacaga	tgtttgccat	ccactcctta	tctggcatgg	aatccacagt	gctgtgtggc	360
atggcttttg	accgctatgt	ggccatctgt	cacccactgc	gccatgccac	agtacttacg	420
ttgcctcgtg	tcacaaaaat	tggtgtggct	gctgtgtgtc	ggggggctgc	actgatggca	480
cccttccctg	tttcatcaa	gcagctgcc	ttctgceget	ccaatatcct	ttcccatccc	540
tactgcctac	accaagatgt	catgaagctg	gcctgtgatg	atatccgggt	caatgtcgtc	600
tatggcctta	tcgtcatcat	ctccgccatt	ggcctggact	cacttctcat	ctccttctca	660
tatctgttta	ttcttaagac	tgtgttgggc	ttgacacgtg	aagcccaggc	caaggcattt	720
ggcacttgcg	tctctcatgt	gtgtgctgtg	ttcatattct	atgtaccttt	cattggattg	780
tccatgggtg	atcgcttttag	caagcggcgt	gactctccgc	tgcccgatcat	cttggccaat	840
atctatctgc	tggttccctc	tgtgtctaac	ccaattgtct	atggagtga	gacaaaggag	900
attcgacagc	gcacccctcg	acttttccat	gtggccacac	acgcttcaga	gccc	954

<210> 409
 <211> 959
 <212> DNA
 <213> Unknown (H38g258 nucleotide)

<220>
 <223> Synthetic construct

<400> 409
 atgtcttcca gactaatgaa tgtgttcagc atggaaacta tcaattttgt tagctgcctt 60
 atcctcatgg gctttccctc aagcccagaa atgcagctcc tctacttcgg tctcttctca 120
 gtagcctata ctctcaccce gatgggaaat gcagccattg tctgtgctgt gtggtaggac 180
 cagcaccttc acactccat gtacaccctc ttgggaaatt tctctctcct ggaaatatgt 240
 tatgttactg caactaaact gctggccaac ttcctctcca caagcaagtc catctcatc 300
 atgagttgtt ttgcacagtt ctactctctc tctttggggt atgatgaggg cttcttcctt 360
 tgcacacagg cctttgacag gtatcttgcc atctgccgcc ctctacgtta tccatgcac 420
 atgactaaac aagtatgcac tggcctcatc atttttgcat ggatcatgtg ctttgtaac 480
 ttctaaactc tgggtgattct catttcacag ctatcctact gtggcccaaa tattatcaac 540
 cattttattt gtgatcccggt cccattgaag atgctgtcct gttctgaaga catcatcatc 600
 acccagctca ttactccac attcaattct gtcttcataa ttggcacctt tctctttatc 660
 ctttgttcct atgctctgggt gattctgggt ataatacggg tgccttcaga ggctggcaaa 720
 cgaaaagctt tctccacttg tgcctctcat ttggcagttg tcaccttatt ttatggctct 780
 atcatgggta tgtatgtag tcttgatca gcacaccag taaaaatgaa aaaatcatta 840
 ccttgttctt ttctgtgata acaccactct gtaatcctct aatataatag ctacaggaaca 900
 aagagatgaa agattatctg aggaaaatct tcaggactgg aaaagatgtt aataaaata 959

<210> 410
 <211> 926
 <212> DNA
 <213> Unknown (H38g259 nucleotide)

<220>
 <223> Synthetic construct

<400> 410
 atgctgaata caacctcagt cactgaattt ctcttttgg gagtgacaga cattcaagaa 60
 ctgcagcctt ttctcttcgt tgttttcctt accatctact tcatcagtggt ggctgggaat 120
 ggagccattc tgatgattgt catctctgat cctagactcc attcccctat gtattttctc 180
 ctgggaaacc tgtcctgcct ggacatctgc tactccagcg taacactgcc aaaaatgctg 240
 cagaacttcc tctctgcaca caaagcaatt tctttcttgg gatgcataag ccaactccat 300
 ttcttccact tcctgggcag cacagaggcc atgttggttg ccgtgatggc atttgaccgc 360
 tttgtggcta tttgcaagcc acttcgctac actgtcatta tgaacctca gctctgtacc 420
 cagatggcca tcacaatctg gatgattggt tttttccatg ccctgctgca ctccctaattg 480
 acctctcgct tgaacttctg tggttctaac cgtatctatc acttcttctg tgatgtgaag 540
 ccattgctaa agctgagctt aatcagtggc tgctcagtag tgtcacaggg acaatcgcca 600
 tgggcccctt ctttctcaca ttactctcct atttctacat tatcacccat ctcttcttca 660
 agactcattc ttttagcatg ctccgcaaag cactgtccac ttgtgcctcc cacttcatgg 720
 tagttattct tttgtatgca cctgttctct tcacctatat tcatcatgcc tcagggacct 780
 ccatggacca ggaccggatc actgccatca tgtatactgt ggctactcca gtactaaacc 840
 cactgatcta cactttgagg aacaaggaag tgaaaggggc ctttaataga gcaatgaaaa 900
 ggtggctttg gcctaaagaa atctttg 926

<210> 411
 <211> 994
 <212> DNA
 <213> Unknown (H38g260 nucleotide)

<220>
 <223> Synthetic construct

<400> 411

atggaaagcg	agaacagaac	agtgataaga	gaattcatcc	tccttcgttt	gacccagttt	60
cgagatat	agctcctggt	ctttgtgcta	gttttaatat	tctacttctt	catcctccct	120
ggaaattttc	tcattatttt	caccataagg	tcagaccctg	ggctcacagc	ccccctctat	180
ttatctctgg	gcaacttggc	cttcctggat	gcacccctact	ccttcattgt	ggctcccagg	240
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ctctttttct	tgcacttctt	tggaggaggg	gagggattac	tccttggtgt	gatggccttt	360
gaccgctaca	tcaccatctg	cctgcctctg	cagtattcaa	ctgtcatgaa	ctctagagcc	420
tgctatgcaa	tgatgttggc	tctgtggctt	gggggttttg	tccactccat	tatccagggtg	480
gtcctcatca	tccgcttgcc	ttttgtggc	ccaaaccagc	tggacaactt	cttctgtgat	540
gtccgacagg	tcacaaagct	ggcttgacc	gacatgtttg	tgggtgagct	tctgatggtc	600
ttcaatagtg	gcctgatgac	actcatgtgc	tttctgggac	ttctggcctc	ctatgcagtc	660
attctttgtc	gcatacgagc	gtcttcttct	gaggcaaaaa	acaaggccat	gtccacatgc	720
accacccata	tcattgttat	attcttcatg	tttggacctg	gcattctcat	ctacacgtgc	780
cccttcaggg	ctttccagc	cgacaagggtg	gtttctctct	tccacacagt	gattcttctt	840
ttgttgaatc	ctgtcattta	tacccttcat	aaccagggaag	tgaaagcttc	catgaaaaag	900
gtgtttaata	aacacatagc	ctgaaaaagg	gcaaaaaaaa	aaagaagaaa	aatagactgt	960
agaattttat	ctgaaattga	tttgtttatt	tcca			994

<210> 412

<211> 945

<212> DNA

<213> Unknown (H38g261 nucleotide)

<220>

<223> Synthetic construct

<400> 412

atggaaattg	tctccacagg	aaacgaaact	attactgaat	ttgtcctcct	tggcttctat	60
gacatccctg	aactgcattt	cttgtttttt	attgtattca	ctgctgtcta	tgtcttcate	120
atcataggga	atatgctgat	tattgtagca	gtggtagct	cccagaggct	ccacaaacct	180
atgtatat	tcttggcgaa	tctgtccttc	ctggatattc	tctacacctc	cgcagtgatg	240
ccaaaaatgc	tggagggctt	cctgcaagaa	gcaactatct	ctgtggctgg	ttgcttgctc	300
cagttcttta	tcttcggctc	tctagccaca	gctgaatgct	tactgctggc	tgcatggga	360
tatgaccgct	acctggcaat	ttgctaccca	ctccactacc	cactcctgat	ggggccaga	420
cgggtacatg	ggctgggtgt	cacaacctgg	ctctctggat	ttgtggtaga	tggactgggt	480
gtggccctgg	tggcccagct	gaggttctgt	ggccccaacc	acattgacca	gttttactgt	540
gactttatgc	ttttcgtggg	cctggcttgc	tcggatccca	gagtggctca	ggtgacaact	600
ctcattctgt	ctgtgttctg	cctcactatt	ccttttggac	tgattctgac	atcttatgcc	660
agaattgtgg	tggcagtgct	gagagttcct	gctggggcaa	gcaggagaag	ggctttctcc	720
acatgctctc	cccacctagc	tgtagtgacc	acattctatg	gaacgctcat	gatcttttat	780
gttgaccctc	ctgctgtcca	ttcccagctc	ctctccaagg	tcttctccct	gctctacact	840
gtggtcaccc	ctctcttcaa	tcctgtgatc	tataccatga	ggaacaagga	ggtgcacag	900
gcacttcgga	agattctctg	tatcaaacaa	actgaaacac	ttgat		945

<210> 413

<211> 936

<212> DNA

<213> Unknown (H38g262 nucleotide)

<220>

<223> Synthetic construct

<400> 413

atgagtgc	aaacacctccat	ggtgactgag	tttcttcttc	tgggttctc	ccacctggcc	60
gacctccagg	gcttgctctt	ctctgtcttt	ctcactatct	acctgctgac	cgtggcaggc	120
aatcttctca	ttgtggtgct	ggtctccact	gatgctgcc	tccagtccc	tatgtacttc	180
ttcttgcgca	ccctctcggc	cttgagatt	ggctatacgt	ctgtcacggg	ccccctgcta	240
cttcaccacc	tccttactgg	cggcgccac	atctctcgct	ctggatgtgc	tctccagatg	300
ttcttcttcc	tcttctttgg	cgccacggag	tgtgctctcc	tggcagccat	ggcctatgac	360
cgctatgcag	ccatctgtga	acccctccgc	taccactgc	tgtgagcca	cgggtgtgt	420
ctacagctag	ctgggtcggc	gtgggcctgt	ggggtgctgg	tggggtggtg	ccacacctt	480

ttcatcttct	ctttgccctt	ctgcggcccc	aataccatcc	cgcagttctt	ctgtgagatc	540
cagcctgtcc	tgcagctggt	atgtggagac	acctcgctta	atgaactgca	gattatcctg	600
gcaacagccc	tcctcatcct	ctgccccctt	ggcctcatcc	tgggctccta	cgggcgtatc	660
ctcgtttacca	tcttccggat	cccatctggt	gcgggcgcgc	gcaaggcctt	ctccacctgc	720
tcctcccacc	tgatcgtggt	ctccctcttc	tatggcaccg	cactctttat	ctatatctgc	780
cctaaggcca	gctacgatcc	ggccactgac	cctctggtgt	ccctcttcta	tgctgtggtc	840
acccccatcc	tcaaccccat	catctacagc	ctgcggaaca	cagagggtcaa	agctgcccta	900
aagagaacca	tccagaaaac	ggtgcctatg	gagatt			936

<210> 414

<211> 948

<212> DNA

<213> Unknown (H38g263 nucleotide)

<220>

<223> Synthetic construct

<400> 414

atgggttaacc	aaagctcccc	catgggcttc	ctccttctg	gcttctctga	acaccagca	60
ctggaaagga	ctctctttgt	ggttgtcttc	acttctacc	tcttgaccct	ggtgggcaac	120
acactcatca	tcctgctgtc	tgtactgtac	cccaggctcc	actctccaat	gtactttttc	180
ctctctgacc	tctccttctt	ggacctctgc	tttaccacaa	gttgtgtccc	ccagatgctg	240
gtcaacctct	ggggcccaca	gaagaccatc	agcttctctg	gatgctctgt	ccagctcttc	300
atcttctctg	ccctggggac	cactgagtgc	atcctctga	cagtgtggc	ctttgaccga	360
tacgtggctg	tctgccagcc	cctccactat	gccaccatca	tccaccccg	cctgtgctgg	420
cagctggcat	ctgtggcctg	ggttatgagt	ctggttcaat	cgatagtcca	gacaccatcc	480
accctccact	tgcccttctg	tcccaccag	cagatagatg	actttttatg	tgagggtcca	540
tctctgatcc	gactctctg	tggagatacc	tcctacaatg	aaatccagtt	ggctgtgtcc	600
agtgtcatct	tcgtggtgt	gcctctcagc	ctcatccttg	cctcttatgg	agccactgcc	660
caggcagtgc	tgaggattaa	ctctgccaca	gcattggaga	aggcctttgg	gacctgtccc	720
tcccattctca	ctgtggtcac	cctcttctac	agctcagtca	ttgctgtcta	cctccagccc	780
aaaaatccgt	atgcccaagg	gaggggcaag	ttctttggtc	tcttctatgc	agtgggcact	840
ccttacttta	accctctcgt	atacaccctg	aggaacaagg	agataaagcg	agcactcagg	900
aggttactag	ggaaggaaag	agactccagg	gaaagctgga	gagctgct		948

<210> 415

<211> 954

<212> DNA

<213> Unknown (H38g264 nucleotide)

<220>

<223> Synthetic construct

<400> 415

atgaagagcg	aactgaacag	gaattactca	gaggtgacag	agttttattct	gctgggattc	60
agaacatcgc	cagaagcaca	gattctctta	ttcttcctgt	tcttgcttat	ctacatgggc	120
attgtgttga	gaaatctcag	catgttagtt	gtcattgaaa	tagactccag	acttcacaca	180
cctgtgtatt	tctttctcag	aaatttgtcc	tatttggatc	tccgctactc	cacagttatt	240
gcttccaaaa	ctgactactt	tattttccaa	ggaaaagaaa	atttcttaca	atggttgagc	300
aacacagttg	tttttctttg	ctctctttgt	tgggactgaa	ggtttttttc	tggatatgat	360
ggcatatgat	cgcttctcag	ctatttgttc	acctttcttc	tatactgtat	gtatgtctca	420
gcaagcttgt	gtttgtttgg	tggttggctc	ctctatctgt	ggatgcatca	actccatgat	480
acaacaggt	tttaccttca	gtttgcattt	ctgtggagaa	aacagattag	agcacttttt	540
ctgtgatgtc	tcagtcatga	tcaagatctc	atgtattgac	atccttgtga	atgaggtagt	600
actgtttatt	ctctctgtc	tcataccacc	caccacaact	gtcattctgg	cttcctatgt	660
gcatactctc	tcactgtcc	tgaagattct	ctcaaccacc	ggcagaagga	agactttctc	720
cacttgcagc	tctcacatca	ctgtggtgag	tttattctat	ggaactgtat	tcttcatgta	780
tgcccaacct	ggggccatct	ccaaagagca	aggttatagt	tgtattctaa	actcttgtca	840
tcctctgtt	aaatatctga	tttatagtct	aagaaatagg	tgcaaaatgc	tttgaaaagg	900
acattgataa	gaaaaatatc	ttttcattgg	cctctagcca	tctataaaac	tata	954

<210> 416
 <211> 531
 <212> DNA
 <213> Unknown (H38g265 nucleotide)

<220>
 <223> Synthetic construct

<400> 416
 atgagcccaa gaatgtgcct ttcatttctg gctgttgcct ggacccttgg tgtcagtcac 60
 tccctgttcc aactggcatt tcttgttaat ttacccttct gtggccctaa tgtgttggac 120
 agctttctact gtgaccttcc tcggcttctc agactagcct gtaccgacac ctacagattg 180
 cagttcatgg tcaactgtta cagtgggttt atctgtgtgg gtactttctt catacttcta 240
 atctcctaca tcttcatect gtttactgtt tggaaacatt cctcaggtgg ttcattcaag 300
 gccctttcca ctctttcagc tcacagcaca gcggtccttt tgttctttgg tccacccatg 360
 tttgtgtata catggccaca ccctaattca cagatggaca agtttctggc tatttttgat 420
 gcagttctca ctcttttct gaatccagtt gtctatacat tcaggaataa ggagatgaag 480
 gcagcaataa agagagtatg caaacagcta gtgatttaca agaagatctc a 531

<210> 417
 <211> 965
 <212> DNA
 <213> Unknown (H38g266 nucleotide)

<220>
 <223> Synthetic construct

<400> 417
 atggaagcag aaaaccttac agaattatca aaatttctcc tcctgggact ctacagatgat 60
 cctgaactgc agcccgtcct ctttgggctg ttctgttcca tgtacctggg cagcgtgctg 120
 gggaacctgc tcatcattct ggccgtcagc tctgactccc acctccacac ccccatgtac 180
 ttcttctctc ccaacctgtc ctttgttgac atctgtttca tctccaccac agtccccaag 240
 atgctagtga gcatccaggc acggagcaaa gacatctcct acatgggggtg cctcactcag 300
 gtgtattttt taatgatgtt tgctggaatg gatactttcc tactggccgt gatggcctat 360
 gaccggtttg tggccatctg ccaccactg cactacacgg tcatcatgaa cccctgcctc 420
 tgtggcctcc tgggtctggc atcttgggtc atcattttct ggttctccct ggttcatatt 480
 ctactgatga agaggttgac cttctccaca ggcactgaga ttccgcattt cttctgtgaa 540
 ccggctcagg tcctcaagggt ggctgtctct aacaccctcc tcaataacat tgtcttgat 600
 gtggccacgg cactgtctggg tgtgttctct gtagctggga tcctcttctc ctactctcag 660
 attgtctcct ccttaatggg aatgtcctcc accaagggca agtacaagc cttttccacc 720
 tgtggatctc acctctgtgt ggtctccttg ttctatggaa caggacttgg ggtctatctg 780
 agttctgtctg tgaccattc ttccagagc agtccaccg cctcagtgat gtacgccatg 840
 gtcaccccca tgctgaaccc cttcatctac agcctgagga acaaggatgt gaagggggcc 900
 ctggaagac tcctcagcag ggccgactct tgtccatgac aaatcagggc ctcagaacta 960
 agagg 965

<210> 418
 <211> 967
 <212> DNA
 <213> Unknown (H38g267 nucleotide)

<220>
 <223> Synthetic construct

<400> 418
 tacacagagc cagagaatct cacaggtgtc ttagaattcc tgctcctggg actcccagat 60
 gatccagaac tgcagcccgt cctcttttggg ctgttctctg ccatgtacct ggtcatgggtg 120
 ctggggaacc tgctcatcat tctggccgtc agctctgact cccatctcca cagccccatg 180
 tacttcttcc tctccaacct gtcttggct gacatcgggt ttgcctctac tactgtcccc 240
 aagatgattg tggacatcca ggctcatagt agactcatct cttacgtggg ctgctgact 300
 cagatgtctt ttttgatctt tttcgcattg atggaaagtc tgctcctgat tgtgatggcc 360

tatgaccggt	tctgtggccat	ctgtcacccc	ctgcactacc	aagtcacat	gagcccacga	420
ctctgtgggt	tcttagtctt	gggtgtcttt	tttcttagcc	ttttggactc	tcagctgcac	480
aatttgattg	tgttacaact	tacctgcttc	aacgatgtgg	aaatctctaa	ttttttctg	540
tgacccttct	taacttctca	agctggcctg	ttctgacacc	tccattaata	acatgggtgt	600
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cacctgcagc	tctcacctgt	cagttgtttg	cttactttat	ggaacagccc	ttggagggtg	780
cctcagttca	gctgtgtccc	tttctccag	gaagggtgca	gtggcctcag	taatgtacat	840
ggtggtcacc	cccatgtcga	accccttcat	ctacagcctg	agaaacaggg	acattcaaag	900
tgccctgcag	aggctgcacg	gcagaataat	gtaatctcct	tatctgttgc	atcttttttg	960
tagtatt						967

<210> 419

<211> 924

<212> DNA

<213> Unknown (H38g268 nucleotide)

<220>

<223> Synthetic construct

<400> 419

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ccacacaccg	agcagctgct	atttatcgta	ttattgggtg	tctacctggg	cactgtgctt	120
ggaaatctgc	ttctaatactc	ccttggtcat	gttgactccc	aacttcacac	acccatgtat	180
ttttttctct	gcaacttgct	tctggctgac	ctctgtttct	ctaccaacat	agttcctcag	240
gcactagtcc	acctgctttc	cagaaagaag	gtcattgcat	tcacactttg	cgcagctcga	300
cttctctttt	tcctcatttt	tgggtgtacc	cagtgcgccc	ttcttgagc	gatgtcctat	360
gatcgctatg	ttgcaatctg	caatcctctg	cgttacctg	acatcatgac	ctggaaagtg	420
tgtgtccagc	tggcaacagg	atcatggacc	agtggcattc	tgggtgtctg	ggtagacacc	480
accttcacac	tgaggctacc	ctaccgaggg	agtaacagca	ttgctcattt	cttttgtgag	540
gcccctgcac	tattgatctt	agcatccaca	gacacccatg	catcagagat	ggccattttt	600
cttacggggg	ttgtgattct	cctcatacct	gtttttctga	ttctggatc	ctatggccgt	660
atcatagtaa	ctgtgggtcaa	gatgaagtca	actgtgggga	gtctcaaggc	attttctacc	720
tgtggctccc	acctcatggt	ggtcatactt	ttttatggat	cagcaattat	cacttacatg	780
acacccaagt	cttccaaaca	gcaggaaaaa	tcggtgtctg	ttttctatgc	aatagtgact	840
cccatgctga	atccctcat	ctatagcctg	agaaacaagg	atgtgaaggc	agctctgagg	900
aaagtagcca	caaggaattt	ccca				924

<210> 420

<211> 954

<212> DNA

<213> Unknown (H38g269 nucleotide)

<220>

<223> Synthetic construct

<400> 420

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ttctcttccc	tacctactga	aatacagtca	ttgctcttcc	tgacatttct	aactatctat	120
ttggttactc	tgaagggaaa	cagcctcatc	attctgggta	ccctagctga	ccccatgcta	180
cacagcccca	tgtacttctt	cctcagaaac	ttatctttcc	tggagattgg	cttcaacctg	240
gtcattgtgc	ccaaaatgct	ggggaccctg	cttgcccagg	acacaacccat	ctccttctct	300
ggctgtgcca	ctcagatgta	tttcttcttc	ttctttgggg	tagctgaatg	cttctcctg	360
gctaccatgg	catatgaccg	ctatgtggcc	atctgcagtc	ccttgactca	cccagtcac	420
atgaacaaaa	ggacacgggc	caaactggct	gctgcttctt	ggttcccagg	ctttcctgta	480
gctactgtgc	agaccacatg	gctcttcagt	ttccattctt	gtggcaccaa	caagggtgaac	540
cacttcttct	gtgacagccc	gcctgtgctg	aagctggctt	gtgcagacac	agcactgttt	600
gagatctacg	ccatcgctcg	aaccattctg	gtggctcatga	tcccctgctt	gctgatcttg	660
tgttcctata	ctcgctattg	tgtgtctatc	ctcaagatcc	catcagctaa	agggaagcat	720
aaagccttct	ctacgtgctc	ctcacacctc	cttggtgtct	ctcttttcta	tatatcttct	780
agcctcacct	acttctggcc	taaatcaaat	aattctcctg	agagcaagaa	gttggttatca	840

ttatcctaca ctgttgtagac tcccatgttg aacccccatta tctacagctt gagaaatagc 900
gaggtgaaga atgccctcag caggaccttc cacaaggctc tagccctcag aaac 954

<210> 421
<211> 780
<212> DNA
<213> Unknown (H38g270 nucleotide)

<220>
<223> Synthetic construct

<400> 421
gcccaccttt ccttcctgga cctcagtttc accaccagct ccatcccccga gctgctctac 60
aaccttaatg gatgtgacaa gaccatcagc tacatgggct gtgccatcca gctcttcttg 120
ttcctgggtc tgggtgggtg ggagtgctg cttctggctg tcatggccta tgaccggtgt 180
gtggctatct gcaagccccct gactacatg gtgatcatga accccagggt ctgccggggc 240
ttgggtgcag tgacctggag ctgtgggggt gccaaactcct tggccatgtc tcctgtgacc 300
ctgcgcttac ccgctgtgg gcaccacgag gtggaccact tcctgcgtga gatgcccgcc 360
ctgacccgga tggcctgcgt cagcactgtg gccatcgaag gcaccgtctt tgtcctggcg 420
gtgggtgttg tgcgtcccc cttggtgttt atcctgctct cttacagcta cattgtgagg 480
gctgtgttac aaattcgggt agcatcagga aggagaagg ccttcggcac ctgcggctcc 540
catctcactg tggctccct tttctatgga aacatcatct acatgtacat gcagccagga 600
gccagttctt cccaggacca gggcatgttc ctcagctctt tctacaacat tgtcaccccc 660
ctcctcaatc ctctcatcta caccctcaga aacagagagg tgaagggggc actgggaagg 720
ttgcttctgg ggaagagaga gctaggaaag gagtaaaggc atctccacct gacttcactt 780

<210> 422
<211> 985
<212> DNA
<213> Unknown (H38g271 nucleotide)

<220>
<223> Synthetic construct

<400> 422
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tgcagcccat cctctttggg ctgttctctg ccatgtgcct ggtcatgggt ctggggaacc 120
ttctcatcat cctggccgtc agctctgact cccacctcca cccccccag tactttttcc 180
tctccaacct gtccctgggt gacatcgggt tccccccac cactgtcccc aagatgattg 240
tggacatcca gtctcacagc agagtcactt cctatgcggg ctgcctgact cagatatctc 300
tttttctgtg ttttggtatg atggaagaca tgcttctgag tgtgatgggt tatgaccggt 360
ttgtggccat ctgtcaccct ctggattatc cagtcacat gaaccatgt ttctgtgggt 420
tcttggtttt gttgtctttt ttttctcagt ctttttagact tccagctgca caattggatt 480
gccttacaaa ttacctgctt caaggatgtg gaaattccca gtttcttctg tgaccttctt 540
caactcccc accttgccgt ttgtgacacc ttcaccaaca acatagtcac gtatttctct 600
gctgccatac ttggttttct tcccatctcg gggactcttt ctcttactat aaaattgttt 660
cctccattct gaaggtttca tcatcagggt ggaagtataa agccttctcc acctgtgggt 720
ctcacctgtc agttgtttgc ttattttatg gaacagccct tggagggtac ctcagttcag 780
acatgtcctc ttatcccaga aaggggtcag tggcttcagt gatgtacaca gtggctgcgcc 840
ccatgctgaa ccggttcacg tacagcctga gaaaaaggga cattaaaagt gccctgcagc 900
agctgcatgg cagaatagtc taatctcatg atcttattat cggttccatt ctttagcatg 960
ggttgaaaaa ggcagcaagg tcaaaa 985

<210> 423
<211> 963
<212> DNA
<213> Unknown (H38g272 nucleotide)

<220>
<223> Synthetic construct

<400> 423

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ggtctggaac	aatttcattt	gtggctctca	ctccctgtgt	gtggcttagg	cacagccaca	120
attgtgggca	atataactat	tctggttgtt	gttgccactg	aaccagtctt	gcacaagcct	180
gtgtaccctt	ttctgtgcat	gctctcaacc	atcgacttgg	ctgcctctgt	ctccacagtt	240
cccaagctac	tggctatctt	ctggtgtgga	gccggacata	tatctgcctc	tgcttgcttg	300
gcacagatgt	tcttcattca	tgccttctgc	atgatggagt	ccactgtgct	actggccatg	360
gcctttgatc	gctacgtggc	catctgccac	ccactccgct	atgccacaat	cctcactgac	420
accatcattg	cccacatagg	ggtggcagct	gtagtgcgag	gctccctgct	catgctccca	480
tgtcccttcc	ttattgggcg	tttgaacttc	tgccaaagcc	atgtgatcct	acacacgtac	540
tgtgagcaca	tggctgtggt	gaagctggcc	tgtggagaca	ccaggcctaa	ccgtgtgtat	600
gggctgacag	ctgcactggt	ggtcattggg	gttgacttgt	tttgacattg	tctctcctat	660
gccctaagtg	cacaagctgt	ccttcgcctc	tcaccccatg	aagctcggtc	caaggcccta	720
gggacctgtg	gttcccatgt	ctgtgtcatc	ctcatctctt	atacaccagc	cctcttctcc	780
ttttttacac	accgcttttg	ccatcacgtt	ccagtccata	ttcacattct	tttggccaat	840
gtttatctgc	ttttgccacc	tgctcttaat	cctgtggtat	atggaggtta	gaccaaacag	900
atccgtaaaa	gagttgtcag	ggtgtttcaa	agtgggcagg	gaatgggcat	caaggcatct	960
gag						963

<210> 424

<211> 982

<212> DNA

<213> Unknown (H38g273 nucleotide)

<220>

<223> Synthetic construct

<400> 424

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cctgtcctcg	cgccactaca	ggtactattg	tttgcccttt	tgtgtctggc	ctatgtgttg	120
gtgctgactg	agaacacact	catcattatg	gcaattagga	accattccac	cctccacaaa	180
cccattgact	tttttctagc	taatatgtcc	tttctggaga	tctggtatgt	actgttccact	240
attcccaaga	tgcttgctgg	ctttgttgga	tccaaacagg	atcatggaca	gctaattctcc	300
tttgagggat	gcatgacaca	gctctacttt	ttccttggct	tgggctgcac	tgagtgtgtc	360
cttctcgctg	ttatggccta	tgatcgctat	atggccatct	gctatcctct	ccactaccca	420
gtcattgtca	gtggccggct	gtgtgtgcag	atggctgctg	gctcttgggc	tggagggttt	480
ggcatctcca	tgggtcaaagt	ttttcttatt	tctggcctct	cttactgtgg	ccccaacatc	540
atcaaccact	ttttctgtga	tgtctctcca	ttgtccaacc	tctcatgcac	tgatatgtcc	600
acagcagagc	ttacagattt	catcctggcc	atttttatct	ttctagggcc	actctctgtc	660
actggggcct	cctatgtggc	cattactggt	gctgtgatgc	acataccttc	ggctgctgga	720
cgctataagg	ccttttccac	ctgtgcctct	catctcactg	ttgtgataat	cttctatgca	780
gccagtatct	tcatctatgc	tgggccaag	gcaactctcag	cttttgacac	caacaagttg	840
gtctctgtac	tgtatgctgt	cattgtacca	ttgtccaatc	ccatcattta	ctgcctgcgc	900
aatcaagagg	tcaagagagc	cctatgctgt	actctgcacc	ctgtaccagc	accaggatcc	960
tgaccccaag	aaagctagca	ga				982

<210> 425

<211> 936

<212> DNA

<213> Unknown (H38g274 nucleotide)

<220>

<223> Synthetic construct

<400> 425

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ccagaactac	agccgttcat	atttgggctg	ttcctgtcca	tgtacctggt	gacggtgctg	120
ggaaacctgc	tcatcatcct	ggccatcagc	tctgactccc	acctccacac	ccccatgtac	180
ttcttctctc	ccaacctgtc	ctggggttgac	atctgtttca	gcacttgcat	cgtccccaag	240
atgctggtga	acatccagac	cgagaacaaa	gccatctcct	acatggactg	cctcacacag	300
gtctatttct	ccatgttttt	tcctattctg	gacacgctac	tcctgaccgt	gatggcctat	360

gaccggtttg	tggtgtctg	ccaccctctg	cactatatga	tcacatgaa	ccccacctc	420
tgtggcctcc	tggtttttgt	cacctggctc	attgggtgca	tgacatccct	cctccatatt	480
tctctgatga	tgcatcta	cttctgtaaa	gattttgaaa	ttccacattt	tttctgcgaa	540
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attgcttcat	ccataaggaa	gatgtcctca	tctgggggaa	aacaaaaagc	actttccacc	720
tgtgggtctc	acctctccgt	cgtttcttta	ttttatggga	caggcattgg	ggtccacttc	780
acttctgcgg	tgactcactc	ttcccagaaa	atctccgtgg	cctcggtgat	gtacactgtg	840
gtcaccceca	tggtgaacc	cttcatctac	agcctgagga	acaaggatgt	gaagggagcc	900
ctggggagtc	tcctcagcag	ggcagcctct	tgtttg			936

<210> 426

<211> 960

<212> DNA

<213> Unknown (H38g275 nucleotide)

<220>

<223> Synthetic construct

<400> 426

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ggcatggagg	acaaacacag	atggatatct	atccccctct	cctccatgta	tttcattatg	120
gtgcttggga	actgcacat	cctcctcacc	atctccacag	agcgtccct	gcacaaaccc	180
atgttctctg	tcctctgtct	gttggccctc	acagacctgg	gcatgtctac	aaccaccatt	240
cccaagggtg	tgtgcatttt	ctggtttggc	cagagtga	tcagctatga	aggatgcctg	300
gttcagctgt	tcttcaccca	ctccatctct	gccatgcagt	cagctgtcct	gatgaccatg	360
gcctttgacc	actatgtggc	catctgcaag	cccttgctgt	atgccaccat	cctttccaat	420
agttgcactg	gactcattgg	cttagtgagt	ttgggtgagag	ctatcctctt	tattctcccc	480
atgcccattc	tccttcagca	aatgccctat	catgccaatc	gtgtcatccc	caccacctcc	540
tgtgagcaca	tggtctgtgt	gaagatgggt	tgtgtagata	ctacagtcaa	caggatatat	600
ggcctggttg	tggtctgtgt	gggtgtgtgg	tagatctctc	agctattgct	tcattcttatg	660
tgctaatacat	ccaggctata	atgcatctct	cttctaagga	agcccaccac	aaagcagtc	720
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ttctcgctca	ccgctttggc	caaggcatcc	cacccatgt	ccacatcatt	cttggcaacc	840
tttacttctc	tgtacctcca	atgctcagtc	ctataattta	tggagtga	actaaggagt	900
tctgggacaa	agtgacaaa	tagggttgct	ggaaagaaga	accacaacc	actgaccatg	960

<210> 427

<211> 948

<212> DNA

<213> Unknown (H38g276 nucleotide)

<220>

<223> Synthetic construct

<400> 427

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agcaatggcc	tactgtctct	ggctatcacc	atggaagccc	ggctccacat	gcccattgtac	180
ctcctgcttg	ggcagctctc	tctcatggac	ctcctgttca	catctgttgt	cactcccaag	240
gcccttgctg	actttctgct	cagagaaaac	accatctcct	ttggaggctg	tgcccttcag	300
atgttctctg	cactgacaat	gggtgggtgct	gaggacctcc	tactggcctt	catggcctat	360
gacaggatg	tggtcatttg	tcatcctctg	acatacatga	ccctcatgag	ctcaagagcc	420
tgtgtgctca	tggtggccac	gtcctggatc	ctggcatccc	taagtgcctt	aatatatacc	480
gtgtatacca	tgactatcc	cttctgcagg	gcccaggaga	tcaggcatct	tctctgtgag	540
atcccacact	tgtgaaggt	ggcctgtgct	gatacctcca	gatatgagct	catggtatat	600
gtgatgggtg	tgaccttctc	gattccctct	cttctgtgta	tactggcctc	ctatacacia	660
attctactca	ctgtgtctca	tatgccatca	aatgagggga	ggaagaaagc	ccttgtcacc	720
tgctcttccc	acctgactgt	gggtgggatg	ttctatggag	ctgccacatt	catgtatgtc	780
ttgcccagtt	ccttccacag	caccagacaa	gacaacatca	tctctgtttt	ctacacaatt	840
gtcactccag	ccctgaatcc	actcatctac	agcctgagga	ataaggaggt	catgctgggccc	900

ttgaggaggg tcctgggaaa atacatgctg ccagcacact ccacgctc

948

<210> 428

<211> 936

<212> DNA

<213> Unknown (H38g277 nucleotide)

<220>

<223> Synthetic construct

<400> 428

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ccggagctgc	agcccatcct	cttcattgctg	ttcctgtcca	tgtacctggc	cacaatgctg	120
gggaacctgc	tcatcatcct	ggccgtcaac	tctgactccc	acctccacac	ccccatgtac	180
ttcctcctct	ctatcctgtc	cttggctgac	atctgtttca	cctccaccac	gatgccaag	240
atgctgggtga	acatccaggc	acaggctcaa	tccatcaatt	acacaggctg	cctcacccaa	300
atctgctttg	tcctgggtttt	tgttggattg	gaaaatggaa	ttctgggtcat	gatggcctat	360
gatcgatttg	tggccatctg	tcacccactg	aggtacaatg	tcattcatgaa	ccccaaactc	420
tgtgggctgc	tgccttctgct	gtccttcacg	gttagtgctc	tggatgctct	gctgcacacg	480
ttgatgggtgc	tacagctgac	cttctgcata	gacctggaaa	ttccccactt	tttctgtgaa	540
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gtcaccacca	tgctgaacct	actcatttac	agcctgagaa	acaaggacat	gttgaaggct	900
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<210> 429

<211> 984

<212> DNA

<213> Unknown (H38g278 nucleotide)

<220>

<223> Synthetic construct

<400> 429

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attcacagct	ggcaacactg	gctatctctg	cccctggcac	tactgtatct	ctcagcactt	120
gctgcaaaaca	ccctcatcct	catcatcatc	tggcagaacc	cttctttaca	gcagcccatg	180
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aagatcctgg	ccatcttctg	gtttgatgcc	aagggtatta	gcctccctga	gtgctttgct	300
cagatttatg	ccattcactt	ctttgtgggc	atggagtctg	gtatcctact	ctgcatggct	360
tttgatagat	atgtggctat	ttgtcacctt	cttcgctatc	catcaattgt	caccagttcc	420
ttaatcttaa	aagctaccct	gttcattggtg	ctgagaaatg	gcttatttgt	cactccagtg	480
cctgtgcttg	cagcacagcg	tgattattgc	tccaagaatg	aaattgaaca	ctgcctgtgc	540
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ttggttctgg	catggcttgg	aatggggagt	gatctaagtc	ttattatact	gtcatatatt	660
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gtgactcatc	tgacagagat	gaaggctact	ttgattccag	ttctacttaa	tgtgttgcac	840
aacatcatcc	ccccttcctt	caaccctaca	gtttatgcac	ttcagaccaa	agaacttagg	900
gcagccttcc	aaaaggtgct	gtttgccctt	acaaaagaaa	taagatctta	gagaccttct	960
ccatgatgta	catgaacctc	agct				984

<210> 430

<211> 947

<212> DNA

<213> Unknown (H38g279 nucleotide)

<220>

<223> Synthetic construct

<400> 430

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agcaatggtc	tgctgctcct	ggccatcacc	atagaagccc	ggctccacat	gcccattgtac	180
ctcctgcttg	ggcagctctc	tctcatggac	ctcctgttca	catctgttgt	cactcccaag	240
gccttgcgga	ctttctgcgc	agagaaaaca	ctatctcctt	tggaggctgt	gcacttcaga	300
tgttcctggc	actgacaatg	ggtagcgctg	aggacctcct	actggccttc	atggcctatg	360
acaggatatg	ggccatttgt	catcctctga	aatacatgac	cctcatgagc	ccaagagtct	420
gctggatcat	ggtggccaca	tcctggatcc	tggcatccct	gattgctata	ggacatacca	480
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tcctattcac	tgtgcttcgt	atgccatcaa	atgaggggag	gaagaaagcc	cttgtcacct	720
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tgcccagttc	cttccacagc	cccaaacaag	acaacatcat	ctctgttttc	tacacaattg	840
tcactccagc	cctgaatcca	ctcatctaca	gcctgaggaa	taaggaggtc	atgcgggcct	900
tgaggagggt	cctgggaaaa	tacatactgc	tggcacattc	cacgctc		947

<210> 431

<211> 897

<212> DNA

<213> Unknown (H38g280 nucleotide)

<220>

<223> Synthetic construct

<400> 431

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tacctcttag	ctctcagtgc	caacatcctt	atcctgatca	tcatacaaa	agaggcagca	120
ctgcaccage	ctatgtacta	tttcttgggc	atcttggcta	tggcagacat	aggcctggct	180
accaccatca	tgctaagat	tttggccatc	ttatgggtca	atgctaagac	catcagtctc	240
ctggagtgtc	ttgctcagat	gtatgccata	cattgctttg	tggccatgga	atcaagtacc	300
tttgtctgca	tggctattga	tagatatgta	gccatttgct	gaccgctacg	atatccatca	360
atcatcactg	aatcttttgt	tttcaaagca	aatgggttca	tggcactgag	aaacagcctg	420
tgtctcatct	cagtgcctct	gttggctgcc	cagaggcatt	actgctccca	gaatcaaatt	480
gagcactgtc	tttgttctaa	ccttggagtc	actagcctat	cttgtgatga	tcgaagaatc	540
aatagcatta	accaggctct	tttggcttgg	acactcatgg	gaagtgcact	gggtttgatt	600
attttatcat	atgctctaat	actttactct	gtcctgaagc	tgaactctcc	agaagctgca	660
tccaaggcct	taagtacctg	cacctccac	ctcatcttaa	tccttttctt	ctacacagtc	720
atcattgtga	tttccattac	tcgtagtaca	ggaatgagag	ttccccttat	tccagttcta	780
cttaatgtgc	tacacaatgt	cattccccct	gcctgaacc	ccatgggtata	tgcactcaag	840
aacaaggaac	tcaggcaagg	cttatacaag	gtacttagac	tgggagtga	gggcacc	897

<210> 432

<211> 980

<212> DNA

<213> Unknown (H38g281 nucleotide)

<220>

<223> Synthetic construct

<400> 432

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tgttgactga	gaacacactc	atcattatgg	caagtaggaa	ccattccacc	ctccacaaac	180
ccatgtactt	tgttctagct	aatatgtcct	cctctggaga	tctggtatgt	cactgtcact	240
attcccaaga	tgcttgctgg	ctttgttggg	tccaacagg	atcatggaca	gctaactctc	300
tttgagggat	gcatgacaca	gctctacttt	ttccttggct	tgggctgcac	tgagtgtgtc	360
cttctcgctg	ttatggccta	tgatcgctat	atggccatct	gctatcctct	ccactaccca	420

gtcattgtca	gtggccggct	gtgtgtgcag	atggctgctg	gctcttgggc	tggagggttt	480
ggcatctcca	tgggtcaaagt	ttttcttatt	tctggcctct	cttactgtgg	ccccaacatc	540
atcaaccact	ttttctgtga	tgtctctcca	ttgtctcaacc	tctcatgcac	tgatattgtcc	600
acagcagagc	ttacagattt	catcctggcc	atttttatte	ttctagggcc	actctctgtc	660
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tctctgtact	gtatgctgtc	attgtaccat	tgtctaatcc	catcatttac	tgccctgcgc	900
atcaagaggt	caagagagcc	ctatgctgta	ctctgcacct	gtaccagcac	caggatcctg	960
acccaagaa	agctagcaga					980

<210> 433

<211> 998

<212> DNA

<213> Unknown (H38g282 nucleotide)

<220>

<223> Synthetic construct

<400> 433

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ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	tcagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcat	tgggtgtgtg	gagatgggtg	tgtcatagc	catggccttt	360
gacagttatg	tggccctatt	aagccccctc	actatctgac	cattatgagc	ccaagaatgt	420
gcctttcatt	tctggctgtt	gcctggaccc	ttgttgcag	tcactccctg	ttccaactgg	480
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ttaacagtgg	gtttatctgt	gtgggtactt	tcttcatact	tctaactcct	tacgtcttca	660
tcctgtttac	tgtttgaaa	cattcctcag	gtggttcac	caaggccctt	tccactcttt	720
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ttctgaatcc	agttgtctat	acattcagga	ataaggagat	gaaggcagca	ataaagagag	900
tatgcaaaca	gctagtgtat	tacaagaaga	tctcataaat	gatacaataa	gcccttctcg	960
ttaaactatga	tatggcttta	tgtttctttc	tttgatat			998

<210> 434

<211> 840

<212> DNA

<213> Unknown (H38g283 nucleotide)

<220>

<223> Synthetic construct

<400> 434

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cccatgtact	tcttcctctg	caacttctcc	ctcatggaga	tgggtggcac	ctccactgtg	120
gtacatagga	tgctggcaga	cctgtatccc	actcacaaga	ccatgtccct	ggccaaatgc	180
ctaaccacgt	cttctcttta	cttctccctg	ggctctgcca	acttccctgat	actcatggtc	240
atggcctttg	atcgctacgt	ggccatctgc	cacccccctg	gctacccaac	catcacgaat	300
ggtccagtgt	gtgtgaagct	ggtggtggcc	tgttgggtgg	ttggtttcct	ctccattgtc	360
tctcccacac	tgagaaaaac	acgactctgg	ttctgtggcc	ctaaccatcat	cggccactac	420
ttctgtgact	ctgccccgct	gctcaagctt	gcctgctctg	acaccgcca	cattgagcgc	480
atggacctct	tctgtccct	gctctttgtg	ctgaccacca	tgtgtcttat	catcctctcc	540
tacatcctca	ttgtggctgc	agtgtgcac	atcccttcc	cctctggatg	ccagaaggcc	600
ttctccacct	gtgcctctca	cctcacagt	gtggttctgg	gctatggcag	tgccatcttc	660
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actgcaatgg	taaccctttt	cctcaacccc	ttcatcttca	ccttccggaa	tgagaagggtc	780
aaggagggtca	ttgaggatgt	gactaaaagg	atcttccctg	gagaccacgc	agcctgtagg	840

<210> 435
 <211> 939
 <212> DNA
 <213> Unknown (H38g284 nucleotide)

<220>
 <223> Synthetic construct

<400> 435
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 ccagagggtcc aactagtcct atttggtata tttctatcct tctatttggt catcctacca 120
 ggaaatatcc ttatcatttg caccatcagt ctagaccctc atctgacctc tcctatgtat 180
 ttccctgttg ctaatctggc ctcccttgat atttggtact ctccattac agccccctgaa 240
 atgctcatag acttcttctt ggagaggaag ataatttctt ttgatggatg cattgcacag 300
 ctcttcttct tacactttgc tggggcttcg gagatgttct tgctcacagt gatggccttt 360
 gacctctaca ctgctatctg ccgacccctc cactatgcta ccatcatgaa tcaacgtctc 420
 tgctgtatcc tgggtggctct ctccctggagg gggggcttca ttcattctat catacagggtg 480
 gctctcattg ttgcacttcc tttctgtggg cccaatgagt tagacagtta cttctgtgac 540
 atcacacagg ttgtccggat tgcctgtgcc aacaccttcc cagaggagtt agtgatgatc 600
 tgtagtagtg gtctgatctc tgtggtgtgt ttgattgtct tgtaaagtgc ctatgccttc 660
 cttctggcct tgttcaagaa actttcaggc tcagggtgaga ataccaacag ggccatgtcc 720
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 gctcgcccat ttgactcgtt tccctagat aaagtgggtg ctgtgttcaa tactttaata 840
 ttccctttac gtaatcccat tatttacaca ttgagaaaca aggaagtaaa ggcagccatg 900
 aggaagtgtg tcaccaaata tattttgtgt aaagagaag 939

<210> 436
 <211> 640
 <212> DNA
 <213> Unknown (H38g285 nucleotide)

<220>
 <223> Synthetic construct

<400> 436
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 cattaanaagc ctctgtatcta ttgttctcct tgtctctgag tctattcttt gggtttggac 120
 aggtgagtggt gtttctcaca atgacacaga gtgtactgtg aatgagcctg tttgcttcat 180
 gttctcctag atgcccttct gcctcagcta gatcttgccc tagacctact atgagcaagt 240
 ggtcatgctg aatctgggtat gtgcagacat cacatatata gtccatacct gtggtctctt 300
 atggcctttt ctgtggatgg atttgatata tttggcatta ttatccacag atatcagaca 360
 ttgcaggctg tactgtagct acctgcaaaa gaatctgtgc ccaaagtatt tagcatatat 420
 gccttccata tttgctgcac cctgtacctg ctcatgatag gattctactc cttttttct 480
 tgttgcttta gctaccatac actcacagtg attcccatct ccttgctcat ccttttactc 540
 attagtgcct tccatgttca ataccatcac ctgtggggtg aagagtaagc atatccaaga 600
 aaacatggta cagagatttt gtgggaaaat ttcctgccat 640

<210> 437
 <211> 989
 <212> DNA
 <213> Unknown (H38g286 nucleotide)

<220>
 <223> Synthetic construct

<400> 437
 atgtgtctct tgaccttgca ggtcactggc ccaatgaatg tctctgagcc aaattccagc 60
 tttgcttttag taaatgaatt tatactccaa gatttatctt ttgagtggaac aattcagatc 120
 ttctcttctt cactcttcac tacaacatat gcactgacca taacaggaaa cggagccatt 180
 gcttgccccc tgtggtgtga ccggcgacgt cacactccca tgtacatgtt cctgggaaat 240

ttctcctttt	tagagatatg	gtatgtctct	tctacagttc	ccaagatggt	gggtcaacttc	300
ctttcagaga	aaaaaaccat	ctcctttgct	ggatgttttc	tccaatttta	tttcttcttc	360
tctttgggta	catctgaatg	cttgattttg	actgtgatgg	cctttgatca	gtaccttggt	420
atctgccatc	ccttgcaacta	tcctaataaa	tcatgactgg	gcattctctgt	gccaaaactgg	480
tcatactgtg	ctgggtttgt	ggattttctgt	gtttcctgat	ccccactggt	ctcatctctc	540
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tagttatttt	tggtaacttc	ctctttatta	ttggatccta	tactcttggt	ctgaaagctg	720
tgttgggtat	gccttcgagc	actgggaaac	ataaagcctt	ctctacctgt	gggtctcatt	780
tggctgtggt	atcactgttc	tatggctctc	ttatgggtcat	gtgtgtgagt	ccaggacttg	840
gacactctat	ggggatgcag	aaaatcaaaa	ctttgttcta	tgctatgggt	acccactctc	900
tcaatccctt	tatctatagc	ctccagaata	aggagataaa	ggcagccctg	aggaaagttc	960
tggggagttc	caacataatc	taagccata				989

<210> 438

<211> 930

<212> DNA

<213> Unknown (H38g287 nucleotide)

<220>

<223> Synthetic construct

<400> 438

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ggactacacc	acattctttt	tgctatatct	ttttcttctc	atttagtgac	attaatggga	120
aacacgggtc	tcattgtgat	tgtctgtgtg	gataaacgtc	tgcagtcccc	catgtatttc	180
ttcctcagcc	acctctctac	cctggagatc	ctgggtcaca	ccataattgt	ccccatgatg	240
ctttggggat	tgctcttcct	gggatgcaga	cagtatcttt	ctctacatgt	atcgctcaac	300
ttttcctgtg	ggaccatgga	gtttgcatta	cttggagtga	tggctgtgga	ccgttatgtg	360
gctgtgtgta	accctttgag	gtacaacatc	attatgaaca	gcagtacctg	tatttgggtg	420
gtaatagtgt	catgggtggt	tggatttctt	tctgaaatct	ggcccatcta	tgccacattt	480
cagtttacct	tccgcaaata	aaattcatta	gaccattttt	actgtgaccg	agggcaattg	540
ctcaaactgt	cctgcgataa	cactcttctc	acagagttta	tccttttctt	aatggctgtt	600
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atcctcaaga	tcccgtcagc	ctctggcccg	aggaaagcct	tctccacttt	tgccctccac	720
ttcacctgtg	ttgtgattgg	ctatggcagc	tgcttgtttc	tctacgtgaa	acccaagcaa	780
acacagggag	ttgagtacaa	taagatagtt	tcctgtgtgg	ttctgtgtgt	aaccccttcc	840
ctgaatcctt	tcattctttac	tcttcggaat	gacaaagtca	aagaggccct	ccgagatggg	900
atgaaacgct	gctgtcaact	cctgaaagat				930

<210> 439

<211> 915

<212> DNA

<213> Unknown (H38g288 nucleotide)

<220>

<223> Synthetic construct

<400> 439

atgtccaaca	caaattggcag	tgcaatcaca	gaattcattt	tacttgggct	cacagattgc	60
ccggaactcc	agtctctgct	ttttgtgctg	tttctgggtg	tttacctcgt	cacctgtcta	120
ggcaacctgg	gcatgataat	gttaatgaga	ctggactctc	gccttcacac	gccccatgtac	180
ttcttcctca	ctaacttagc	ctttgtggat	ttgtgctata	catcaaatgc	aaccccgagc	240
atgtcgacta	atatcgatc	tgagaagacc	atttcctttg	ctgggtgtgt	tacacagtgc	300
tacattttca	ttgcccttct	actcactgag	ttttacatgc	tggcagcaat	ggcctatgac	360
cgctatgtgg	ccatatatga	ccctctgcgc	tacagtgtga	aaacgtccag	gagagtgtgc	420
atctgcttgg	ccacatttcc	ctatgtctat	ggcttctcag	atggactctt	ccaggccatc	480
ctgaccttcc	gacctgacct	ctgtagatcc	agtgatcatc	accacttcta	ctgtgtgac	540
ccgccgctca	ttagcttttc	ttgttctgat	acttatgtca	aagagcatgc	catgttcata	600
tctgtctggc	tcaacctctc	cagctccctc	accatcgctc	tgggtgtccta	tgcttctatt	660
cttgcctgca	tcctccggat	caaatcagca	gaggaagggc	acaaggcatt	ctccacctgt	720

ggttcccata	tgatggctgt	caccctgttt	tatgggactc	tcttttgcac	gtatataaga	780
ccaccaacag	ataagactgt	tgaggaatct	aaaataatag	ctgtctttta	cacctttgtg	840
agtcgggtac	ttaatccatt	gatctacagt	ctgaggaata	aagatgtgaa	gcaggccttg	900
aagaatgtcc	tgaga					915

<210> 440

<211> 939

<212> DNA

<213> Unknown (H38g289 nucleotide)

<220>

<223> Synthetic construct

<400> 440

atggcaaatc	tgagccagcc	ctccgaattt	gtcctcttgg	gcttctcctc	ctttggtgag	60
ctgcaggccc	ttctgtatgg	ccccttcctc	atgctttatc	ttctcgccct	catgggaaac	120
accatcatca	tagttatggt	catagctgac	accacacctc	atacaccat	gtacttcttc	180
ctgggcaatt	ttccctgct	ggagatcttg	gtaaccatga	ctgcagtgcc	caggatgctc	240
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ccctttctca	atccctttat	ccttaccttc	tgcaatcaga	cagttaaaac	agtgctacag	900
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<210> 441

<211> 948

<212> DNA

<213> Unknown (H38g290 nucleotide)

<220>

<223> Synthetic construct

<400> 441

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caagatatcc	agctcttggg	ctttgtgctg	atcttaattt	tctaccttat	catcctccct	120
ggaaattttc	tcattatatt	caccataagg	tcagaccctg	ggctcacagc	ccccctctat	180
ttattttctg	gcaacttggc	cttcctggat	gcctcctact	ccttcattgt	ggctcccagg	240
atgttgggtg	acttcctctc	tgagaagaag	gtaactcctc	acagaggctg	catcactcag	300
ctctttttct	tgcaacttcc	tgaggagggg	gagggtatcc	tccttgttgt	gatggccttt	360
gaccgctaca	tcgccatctg	ccggcctctg	cactgttcaa	ctgtcatgaa	ccctagagcc	420
tgctatgcaa	tgatgttggc	tctgtggcct	gggggttttg	tccactccat	tatccagggtg	480
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accactcgtg	tcattattat	acttcttatg	tttggacctg	ctatcttcat	ctacatgtgc	780
cccttcaggg	ccttaccagc	tgacaagatg	gtttctctct	ttcacacagt	gatctttcca	840
ttgatgaatc	ctatgattta	tacccttcgc	aaccaggaag	tgaaaacttc	catgaagagg	900
ttattgagtc	gacatgtagt	ctgtcaagtg	gattttataa	taagaaac		948

<210> 442

<211> 1034

<212> DNA

<213> Unknown (H38g291 nucleotide)

<220>

<223> Synthetic construct

<400> 442

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atcctaggca	attgcacaat	cctctttggt	atcaggactg	agccctcact	ccatgcaccc	180
atgtactatt	tcctttccat	gttggctgtc	tctgatctgg	gcctgtccct	ctcctaccta	240
cccactatgc	tgaggatctt	tgtattcaat	gccacaggaa	tctcctcaaa	tgctcgcttt	300
gctcaagaat	tctttattca	tgattcaca	gatatggagt	cctcagtgtc	tctcgtcatg	360
tcttttgacc	ggttttggcc	atatgccacc	ctctgaggta	catatctgag	gtactggtga	420
gctgtatcct	caccagtgtc	agagtggcca	aaatggggct	gttggtttctc	attaaaagag	480
aaacaacact	aaactcatta	aaagaaacaa	ctaactcatg	ctgttagtac	tcccatttcc	540
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tcattgctga	tgttttcttg	ctagtgtccac	ctcttatgaa	tcccattgta	tattgtgtga	960
agacacagca	aattcatgaa	aaagtttttag	gaaaactggg	tctacaacaa	cggtgtcagt	1020
aaacgtggta	caag					1034

<210> 443

<211> 713

<212> DNA

<213> Unknown (H38g292 nucleotide)

<220>

<223> Synthetic construct

<400> 443

ccacttattt	gaccagatcc	attcatcttt	acacaattgt	gttcattcct	taataaatat	60
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atcctaaatc	tgctccttatt	tcctttggga	ttaaaggcat	gtggagcaat	gttaattctt	180
gtttcctttc	tagccttccc	agagagaaag	agctaggatt	gaaacagcga	ggggaactac	240
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ttcacacagt	ctattaatgg	acatttccat	tgttattgct	tctttgatcc	agattgatcc	480
ctactccagt	atcccctcag	cgtctggcca	aaaaataatc	cttctccact	catgcctccc	540
atttcacctg	tgtggggatt	gactatgaca	gctgcttggt	tctctacgtg	aaacccaagc	600
aaatttgggc	agcagaataa	aacaaggtag	ttttcctggt	tattttcctg	ttgacccctt	660
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<210> 444

<211> 931

<212> DNA

<213> Unknown (H38g293 nucleotide)

<220>

<223> Synthetic construct

<400> 444

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ggaatgcaat	tgatgttctt	tgtcttattt	ctcctcttct	acgtcgtgat	catgggtggga	120
aatttgctca	ttttgcttat	ggtcttttct	gactcccgac	tacacacacc	catgtatttc	180
ttcctcagta	acctgtcttt	tgtggacatt	gcctgttccct	cagccacagc	acccaagatg	240
attgaagact	ttgtttctga	gaaaaagact	atttcctact	ggggctgtat	aactcagatg	300
tttaccttcc	acttttttgg	ttgtgctgag	atttttgttt	tgactgtcat	ggcttttcat	360

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cgctatgctg ctatctgcca acccctccgt tacactgtca tcatgagtgc taatgcttat 420
actgtgctgg catcactgtc ctggttgggg gccctgggtc attcctttgt tcagaccctc 480
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ctgtttagtc ttcaaaaaca gtctgcagag agctgacaca aagttctctc tacctgtgga 720
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ctactttccc attggataaa gctgtgtctg tgttctatac caccatcacc ccaatgctga 840
acccactcat ctatactctg aggaatgagg agtaaagaat gccatgagggc ggctatggag 900
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<210> 445

<211> 968

<212> DNA

<213> Unknown (H38g294 nucleotide)

<220>

<223> Synthetic construct

<400> 445

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tcttaattat tcgctttgtc ctcagaattg cctcccctga agaattggac aagggtcttca 720
gcacctgtgt ctcccacgtg ggagcagttg ctttcttcta catccacatg ctgagcctgt 780
ccttgggtga tcgctatggt cggtcagccc ccagagtagt ccattcagtg atggctaacg 840
tatacctgct ttacccccct gtgctcaacc ccatcatcta cagtgtaaaa acaaaacaaa 900
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caaacctg

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<210> 446

<211> 963

<212> DNA

<213> Unknown (H38g295 nucleotide)

<220>

<223> Synthetic construct

<400> 446

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acgggtgctga ggaacctgct cagcatectg gctgtctgct ctgactcccc cctccacacc 180
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ctgacgcaga tgtctttctt ggtccttttt gcatgtatag aaggcatgct cctgactgtg 360
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tataaaatca tcccctccat tctaaggatt tcatcgtag atgggaagta taaagccttc 720
tccacctgtg gctctcacct agccgttgtt tgctgatttt atggaacagg cattggcatg 780
tacctgactt cagctgtgtc acaaccccc aggaatgggt tgggtggcatc agtgatgtat 840

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gctgtggtca ccccatgct gaaccttttc atctacagcc tgagaaacag gaacatacaa	900
agtgcctctg ggaggctgca cagcagaaca gtcgaatctc atgatttgtt ccatcctttc	960
tct	963

<210> 447

<211> 975

<212> DNA

<213> Unknown (H38g296 nucleotide)

<220>

<223> Synthetic construct

<400> 447

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ctcttgggaa acagtatgat cttctctgtc atcattacta agcggagact ccacaaaccc	180
atgtattatt tcctctccat gctggcagct gttgatctat gtctgacct tacgaccctt	240
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attcaaatgt tctttgtgca tgctttctcc ttgctggagt cctcgggtgt ggtagccatg	360
gcctttgacc gcttcgtggc tatctgtaac ccactgaact atgctactat cctcacagac	420
aggatgggcc tgggataggg gctggtcac tcgattagac cagcagtttt cttacttccc	480
cttctttagc ccataaacac tgtgtctttt catgggggtc acgagctttc ccatccattt	540
tgctaccacc cagaagtgat caaatacaca tattccaaac cttggatcag cagtttttgg	600
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gtcctgatcc tccgtactgt tctgggcatt gtggcccgaa agaagcaaca aaaagctctc	720
agcacttggt tctgtcacat ctgtgcagtc actattttct atgtgccact gatcagcctc	780
tctttggcac accgcctctt ccactccacc ccaaggggtc tctgtagcac tttggccaat	840
atttatctgc tcttaccacc tgtgtgtaac cctatcattt acagcttgaa gaccaagaca	900
atccgccagg ctatgttcca gctgtccaa tccaaggggt catgggggtt taatgtgagg	960
ggtcttaggg gaaga	975

<210> 448

<211> 945

<212> DNA

<213> Unknown (H38g297 nucleotide)

<220>

<223> Synthetic construct

<400> 448

atggagacgt gggatgaacca gtcctacaca gatggcttct tcctcttagg catcttctcc	60
cacagtactg ctgacctgt cctcttctcc gtggttatgg cggctctcac agtggccctc	120
tgtgggaatg tcctcctcat cttcctcacc tacatggacc ctcacctca ccccccatg	180
tacttcttcc tcagccagct ctccctcatg gacctcatgt tggctgtgac caatgtgcca	240
aagatggcag ccaacttccg gtctggcagg aagtcacatc cctttgtggg ctgtggcata	300
caaattggcc tctttgtctg tcttgtggga tctgaggggc tcttgtggg actcatggct	360
tatgaccgct atgtggccat tagccaccca cttcactatc ccacctcat gaatcagagg	420
gtctgtctcc agattactgg gagctcctgg gcctttggga taatcgatgg cttgatccag	480
atgggtgtag taatgaattt cccctactgt ggcttgagga aggtgaacca tttcttctgt	540
gagatgctat ccttgttgaa gctggcctgt gtagacacat ccctgtttga gaaggtgata	600
tttgttctgt gtgtcttcat gcttctcttc ccattctcca tcactgtggc ctctatgct	660
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gtccttactc ccatgtctaa cccctcatt tacagcttga ggaacaggga ggtgatgggg	900
gcaactgagga aggggctgga ccgctgcagg atcggcagcc agcac	945

<210> 449

<211> 965

<212> DNA

<213> Unknown (H38g298 nucleotide)

<220>

<223> Synthetic construct

<400> 449

atgtcaccac	tcaaccaa	tactgaga	caccagag	tcttcacc	gactgggatt	60
ccaggaatgc	cagagaaaga	cttatggatg	gccttgcccc	tctgtcttct	ttatagcacc	120
acgatcttgg	gaaatgtcac	catccttgtt	gtcatcaaag	ttgagcaaag	tctccatgag	180
cccatgtatt	tttctagcca	tgtagctgc	cactgacctc	agcctttcac	tgtcttccat	240
gcctaccatg	gtcagtggtc	actggttcaa	ctggcggttca	ataactttta	atggctgcct	300
tatccagatg	ttcttcatcc	acacatttgg	gggagtggaa	tcaggtgttc	tggtggccat	360
ggcctttgat	cgctttgtgg	ccatccgctt	tcctttgcac	tatgctacaa	ttctactca	420
cagtgtcatc	agcaagattg	cagcagccat	cctgctacgg	agtgtggggg	ctgtgctccc	480
tgtgcctttt	ctcatcaaaa	ggttaccttt	ctgtcactcc	aatgtcctct	cccatgcata	540
ctgcctccat	caggatgcca	tgaggcttgc	ctgtgctgac	actggtgtca	atagcatcta	600
tggcctgttg	gctgtgatct	tcatcattgt	actagatgcc	ttaatacttt	tggcctctta	660
cattctaate	ctgcaggcag	tattgagcat	tgcttcccag	gaagacaggc	tcaaggctct	720
caacacctgt	ctcttcata	tctgcagtgc	tgcttttcta	tgtgcctctc	attggtatga	780
ccctaattca	tcgctatggg	aagcatttgt	caccactaat	acacacattc	atggccaata	840
tctacctgct	tctccctcct	gtgtcacaac	ccattgtgta	cagtgttagg	accaagcaga	900
tctgatatga	gattgtccag	gccttttgtg	gggctagggt	tagcccttaa	tggtcatctac	960
tattt						965

<210> 450

<211> 936

<212> DNA

<213> Unknown (H38g299 nucleotide)

<220>

<223> Synthetic construct

<400> 450

atgtctgttc	tcaataactc	cgaagtcaag	cttttccctc	tgattgggat	cccaggactg	60
gaacatgccc	acatttggtt	ctccatcccc	atttgccctc	tgtacctgct	tgccatcatg	120
ggcaactgca	ccattctctt	tattataaag	acagagccct	cgcttcatga	gcccattgat	180
tatttccttg	ccatgttggc	tgtctctgac	atgggcctgt	ccctctcctc	ccttccctacc	240
atgttgaggg	tcttcttgtt	caatgccatg	ggaatttcac	ctaagcctg	ctttgctcaa	300
gaattcttca	ttcatggatt	cactgtcatg	gaatccctcag	tacttcta	tatgtctttg	360
gaccgctttc	ttgccattca	caatccctta	agatacagtt	ctatccctac	tagcaacagg	420
gttgctaaaa	tgggacttat	tttagccatt	aggagcattc	tcttagtgat	tccatttccc	480
ttcaccttaa	ggagattaaa	atattgtcaa	aagaatcttc	tttctcactc	atactgtctt	540
catcaggata	ccatgaagct	ggcctgctct	gacaacaaga	ccaatgtcat	ctatggcttc	600
ttcattgctc	tctgtactat	gctggacttg	gcactgattg	ttttgtctta	tgtgctgate	660
ttgaagacta	tactcagcat	tgcacttttg	gcagagaggc	ttaaggccct	aaatacctgt	720
gtctcccaca	tctgtgctgt	gctcaccttc	tatgtgcccc	tcataccctc	ggctgccatg	780
catcactttg	ccaagcacaa	aagccctctt	gttggtgatcc	ttattgcaga	tatgttcttg	840
ttggtgccgc	cccttatgaa	ccccattgtg	tactgtgtaa	agactcgaca	aatctggggg	900
aagatcttgg	ggaagttgct	taatgtatgt	gggaga			936

<210> 451

<211> 923

<212> DNA

<213> Unknown (H38g300 nucleotide)

<220>

<223> Synthetic construct

<400> 451

atgaaaataa	atgacagctc	aggggaagac	ttcatcttag	ttggcttctc	agaatatccc	60
caggctgagt	tcatactttc	tctgtttgtc	tccgggttct	acaccatgac	attcacaggg	120
aacacagcca	tcactttggt	ctctctgctg	gactaccggc	tccgcacccc	aatgtacttc	180

ttcctccgaa	agctctcatt	tctggacatg	tgtttcacca	cctgcattgt	ccttcagatg	240
ctggtgaaca	tctggggaga	gagtaagaag	gtcagctatg	taggctgcat	ggttcagtat	300
tctgtagcct	tggctcttgg	ctccacagag	tgtgtgcttc	ttgctatcat	ggctgtggac	360
cgttatgttg	ccgtccgctg	gccccttcac	tatgttacaa	tcattgcacca	acagatctgc	420
cactttctcg	cagccttgtc	ctggttttct	gggttagcca	actctctctt	tcactcttca	480
ctaaccacca	ttttgcctct	gtgtggccac	cgccgtgtgg	accattttctt	tgtgaggtec	540
tgtcatttgt	caagctgtcc	tgcgtggaca	ccggcccaac	tgaattgaag	atgttaattg	600
ctcgtgtgat	catccttgcc	cttcacgtgt	gcaccatcct	cacctcctat	gcctgcattg	660
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tgaagagtaa	ctactctcag	attcagggaa	agctgcttcc	tcttgtttat	accattgtcg	840
ccccaccta	gaaccaccta	atctatgcac	tgaggaaaca	agttgtaaag	agggcaattg	900
gaaaattgat	ctggaaggat	tca				923

<210> 452

<211> 951

<212> DNA

<213> Unknown (H38g301 nucleotide)

<220>

<223> Synthetic construct

<400> 452

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tggtgcactc	agatatccct	gttttccctg	ttcttgggtca	catacctcat	gacagtgtcg	120
gggaactgtc	tatttgtcct	tctgatcaga	ctggacagcc	gactccacac	tcccatgtat	180
ttctttctca	ccaacctctc	ccttgctgat	gtctcctatg	ccacaagcgt	agtccccag	240
ctgtcggcac	attttcttgc	agaacataaa	gccatcccat	tccagagctg	tgtagcccag	300
ttatttttct	ccctggcctt	gggtgggatt	gagtttgttc	tcctggcagt	gatggcctat	360
gaccgcgatg	tggtctgtgc	tgaccgcctg	cgatactcgg	ccatcatgca	tgtagggctg	420
tgtgctaggt	tggccatcac	atcctgggtc	agtggctcca	tcaactctct	tgtgcagact	480
gctatcacct	ttcagctgcc	catgtgcact	aacaagttta	ttgatcacat	atcctgtgaa	540
ctcctagctg	tggtcaggct	ggcttgtgtg	gacacctcct	ccaatgaggc	tgccatcatg	600
gtgtctagca	ttgttcttct	gatgacacct	ttctgcctgg	ttctgttgtc	ctacatccgg	660
atcatctcca	ccatccataa	gatccagtcc	agagaaggaa	gaaagaaagc	cttccacacg	720
tgtgcctctc	acctcacggg	ggttgccctg	tgctacggca	caacgatttt	cacttacatc	780
cagccccact	ctgggtccctc	agtccttcaa	gagaagctga	tctctgtctt	ctatgccatt	840
gttatgcctc	tgctgaaccc	tgtgatttat	agtcctaagga	ataaagagggt	gaagggggcc	900
tggcataaac	tattagagaa	attctctggg	ttaacatcca	agctgggaac	t	951

<210> 453

<211> 918

<212> DNA

<213> Unknown (H38g302 nucleotide)

<220>

<223> Synthetic construct

<400> 453

atggaaggga	aaaatcaaac	caatatctct	gaattttctcc	tcctgggctt	ctcaagttgg	60
caacaacagc	aggtgctact	ctttgcactt	ttctgtgtgc	tctatttaac	agggctgttt	120
ggaaacttac	tcatcttgct	ggccattggc	tcggatcact	gccttcacac	acccatgtat	180
ttcttccttg	ccaatctgtc	cttggtagac	ctctgccttc	cctcagccac	agtccccag	240
atgctactga	acatccaaac	ccaaacccaa	accatctcct	atcccggctg	cctggctcag	300
atgtatttct	gtatgatgtt	tgccaatatg	gacaattttc	ttctcacagt	gatggcatat	360
gaccgttaag	tggccatctg	tcacctttta	cattactcca	ccattatggc	cctgcgcctc	420
tgtgcctctc	tggtagctgc	accttgggtc	attgccattt	tgaaccctct	cttgcacact	480
cttatgatgg	cccattctga	cttctgctct	gataattgta	tccaccattt	cttctgtgat	540
atcaactctc	tcctccctct	tcctgttccc	gacaccagtc	ttaatcagtt	gagtggtctg	600
gtacagggtg	ggctgatctt	tgtgggtacct	tcagtgtgta	tcctgggtatc	ctatatcctc	660
attgtttctg	ctgtgatgaa	agtccttctt	gcccaggaa	aactcaaggc	tttctctacc	720

tgtggatctc	accttgccct	ggtcattctt	ttctatggag	caaacacagg	ggcttatatg	780
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gtagcacctg	tggtgaatcc	attcatttac	agtttaagaa	acaatgaact	gaaggggact	900
ttaaaaaaga	ccctaagc					918

<210> 454

<211> 933

<212> DNA

<213> Unknown (H38g303 nucleotide)

<220>

<223> Synthetic construct

<400> 454

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ccagaactga	agttaatccc	tttcagcctg	ttcctgtcca	tgtacctggt	caccatcctg	120
gggaacctgc	tcattctcct	ggctgtcatc	tctgactccc	acctccacac	ccccatgtac	180
ttccttctct	ttaatctctc	ctttactgac	atctgtttta	ccacaaccac	agtcccaaaag	240
atcctagtga	acatccaagc	tcagaatcag	agtatcactt	acacaggctg	cctcaccacag	300
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gaccgctatg	tggccatttg	ccaccactg	aggtacacag	tcctcatgaa	tgtccatttc	420
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gtccctcaaa	tgatgaaccc	cttcactctac	agcctgagaa	ataaggagat	gaagaaagct	900
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<210> 455

<211> 939

<212> DNA

<213> Unknown (H38g304 nucleotide)

<220>

<223> Synthetic construct

<400> 455

atggaagcga	gaaaccaaac	agctatttca	aaattccttc	tcctgggact	gatagaggat	60
ccggaactgc	agcccgctct	tttcagcctg	ttcctgtcca	tgtacttggg	caccatcctg	120
gggaacctgc	tcattctcct	ggctgtcatc	tctgactctc	acctccacac	ccccatgtac	180
ttcttctctt	ccaatctctc	ctttttggac	atttgtttta	gcacaaccac	gatcccaaaag	240
atgctgggtga	acatccaagc	tcagaatcgg	agcatcacgt	actcaggctg	cctcaccacag	300
atctgctttg	tcttggtttt	tgctggcttg	gaaaattgtc	tccttgagac	aatggcctat	360
gaccgctatg	tggccatttg	tcacccctt	agatacacag	tcatacatgaa	cccccgctc	420
tgtggcctgc	tgattcttct	ctctctgttg	actagtgttg	tgaatgccct	tcttctcagc	480
ctgatgggtg	tgaggctgtc	cttctgcaca	gacctggaaa	tcccgcctct	cttctgtgaa	540
ctggctcagg	tcatacaact	cacctgttca	gacacctca	tcaataacat	cctgatatat	600
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agttctgtgg	ttactgactc	acctaggaag	gctgcagtgg	cttcagtgtg	gtattctgtg	840
ttccctcaaa	tggtgaaccc	ctttatctat	agtctgagga	ataaggacat	gaaaggaacc	900
ttgagggaag	tcatagggag	gataccttct	cttctgtgg			939

<210> 456

<211> 939

<212> DNA

<213> Unknown (H38g305 nucleotide)

<220>

<223> Synthetic construct

<400> 456

atggaaccaa	gaaaccaaac	cagtgcattct	caattcatcc	tcctgggact	ctcagaaaag	60
ccagagcagg	agacgcttct	cttttccctg	ttcttctgca	tgtacctggt	catggctgtg	120
gggaacctgc	tcattcatct	ggccatcagc	atagactccc	acctccacac	ccccatgtac	180
ttcttctctg	ccaacctgtc	cctggttgat	ttctgtctgg	ccaccaacac	catccctaag	240
atgctgggtga	gccttcaaac	cgggagcaag	gccattctct	atccctgctg	cctgatccag	300
atgtacttct	tccatttctt	tggcatcgtg	gacagcgtca	taatcgccat	gatggcttat	360
gaccggttcg	tggccatctg	ccacccattg	cactacgcca	agatcatgag	cctacgcctc	420
tgtcgccctg	tggtcggcgc	cctctgggcg	ttttcctgct	tcattctcact	cactcacatc	480
ctcctgatgg	cccgctctct	tttctggcgc	agccatgagg	tgcctcacta	cttctgcgac	540
ctcactccca	tcctccgact	ttcgtgcacg	gacacctctg	tgaataggat	cttcactctc	600
attgtggcag	ggatgggtgat	agccacgccc	tttgtctgca	tcctggcctc	ctatgctcgc	660
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tgtccctcct	cggctcctac	cactgtgaag	gagaaagctt	ctgcggtgat	gtacacagca	840
gtcaccacca	tgtgaatcc	cttcattctac	agcttgaggga	acagagacct	gaaaggggct	900
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<210> 457

<211> 295

<212> DNA

<213> Unknown (H38g306 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(295)

<223> n = A,T,C or G

<400> 457

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ggcctggagc	acctgcacat	ctggatctcc	atcccttctt	cagcatatac	actggccctg	120
cttggaact	gcactctcct	tctcatcatc	caggctgatg	cagccctcca	tgaacctatg	180
tacctctttc	tggccatggt	ggcagccatc	gaccagctct	ctatctcctc	agcactgcgc	240
ccgggacaga	cgggtgattct	ggttcacgga	tcngaagaat	aaaccctttg	ccggg	295

<210> 458

<211> 960

<212> DNA

<213> Unknown (H38g307 nucleotide)

<220>

<223> Synthetic construct

<400> 458

atgccatctg	cctctgccat	gatcattttc	aacctgagca	gttacaatcc	aggacccttc	60
attctggtag	ggatcccagg	cctggagcaa	ttccatgtgt	ggattggaat	tcccttctgt	120
atcatctaca	ttgtagctgt	tgtgggaaac	tgcactcttc	tctacctcat	tgtgggtggag	180
catagtcttc	atgaacctat	gttcttcttt	ctctccatgc	tggccatgac	tgacctcatc	240
ttgtccacag	ctggtgtgcc	taaagcactc	agtatctttt	ggctaggggc	tcgcgaaatc	300
acattcccag	gatgccttac	acaaatgttc	ttccttcact	ataactttgt	cctggattca	360
gccattctga	tggccatggc	atttgatcac	tatgtagcta	tctgttctcc	cttgagatat	420
accaccatct	tgactcccaa	gaccatcatc	aagagtgtca	tgggcatctc	ctttcgaagc	480
ttctgcatca	tcctgccaga	tgtattcttg	ctgacatgcc	tgcctttctg	caggacacgc	540
atcatacccc	acacatactg	tgagcatata	ggtgttgccc	agctcgccctg	tgtgatatac	600
tcatacaact	tctgggtatgg	cttttgtgtt	cccatcatga	cggctcatctc	agatgtgatt	660

ctcattgctg	tttcctacgc	acacatectc	tgtgctgtct	ttggccttcc	ctcccaagag	720
gcctgccaga	aagccctcgg	cacttggtgt	tctcatgtct	gtgtcaccct	catgttttat	780
acacctgcct	ttttctccat	cctcgcccat	cgctttggac	acaatgtctc	tcgcaccttc	840
cacatcatgt	ttgccaatct	ctacattggt	atcccacctg	cactcaaccc	catgggtttac	900
ggagtgaaga	ccaagcagat	cagagataag	gttatacttt	tgttttctaa	gggtacagga	960

<210> 459

<211> 936

<212> DNA

<213> Unknown (H38g308 nucleotide)

<220>

<223> Synthetic construct

<400> 459

atgagcggga	caaaccagtc	gagtgtctcc	gagttcctcc	tcttgggact	ctccaggcag	60
ccccagcagc	agcatctcct	ctttgtgttc	ttcctcagca	tgtacctggc	cactgtcctg	120
gggaacctgc	tcatcatcct	gtccgtaagc	atagactcct	gcctgcacac	ccccatgtac	180
ttcttctcca	gcaacctgtc	ttttgtggac	atctgtctct	ccttcaccac	cgcccccaag	240
atgctggcca	atcacatact	cgagactcag	accatctcct	tctgtggctg	tctcacacag	300
atgtatttcg	ttttcatggt	cggtggacatg	gacaatttcc	tcttagctgt	gatggcctat	360
gaccactttg	tcgccgtgtg	ccacccctta	cattacacag	caaagatgac	ccatcagctc	420
tgtgccctgc	tggttgctgg	attatgggtg	gttgccaacc	tgaatgtcct	tctgcacacc	480
ctgctgatgg	ctccactctc	attctgtgca	gacaatgcc	tcaactcact	cttctgcgat	540
gtgactcccc	tactgaaact	ctcctgtcca	gacacacacc	tcaatgaggt	cataatcctt	600
agtgagggtg	ccctgggtcat	gatcacecca	ttcttttgca	tcttggcttc	ttatatgcac	660
atcacctgca	ctgtcctgaa	ggteccatcc	acaaagggaa	ggtggaaagc	cttctccacc	720
tgtgggttctc	acctggctgt	ggttctctc	ttctacagca	ccatcattgc	tgtgtatttt	780
aacctctgt	cctccactc	agctgagaaa	gacactatgg	ctactgtgtt	gtatacagta	840
gtgactccca	tgctaaaccc	tttcatctac	agcctgagga	acagggtactt	gaaaggggct	900
ctgaaaaaag	tagttggcag	ggtgggtgtt	tctgtc			936

<210> 460

<211> 762

<212> DNA

<213> Unknown (H38g309 nucleotide)

<220>

<223> Synthetic construct

<400> 460

atgtacttct	tcttgcgcca	actctcagtg	gtggagctct	tctacaccac	tgacatcgtg	60
cccaggaccc	tgcccaatct	gggtctcccg	catccccagg	ccatctcttt	ccagggctgt	120
gcagcccata	tgtacgtctt	cattgtcctg	ggcatctcgg	agtgtgcct	gtcactgcc	180
atggcctatg	accgatatgt	tgccatctgc	cagcccctac	gctattccac	cctcttgagc	240
ccacgggcct	gcatggccat	ggtgggtacc	tcttggctca	caggcatcat	cacggccacc	300
acccatgcct	ccctcatctt	ctctctacct	tttcgcagcc	acccgatcat	ccgcacttt	360
ctctgtgaca	tcttgcagtg	actgaggctg	gcaagtgtg	ggaagcacag	gagcgagatc	420
tccgtgatga	cagccaccat	agtcttcatt	atgatccct	tctctctgat	tgtcacctct	480
tacatccgca	tcttgggtgc	catectagca	atggcctcca	cccagagccg	ccgcaaggtc	540
ttctccacct	gtctctccca	tctgtctgtg	gtctctctct	tctttggaac	agccagcatc	600
acctacatcc	ggcgcagggc	aggctcctct	gttaccacag	accgcgtcct	cagtctcttc	660
tacacagtca	tcacacccat	gctcaacccc	atcatctaca	cccttcggaa	caaggacgtg	720
aggagggccc	tgcgacactt	ggtgaagagg	cagcgccctc	ca		762

<210> 461

<211> 998

<212> DNA

<213> Unknown (H38g310 nucleotide)

<220>

<223> Synthetic construct

<400> 461

atggatggag	agaatcactc	agtggatatc	gagttttt	gttctgggact	cactcattca	60
tgggagatcc	agtcctcct	cctagtgtt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	tcagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgtctca	300
atcttcttca	tccacgtcat	tgggtgtgtg	gagatgggtg	tgctcatagc	catggccttt	360
gacagtatat	tggccctatt	aagccctctc	actatctgac	cattatgagc	ccaagaatgt	420
gcctttcatt	tctggctgtt	gcctggaccc	ttgttgtcag	tactccctg	ttccaactgg	480
catttcttgt	taatttacc	ttctgtggcc	ctaagtgtt	ggacagcttc	tactgtgacc	540
ttctcagct	tctcagacta	gcctgtaccg	acacctacag	attgcagttc	atggtcactg	600
ttaacagtgg	gtttatctgt	gtgggtactt	tcttcatact	tctaactctc	tacgtcttca	660
tcctgtttac	tgtttgaaa	cattcctcag	gtgggttcac	caaggccctt	tccactcttt	720
cagctcacag	cacagcggtc	cttttgttct	ttgggtccacc	catgtttgtg	tatacatggc	780
cacacctaa	ttcacagatg	gacaagtttc	tggctatttt	tgatgcagtt	ctcactcctt	840
ttctgaatcc	agttgtctat	acattcagga	ataaggagat	gaaggcagca	ataaagagag	900
tatgcaaaca	gctagtgtat	tacaagaaga	tctcataaat	gatacaataa	gcccttctcg	960
ttaaacatga	tatggcttta	tgtttctttc	tttgatat			998

<210> 462

<211> 933

<212> DNA

<213> Unknown (H38g311 nucleotide)

<220>

<223> Synthetic construct

<400> 462

atggaagagt	acaacacatc	ctctacagac	ttcactttca	tggggctgtt	caacagaaag	60
gaaacctcag	gtcttatttt	tgccatcatc	tctatcatct	tcttcaccgc	actgatggcc	120
aatgggggta	tgaatcttcc	gatccaaaca	gatttgcgcc	ttcatacacc	catgtacttc	180
ctcctcagcc	acctttcctt	aattgacatg	atgtatat	ccactattgt	gcctaagatg	240
ctgggttaatt	acctgctgga	tcaaaggacc	atttcctttg	tgggggtgcac	agctcaaac	300
ttcctctacc	ttacccttgt	gggagctgaa	ttcttctgc	tgggcctcat	ggcctatgac	360
cgctatgtgg	ccatttgcaa	ccctctgaga	tacctgtcc	tcattgagccg	ccgggtctgt	420
tggatgatta	tagcaggttc	ctggtttggg	ggctctttgg	atggcttctt	cctaaccctc	480
atcaccatga	gctttccctt	ctgcaattcc	cgggagatta	accacttctt	ctgcgaggca	540
ccagcagtc	tgaagtggc	atgtgcagac	acagccctct	acgagacagt	gatgtatgtg	600
tgctgtgttt	tgatgtgtgt	gattcctttc	tctgtagtcc	ttgcttctta	tgcccgaatc	660
ctgactacag	ttcagtgcac	gagctcagtg	gagggcagga	agaaggcatt	tgccacttgc	720
tcattcccaca	tgactgtggg	gtccttgttc	tacggggctg	ccatgtacac	ctacatgctg	780
ccacattctt	accacaagcc	agcccaggac	aaagtcctct	ctgtgtttta	caccattctc	840
acacccatgc	tgaacccctt	catctacagc	cttagaaaaca	aggatgtgac	tggagctctg	900
aagagggcct	tggggagggt	caagggtcct	caa			933

<210> 463

<211> 883

<212> DNA

<213> Unknown (H38g312 nucleotide)

<220>

<223> Synthetic construct

<400> 463

atccaatgca	agggctaata	gaagtgaatt	aagacattct	ctgtaactcc	aatatttaa	60
ggaaaccggg	aaatagccag	attcctctcc	aacctgtcct	tggctggcat	cggtttcccc	120
tccaccatag	tctccaagat	gattgtggac	atccagtctc	acagcagagt	catctcctat	180
gcgggctgcc	tgactcaggt	atctcttttt	gccgtttttg	gatgcagga	agacatgctt	240
ctgagtgtga	tggcttatga	ccggtttgtg	gacatctgtc	accctctgga	ttatccagtc	300

atcatgaacc	catgtttctg	tggcttccta	gttttggtgt	ctttttttct	cagtctttta	360
gactcccagc	tgcacaattg	gattgcctta	caaattacct	gcttcaagga	tgtggaaatt	420
cccaatttct	tctgtgaccc	ttctcaactc	ccccaccctt	gcctgttggtg	acaccttcac	480
caatgacata	gtcatgtatt	tccttgctgc	catatttggt	ttctttccca	tttcggggcc	540
ttttctctta	ctataaaatt	gtttcctcca	ttctgagggt	ttcatcatca	gggtgggaagt	600
ataaagcctt	ctccacctgt	ggctctcacc	tgtcagttgt	ttgcttattt	tatggaacag	660
gctttggagg	ggacctcagt	tcagacatgt	cctcttatcc	cagaaaaggt	gcagtggcct	720
cagtgatgta	cacggtgggt	actcccatgc	tgaaccatt	catttacagc	ctaacaggga	780
aattaaaagt	gccctgcggc	agctgcactg	cagaatagtc	taatctcatt	ttcttattat	840
ctgttcatt	ccttcgtag	tgtgagttag	aaaaggcagc	aag		883

<210> 464

<211> 942

<212> DNA

<213> Unknown (H38g313 nucleotide)

<220>

<223> Synthetic construct

<400> 464

atgaccctgg	gatccctggg	aaacagcagc	agcagcgttt	ctgctacctt	cctgctgagt	60
ggcatccctg	ggctggagcg	catgcacatc	tggatctcca	tccactgtg	cttcatgtat	120
ctggtttcca	tcccgggcaa	ctgcacaatt	ctttttatca	ttaaaacaga	gcgctcactt	180
catgaacctc	tgtatctctt	cctgtccatg	ctggctctga	ttgacctggg	tctctccctt	240
tgcactctcc	ctacagtcct	gggcatcttt	tgggttgag	cacgagaaat	tagccatgat	300
gcctgctttg	ctcagctctt	tttcattcac	tgcttctcct	tcctcgagtc	ctctgtgcta	360
ctgtctatgg	cctttgaccg	ccttggtggt	atctgccacc	ccttgcacta	tgtttccatt	420
ctcaccaaca	cagtcattgg	caggattggc	ctggctctct	tgggtcgtag	tgtagcactc	480
atttttccat	taccttttat	gctcaaaaga	ttcccctatt	gtggctcccc	agttctctca	540
cattcttatt	gtctccacca	agaagtgatg	aaattggcct	gtgccgacat	gaaggccaac	600
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aaggccctta	acacctgtgt	ttcccacatc	tgtgctgtgc	tgtctctcta	cactcccatg	780
attggcctct	ctgtcatcca	tcgctttgga	aagcaggcac	cccacctggg	ccagggtggc	840
atgggtttca	tgtatcttct	ctttcctcct	gtgatgaatc	ccattgtcta	cagtgtgaag	900
accaaacaga	tccgggatcg	agtgacgcac	gccttttgtt	ac		942

<210> 465

<211> 990

<212> DNA

<213> Unknown (H38g314 nucleotide)

<220>

<223> Synthetic construct

<400> 465

atgggactct	tcagacaatc	caaacatcca	atggccaata	tcacctggat	ggccaaccac	60
actggatggg	cggatttcat	cctgttgagg	ctcttcagac	aatccaaaca	tccagcacta	120
ctttgtgtgg	tcatttttgt	ggttttcctg	atggcggtgt	ctggaaatgc	tgtcctgata	180
cttctgatac	actgtgacgc	ccacctccac	acccccatgt	actttttcat	cagtcaattg	240
tctctcatgg	acatggcgta	catttctgtc	actgtgcccc	agatgctcct	ggaccaggtc	300
atgggtgtga	ataagatctc	agcccctgag	tgtgggatgc	agatgttctt	ctacgtgaca	360
ctagcagggt	cagaattttt	ccttctagcc	accatggcct	atgaccgcta	cgtggccatc	420
tgccatcctc	tccgttacc	tgtcctcatg	aacctatagg	tgtgtctctt	cctgtcatca	480
ggctgctggg	tcctgggctc	agtggatggc	ttcacattca	ctcccatcac	catgaccttc	540
cccttccgtg	gatcccgagg	gattcatcat	ttcttctgtg	aagtctcctg	tgtattgaat	600
ctctcctgct	cagacacctc	actctatgag	attttcatgt	acttgtgctg	tgtcctcatg	660
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gtggctcatc	tcttctatgg	ggctgccatc	tacacctaca	tgtccccag	ctcctaccac	840
acccctgaga	aggacatgat	ggtatctgtc	ttctatacca	tcctcactcc	agtggatgaac	900

cctttaatct atagtcttag gaataaggat gtcattggggg ctctgaagaa aatgttaaca 960
gtggaacctg cctttcaaaa agctatggag 990

<210> 466

<211> 591

<212> DNA

<213> Unknown (H38g315 nucleotide)

<220>

<223> Synthetic construct

<400> 466

gctgccatgg	cttaagaccg	gtacatagca	atctgtaacc	cgctgctcta	tacagtgatt	60
atgtccaaga	agggtttgtg	ccagcttgca	attggagcat	ttttgggggg	cactatgagc	120
tcaattattc	ataccacgaa	cactttccat	ctgtcattct	gtccagaga	tattaaccat	180
ttcttttgtg	atatctcccc	actcttctct	ctgtcctgca	ctgacacata	catgcatgac	240
atcattctgg	tggctcttgc	cagttttgtg	gaagcaatct	gtcttctatc	agttctcctt	300
tccttatgtc	tcattatggc	agctattctt	agaacagggt	ctgtggaggg	aagaagaaga	360
gggttctcca	cttgtgcttc	ccacctgact	gtggctacta	tgtatcatgg	taccttgatc	420
ttcatttatt	tgcgtcccag	cactggccat	tcactggata	ttgacaaagt	gacctctgtg	480
ttctataact	tgattatacc	tatgttgaac	cctctaattt	acagtctaag	gaacaaagat	540
gtcaaaaatg	cttttagaaa	agtgattggc	cgaaaattac	ttccttaagg	t	591

<210> 467

<211> 938

<212> DNA

<213> Unknown (H38g316 nucleotide)

<220>

<223> Synthetic construct

<400> 467

atgatgactc	ttaagaactg	cactgtgttt	actgacttta	tattcttagg	actttcaggt	60
acacaggata	tacagcaggg	gctctttgtg	cttttcttcc	tgatttatgg	cataactgtg	120
attgtcaatc	tagggatgat	cctactgatc	aagatggatc	tcagacttca	cacacccgtg	180
tattatttcc	tgagcaattt	gtctttctgt	gatgtctgct	actcttccac	gtctctccca	240
aatgctagct	gatttcttat	cggaccaaaa	gtggattccg	tataatttat	gtgccattca	300
gatgtattta	tttggagtct	ttgcagatgt	ggaatgtctc	atgttggctg	tcattggccta	360
tgatcgttat	gttgccattt	gcaatccact	tctttatacg	atcactatgc	ccaggaggat	420
ctgcacccag	ctagtggctc	ttgcctatgt	tgtaggtttg	gtggattctg	caatccacac	480
ctgctgcaca	ttcagattgt	cattctgcaa	ttctaattgc	atcaatcact	ttttctgtga	540
catccacccc	ttgctagccc	tcaatccctac	tattaattgc	tattaatgag	atagtgatgt	600
tcacattcgt	tggctgtgtt	gcggggtgca	gcattgtcac	tgtcttctc	tcctacagct	660
acatcataat	taccatcctt	aaaatgagct	cagctgaggg	cagacggaaa	gccttctcta	720
cctgcacctc	ccacttgatg	gccgtggctg	tatttcatgg	cacactcctg	ttcatgtatt	780
tccgacccag	ttcaagttac	tcaatggaaa	cagacaaaat	ggcctctgtt	ttctacacag	840
ttgtcatacc	tatgttaaat	ccactgatct	acagcttaag	gaatagggat	gtgaaagggtg	900
ctctgaaaaa	agcaataagc	actaaattat	attctgta			938

<210> 468

<211> 969

<212> DNA

<213> Unknown (H38g317 nucleotide)

<220>

<223> Synthetic construct

<400> 468

atgtcaacat	taccaactca	gatagccccc	aatagcagca	cttcaatggc	ccccaccttc	60
ttgctgggtg	gcatgccagg	cctatcaggt	gcacctcct	ggtggacatt	gcccctcatt	120
gctgtctacc	ttctctctgc	actgggaaat	ggcaccatcc	tctggatcat	tgccctgcag	180

cccgccctgc	accgccaat	gcacttcttc	ctcttcttgc	ttagtggtgc	tgatattgga	240
ttgggtactg	ccctgatgcc	cacactgctg	ggcatcgccc	ttgctgggtg	tcacactgtc	300
cctgcctcag	cctgccttct	acagatgggt	tttatccatg	tcttttctgt	catggagtcc	360
tctgtcttgc	tcgccatgtc	cattgatcgg	gcactggcca	tctgccgacc	tctccactac	420
ccagcgctcc	tcaccaatgg	tgtaattagc	aaaatcagcc	tggccatttc	ttttcgatgc	480
ctgggtctcc	atctgccctc	gccattcctg	ctggcctaca	tgccctactg	cctcccacag	540
gtcctaaccc	attcttattg	cttgcatcca	gatgtggctc	gtttggcctg	cccagaagct	600
tgggggtgag	cctacagcct	atthgtgggt	ctttcagcca	tgggtttgga	ccccctgctt	660
atthtcttct	cctatggcct	gattggcaag	gtgttgcaag	gtgtggagtc	cagagaggat	720
cgctggaagg	ctggtcaaac	ctgtgctgcc	cacctctctg	cagtgtcctc	cttctatata	780
cctatgatcc	tcttggcact	gattaacat	cctgagctgc	caatcactca	gcatacccat	840
actcttctat	cctatgtcca	tttccttctt	cctccattga	taaaccctat	tctctatagt	900
gtcaagatga	aggagattag	aaagagaata	ctcaacagg	tgcagcccag	gaagggtgggt	960
ggtgctcag						969

<210> 469

<211> 384

<212> DNA

<213> Unknown (H38g318 nucleotide)

<220>

<223> Synthetic construct

<400> 469

tctcgctcag	atacacaggt	caatgagtta	gtgttattca	ccgtctttgg	ttttattgaa	60
ctgagtacca	tttcaggagt	tttcatttct	tattgttata	tcacccctatc	agtcttggag	120
atacactctg	ctgaggggag	gttcaaagct	ctctctacat	gcacttccca	cttatctgag	180
gttgcaattt	tccagggaac	tctgtctctt	atgtatttcc	ggccaagtcc	ttcctattct	240
ctagatcaag	ataaaatgac	ctcattgttt	tacacccttg	tggttcccat	gttgaacccc	300
ctgatttata	gcctgaggaa	caaggatgtg	aaagaggccc	tgaaaaaact	gaaaaataaa	360
atthtatttt	aaggaaatag	taaa				384

<210> 470

<211> 946

<212> DNA

<213> Unknown (H38g319 nucleotide)

<220>

<223> Synthetic construct

<400> 470

atgtttctgc	tcaatacctc	agaagttgaa	gtctccacat	tcctattgat	tgggatacca	60
ggacttgagc	atgcacacat	ttggatctct	atccccatct	gccttatgta	cctcatggcc	120
atcctgggca	actgcacat	cctatttgtt	atcagaacag	agcattccct	gcaagagccc	180
atgtactatt	tcctctccat	gctggccctg	tcagacctgg	gcctgtcttt	ctcctcccta	240
cccacgatgc	tgagaatctt	cttgttcaac	aacatgggga	tttctgctga	tacatgcatt	300
gcccaggaat	tcttcatcca	tggattcaca	gacatggagt	cttcagttct	cctaatacat	360
tcctttgatc	acttagtagc	catttgcaac	cccctaagat	atagctctat	tctcaccagc	420
ttcaggggtt	tgcaaattgg	actggctttt	gccattaaaa	gcattctcct	agtgtctacc	480
cttttacttt	aaagagactc	agatactgta	ataaacacct	tttatcccac	tcctactgcc	540
ttcaccagga	tgtaatgaag	ctggcctgct	ctgacaacag	ggttaacttt	tactatggtt	600
tgttcgttgc	actctgcatg	atgtcagaca	gtgtttttat	tgctatttcc	tatatgtgtt	660
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ctgtgtgtct	catatctgtg	ctgtactcgt	cttctatgtg	cccatcatca	ccttggtctac	780
catgcgtcgc	tttgctaagc	ataaatcccc	tttagctatg	attctgatag	cagatgcatt	840
cttgcgtgga	ccacccttga	tgaatcccat	tgtgtattgt	gtaaaaactc	ggcagattag	900
agtaaaggtc	ctggaaaaat	tggctctgaa	gcctaaatga	tggggc		946

<210> 471

<211> 942

<212> DNA

<213> Unknown (H38g320 nucleotide)

<220>

<223> Synthetic construct

<400> 471

atgatggcat	ctgaaagaaa	tcaaagcagc	acacccactt	ttattctctt	gggtttttca	60
gaatacccag	aaatccaggt	tccactcttt	ctggttttct	tgttcgtcta	cacagtcact	120
gtagtgggga	acttgggcat	gataataatc	atcagactca	attcaaaaact	ccatacaatc	180
atgtgctttt	tccttagtca	cttgtccttg	acagacttct	gtttttccac	tgtagttaca	240
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gcttatgacc	gttttggtgg	agtttgtaaa	cccttgctgt	ataccactat	tatgtctcag	420
aagctctgtg	ctcttctggt	ggctgggtcc	tatacatggg	ggatagtgtg	ctccctgata	480
ctcacatatt	ttcttcttga	cttatcggtt	tgtgaatcta	ccttcataaa	taattttatc	540
tgtgaccact	ctgtaattgt	ttctgcctcc	tactcagacc	cctatatcag	ccagaggcta	600
tgctttatta	ttgccatatt	caatgagggt	agcagcctaa	ttatcattct	gacatcatat	660
atgcttattt	tcactaccat	tatgaagatg	cgatctgcaa	gtgggcgcca	gaaaactttc	720
tccacctgtg	cctccacact	gacagccatc	actatcttcc	atggaactat	ccttttcctt	780
tactgtgttc	ctaattcctaa	aacttctagc	ctcatagtta	cagtggcttc	tgtgttttac	840
acagtggcga	ttccaatgct	gaacccattg	atctacagcc	ttaggaacaa	agatatcaat	900
aacatgtttg	aaaaattagt	gtcaccaaaa	ttgatttacc	ac		942

<210> 472

<211> 965

<212> DNA

<213> Unknown (H38g321 nucleotide)

<220>

<223> Synthetic construct

<400> 472

cacacagagc	cacggaatca	cacaggggtc	tgagaatttc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctgggc	120
acgggtgctg	ggaacctgct	cagcatcctg	gctgtccgct	ctgactcccc	cctccacaac	180
cccattgtact	tcttcctctc	caacctgtgc	tgggctgaca	tcgggtttcac	ctcggccacg	240
gttgccaaga	tgattgtgga	atgcagtcgc	atagcagagt	catctctcat	gcgggctgcc	300
tgacgcagat	gtctttcttg	gtcctttttg	catgtataga	aggcatgctc	ctgactgtga	360
tggcctatga	ctgctttgta	gccatctgtc	gtcctctgca	ctacccagtc	atcgtgaatc	420
ctcacctctg	tgtcttcttc	gttttggtgt	cctttttcct	tagcctgttg	gattcccagc	480
tgcacagttc	gattgtgtta	caattcacca	tcatacaaga	tgtggaaatc	tctcattttg	540
tctgtgaccc	ctctcatctt	ctcaaacttg	cctgttctga	cagcgtcatc	aatagcatat	600
tcataatatt	cgatagtact	atgtttgggt	ttcttcccat	ttcagggatc	ctttgggtctt	660
actataaaat	cgtcccctcc	attctaagga	tttcatcatc	agatgggaag	tataaagcct	720
tcgccacctg	tggctctcac	ctagcagttg	tttctgatt	tgatggaaca	ggcattggta	780
tgtacctgac	ttcagctgtg	gcaccacccc	ctagggaatg	agtgggtggc	tcagtgatgt	840
aggctgtggt	caccccatg	ctgaaccttt	tcacttacag	cctgagaaac	agggacatac	900
aaagtgcctt	gcggaggctg	ctcagcagaa	cagtcgaatt	tcatgatctg	tttcattctt	960
tttct						965

<210> 473

<211> 990

<212> DNA

<213> Unknown (H38g322 nucleotide)

<220>

<223> Synthetic construct

<400> 473

atgtcgggtcc	tcaataatac	cattgctgag	cctctgatct	tcctcctgat	gggcattcca	60
ggcctgaaag	ccaccagta	ctggatctcc	atcccttttt	gtctcctata	tggtgttgcc	120

gtctctggaa	atagcatgat	cctgtttgtg	gtcctctgtg	aacggagcct	ccataagcct	180
atgtactatt	tcctctctat	gcttttcagcc	acagacctga	gcttgtccct	gtgtacactt	240
tctactaccc	ttggtgtcct	ctggtttgaa	gcccagagaa	tcaacctaaa	tgctgcatt	300
gcccgatgt	tctttctaca	cggatttact	ttcatggagt	ctggggttct	actggccatg	360
gcttttgatc	gttttgtggc	catctgttac	ccactgagat	acactacat	ccttaccaat	420
gcccgattg	ccaagattgg	gatgagcatg	ttgataagaa	atgttgccgt	catgttgcca	480
gtcatgctct	ttgtcaagag	gttgctcttc	tgcagttcta	tggtccttcc	acattcttac	540
tgctaccatg	ttgatctcat	ccaactctcc	tgcacagaca	ataggatcaa	cagcatcctt	600
ggtctgtttg	cgcttttgtc	cactacaggg	tttgactgcc	cttgcatcct	gctctcctat	660
atcctgatca	ttcgatctgt	cctcagcatt	gcttcctcag	aagagaggcg	gaaagccttc	720
aacacctgca	catcccacat	cagtgtgtgt	tccacttctt	acctccctct	catcagtttg	780
tctcttgtcc	atcgctatgg	ccattcagca	cctccatttg	tccacatcat	catggccaat	840
gtctttctgc	taatccctcc	tgtgctcaac	cctattattt	acagtgtaaa	gattaagcag	900
attcaaaagg	ccattatcaa	ggtcttaatt	cagaagcact	ccaaatctaa	tcatacagcta	960
tttctgatta	gagataaagc	catttatgaa				990

<210> 474

<211> 942

<212> DNA

<213> Unknown (H38g323 nucleotide)

<220>

<223> Synthetic construct

<400> 474

atgatgatgg	ttttaaggaa	tctgagcatg	gagccacact	ttgccctttt	aggtttcaca	60
gattacccaa	agcttcagat	tcctctcttc	cttgtgtttc	tgctcatgta	tgttatcaca	120
gtggtaggaa	accttgggat	gatacataata	atcaagatta	accccaaatt	tcacactcct	180
atgtactttt	tccttagtca	cctctctttt	gttgattttt	gttactcttc	cattgtcact	240
cccaagctgc	ttgagaactt	ggtaatggca	gataaaaagca	tcttctactt	tagctgcatg	300
atgcagtact	tcctgtcctg	cactgctgtg	gtgacagagt	ctttcttgct	ggcagtgatg	360
gcctatgacc	gctttgtggc	catctgcaat	cctctgcttt	atacagtggc	catgtcacag	420
aggcttctgt	ccctgctggg	ggctgggtca	tatctctggg	gcatgtttgg	ccccttggtta	480
ctcctttgtt	atgctctccg	gttaaaacttc	tctggaccta	atgtaatcaa	ccacttcttt	540
tgtgagtata	ctgctctcat	ctctgtgtct	ggctctgata	tactcatccc	ccacctgctg	600
cttttcagct	tcgccacctt	caatgagatg	tgtacactac	tgatcatcct	cacttcctat	660
gttttcattt	ttgtgactgt	actaaaaatc	cgttctgtta	gtgggcgcca	caaagccttc	720
tccacctggg	cctcccacct	gactgctatc	accatcttcc	atgggaccat	ccttttcctt	780
tactgtgtac	ccaactccaa	aaactctcgg	caaacagtca	aagtggcctc	tgtattttac	840
acagttgtca	accccatgct	gaaccctccg	atctacagcc	taaggaataa	agacgtgaag	900
gatgctttct	ggaagttaat	acatacacia	gttccatttc	ac		942

<210> 475

<211> 942

<212> DNA

<213> Unknown (H38g324 nucleotide)

<220>

<223> Synthetic construct

<400> 475

atgggtgctgg	cttcaggga	cagctcttct	catcctgtgt	ccttcaccc	gcttggaatc	60
ccaggcctgg	agagtttcca	gttgtggatt	gcctttccgt	tctgtgccac	gtatgctgtg	120
gctgttgttg	gaaatatcac	tctcctccat	gtaatcagaa	ttgaccacac	cctgcatgag	180
cccatgtacc	tctttctggc	catgctggcc	atcactgacc	tggtcctctc	ctcctccact	240
caacctaa	tggttgccat	attctggttt	catgctcatg	agattcagta	ccatgcctgc	300
ctcatccagg	tgttcttcat	ccatgccttt	tcttctgtgg	agtctgggg	gctcatggct	360
atggccttgg	actgctacgt	ggctacctgc	ttccactctc	gacactctag	catcctgacc	420
ccatcggtcg	tgatcaaa	ggggaccatc	gtgatgctga	gagggtgctg	gtgggtgagc	480
cccttctgct	tcattgtgtc	taggatgccc	ttctgccaac	accaagccat	tccccagtca	540
tactgtgagc	acatggctgt	gctgaagttg	gtgtgtgctg	atacaagcat	aagtcgtggg	600

tatgggctct	ttgtggcctt	ctctgtggct	ggctttgata	tgattgtcat	tggtatgtca	660
tacgtgatga	ttttgagagc	tgtgcttcag	ttgccctcag	gtgaagcccg	cctcaaagct	720
tttagcacac	gtgcctccca	tatctgtgtc	atcttggctc	tttatatccc	agcccttttt	780
tctttcctca	cctaccgctt	tggccatgat	gtgcccgcag	ttgtacacat	cctgtttgct	840
aatctctatc	tactgatacc	tcccatgctc	aaccccatca	tttatggagt	tagaaccaaa	900
cagatcgggg	acagggttat	ccaaggatgt	tgtggaaaca	tc		942

<210> 476

<211> 860

<212> DNA

<213> Unknown (H38g325 nucleotide)

<220>

<223> Synthetic construct

<400> 476

tatatattgt	tagacatata	tatatgtcta	aacaacactc	atgtctaatt	gtgtgtagag	60
tcactagagg	caatttaaaa	taagttttta	tttttctttt	tttctattgg	caataacatg	120
attttagtga	taaattttta	taattatgaa	aacataacag	tactttttta	aacataaaca	180
tttaaagaaa	aagttttcat	gattcttgta	tacatcttaa	catacatact	ctccctttta	240
agtaagttct	ttgcattggt	taaatctttg	cagacaaagc	ttttcaagag	caagtcagtg	300
gaaactagta	gagcaggagt	tgagaaagcc	ctgtgcatta	tacactcacc	atgtcccaga	360
agttttgctc	catccatcca	gcaggatggt	agaccagggc	atataatcta	tccccgggtca	420
ctcattttct	cattgtattg	cctattgtgg	gcacaatgta	gttaatatat	tttaaaataa	480
atattctggt	gccatttcag	attcgtgagt	tcactctggat	agcggatttt	tgtttgtttg	540
tttgttttgc	tttagtcaat	tttgattaat	taaggaaatct	cagagtcctc	actccttagc	600
tttcatattc	aacttggtta	aaaggcactt	tctgccagtg	cacatcaacc	tttctccacc	660
atttcccaca	tttccaccat	ccttcctcac	tctagtgcac	taactccaaa	aactcacagg	720
caactgtgaa	agcacactct	gtatgttatg	ccatgttaat	ccccatgctg	aactcacaga	780
cttgtagcat	gcggtacaaa	aatgtgaatg	aatctctgca	gaagctgatg	gacttcaaaa	840
tatttttagca	ttgaaagcaa					860

<210> 477

<211> 966

<212> DNA

<213> Unknown (H38g326 nucleotide)

<220>

<223> Synthetic construct

<400> 477

agtcacacag	agccatagaa	tctcacaagt	gtctcagaat	tccttctcca	gggactctca	60
gaggatccag	aactgcagcc	cgctcctcgt	gggctgtccc	tgteccatgta	cctgggtcacg	120
gtgctgagga	acctgctcat	catcctggct	gtcagctctg	actcccacct	ccacaccccc	180
atgtacttct	tcctctccaa	cctctcctgg	gctgacattg	gtttcacctc	ggccatgggt	240
cccaagatga	ttgtggacat	gcagtcgcat	agcagagtca	tctcttaagc	gggctgcctg	300
acacagatgt	ctttctttgt	cctttttgca	tgtatagaag	acatgctcct	gactgtgatg	360
gcctatgacc	aatttggtgg	catctgtcac	ccctgcacta	cccagtcate	atgaatcctc	420
acctctgtgt	cttcttagtt	ttggtttctt	tttcccttag	cctgtttggat	tcccagctgc	480
acagttggat	tgtgtttacaa	ttcaccttct	tcaagaatgt	ggaaatctct	aattttttct	540
gtgatccatc	tcaacttctc	aaccttgcc	gttctgacgg	catcatcaat	agcatattta	600
tatatattga	tagtattctg	ttcagttttc	ttcccatctc	agggatcctt	ttgtcttact	660
ataaaaattgt	cccctccatt	ctaagaattt	catcgtcaga	tgggaagtat	aaagccttct	720
ccatctgtgg	ctctcacctg	gcagttgttt	gcttatttta	tggaaacagg	attggcgtgt	780
acctaacttc	agctgtgtca	ccacccccag	gaatgggtgtg	gtggcgctcag	tgatgtatgc	840
tgtgggcacc	cccagctgta	actcttttat	ctacagcctg	agaaacaggg	acattcaaa	900
cgccctgtgg	aggctgcgca	gcagaacagt	cgaatctcat	gatctgttcc	atccttattc	960
ttgtgt						966

<210> 478

<211> 951

<212> DNA

<213> Unknown (H38g327 nucleotide)

<220>

<223> Synthetic construct

<400> 478

atgcaacccat	ataccaaaaa	ctggacccag	gtaactgaat	ttgtcatgat	gggctttgct	60
ggcatccatg	aagcacacct	cctcttcttc	atactcttcc	tcaccatgta	cctgttcacc	120
ttgggtggaga	atttggccat	catttttagtg	gtgggtttgg	accaccgact	acggagaccc	180
atgtatttct	tcctgacaca	cttgctctgc	cttgaaatct	ggtacacttc	tggtacagtg	240
cccaagatgc	tggtctggtt	tattgggggtg	gatggtggca	agaatatctc	ttatgctggt	300
tgcctatccc	agctcttcat	cttcaccttt	cttggggcaa	ctgagtgttt	cctactggct	360
gccatggcct	atgatcggtt	tgtggccatt	tgtatgcctc	tccactatgg	ggcttttgtg	420
tcctggggca	cctgcatccg	tctggcagct	gcctgttggc	tggtagggtt	cctcacaccc	480
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ttctcctgtg	atgcctcacc	cttgctagcc	ttgtcgtgct	cagatgtcac	ttggaaggag	600
actgtggatt	tcctgggtgc	tctggctgtg	ctactggcct	cctctatggt	cattgctgtg	660
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tttatgtatg	tccagaccaa	ggtgacctcc	tccatcaact	tcaacaaggt	ggtatctgtc	840
ttctactctg	ttgtcacgcc	catgctcaat	cctctcatct	acagtcttag	gaacaaggaa	900
gtgaagggag	ctctgggtcg	agtcttttct	ctcaactttt	ggaagggaca	g	951

<210> 479

<211> 936

<212> DNA

<213> Unknown (H38g328 nucleotide)

<220>

<223> Synthetic construct

<400> 479

atggatggag	agaatcactc	agtggatatct	gagtttttgt	ttctgggact	cactcattca	60
tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcatttgtgt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	ccagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcgt	tgggtgtgtg	gagatgggtc	tgctcatagc	catggccttt	360
gacagatatg	tggccctatg	taagcccctc	cactatctga	ccattatgag	cccaagaatg	420
tgcctttcat	ttctggctgt	tgcctggacc	cttgggtgtc	gtcactccct	gttccaactg	480
gcatttcttg	ttaatttacc	cttctgtggc	cctaattgtg	tggacagctt	ctactgtgac	540
cttctcagc	ttctcagact	agcctgtacc	gacacctaca	gattgcagtt	catggctact	600
gttaacagtg	ggtttatctg	tgtgggtact	ttcttcatac	ttctaacttc	ctacatcttc	660
atcctgttta	ctgtttgga	acattcctca	ggtagttcat	ccaaggccct	ttccactctt	720
tcagctcaca	gcacagcgg	ccttttgttc	tttgggtccac	ccatgtttgt	gtatacatgg	780
ccacacccta	attcacagat	ggacaagttt	ctggctatatt	ttgatgcagt	tctcactcct	840
tttctgaatc	cagttgtcta	tacattcagg	aataaggaga	tgaaggcagc	aataaagaga	900
gtatgcaaac	agctagtgat	ttacaagaag	atctca			936

<210> 480

<211> 668

<212> DNA

<213> Unknown (H38g329 nucleotide)

<220>

<223> Synthetic construct

<400> 480

gtgaggcacc	ccctgcgatg	cggaagtaa	gagccagccc	ctctcccacc	cctggctctt	60
aggaacccca	tcatgacctc	gtgtttctgt	ggctttctag	ttttgtcttt	tttttttttt	120

ttctcagtc	tttagacgcc	cagctgcaca	acttgattgc	cttacaaatg	acctgcttcc	180
aggatgcgga	aattcctagt	ttcttctgtg	acccttctca	actcccccat	cttgcatggt	240
gtgacacctt	caccaataac	ataatcatgt	atttgccctg	tgccatattt	ggttttcttc	300
ccatctcggg	gacccttttc	tcttactata	aaattgtttc	ctccattctg	aggggttcat	360
catcacgtgg	gaagtataag	gccttctcca	cctgtgggtc	tcacctgtca	gttggttgct	420
gattttacgg	aacaggcttt	ggagggtacc	tcagttcaga	tgtgtcatct	tccccgagaa	480
aggctgcagt	ggcctcagtg	atgtacacgg	tgatcacctc	catgctgaac	cccttcatct	540
acagcctgag	aaacagggat	attaaagggt	tcctgcgcca	gccgcacggc	agcaccgtcc	600
aatttcagta	tcttcttata	tgttccattc	cttttgtagt	gtgggttaaa	aaaggcagca	660
aggtcaaa						668

<210> 481

<211> 840

<212> DNA

<213> Unknown (H38g330 nucleotide)

<220>

<223> Synthetic construct

<400> 481

atgtacctgg	tcacgggtgct	gaggaacctg	ctcatcatcc	tggtgtgcag	ctctgactcc	60
cacctccaca	cccccatgtg	cttcttcctc	tccaacctgt	gctgggctga	catcggtttc	120
acctcggcca	tggttcccaa	gatgattgtg	gacatgcagt	cgcatagcag	agtcactctt	180
tatgcgggct	gcctgacaca	gatgtctttc	tttgtccttt	ttgcatgtat	agaagacatg	240
ctcctgacag	tgatggccta	tgaccgattt	gtggccatct	gtcacccctc	gcactaccac	300
gtcatcatga	atcctcacct	tggtgtcttc	ttagttttgg	tgctcctttt	cctcagcctg	360
ttggattccc	agctgcacag	ttggattgtg	ttacaattca	ccttcttcaa	gaatgtggaa	420
atctccaatt	ttgtctgtga	cccattctca	cttctcaacc	ttgcctgttc	tgacagtgtc	480
atcaatagca	tattcatata	tttagatagt	attatgtttg	gttttcttcc	catttcaggg	540
atccttttgt	cttacgctaa	caatgtcccc	tccattctaa	gaatttcac	atcagatagg	600
aagtctaaag	ccttctccac	ctgtggctct	cacctggcag	ttgtttgctt	attttatgga	660
acaggcattg	gcgtgtacct	gacttcagct	gtgtcaccac	ccccaggaa	tggtgtgggtg	720
gcatcagtg	tgtacgctgt	ggtcaccccc	atgctgaacc	ctttcatcta	cagcctgaga	780
aatagggaca	ttcaaagtgc	cctgtggagg	ctgcgcagca	gaacagtcga	atctcatgat	840

<210> 482

<211> 924

<212> DNA

<213> Unknown (H38g331 nucleotide)

<220>

<223> Synthetic construct

<400> 482

atggaaacac	agaacctcac	agtggtgaca	gaattcattc	ttcttgggtc	gacctcagtc	60
caagatgctc	aacttctggg	ctttgtgcta	gtcttaattt	tctaccttat	catcctccct	120
ggaaatttcc	tcattcattt	caccataaag	tcagacctg	ggctcacagc	ccccctctat	180
ttctttctgg	gcaacttgge	cttactggat	gcatcctact	ccttcattgt	ggttcccagg	240
atgtttgggtg	acttccctct	tgagaagaag	gtaatctcct	atagaagctg	catcactcag	300
ctctttttct	tgatttttct	tggagcgggg	gagatgttcc	tcctcgttgt	gatggccttt	360
gaccgctaca	tcgccatctg	ccggccttta	cactattcaa	ccatcatgaa	ccctagagcc	420
tgctatgcat	tatcggtggg	tctgtggctt	gggggcttta	tccattccat	tgtacaagta	480
gcccttatcc	tgactttgcc	tttctgtggc	ccaaaccagc	tcgataactt	cttctgtgat	540
gttccacagg	tcataagct	ggcctgcacc	aatacctttg	tggtggagct	tctgatgggtc	600
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atcctctgtc	gtataaggga	gactcctctt	gaaggaaaga	gcaaggctat	ttccacatgc	720
accacccata	ttatcattat	atttctcatg	tttggaacct	ctattttcat	ctacacttgc	780
cccttccagg	ctttccagc	tgacaaggta	gtttctcttt	tcatactgt	catctttcct	840
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ttgttaagtc	aacatatggt	ttgc				924

<210> 483
 <211> 457
 <212> DNA
 <213> Unknown (H38g332 nucleotide)

<220>
 <223> Synthetic construct

<400> 483
 gggatgagaa aggaacaagc tgtctgtggt agtcatccat gattgagatg atgtgtggac 60
 cctgagtcag actacctggt tcaaatgcag gctctctact ttttaccat ttgatcttgg 120
 cctgtggctc tctacttctt atccatttca tcttggactt gtggcctctc atacctcatc 180
 ttccttacag tctccatat gaaatcccc taaagtagga acaaagcttt ggccaactgc 240
 tctcccac tttcctggt ctttacttag gaactgtgtg tttaataac gtgacacagg 300
 gtttctccca catccctgag cagaaacaag ctgtgtctgt attttgcact gtactcaccc 360
 ccatgctaaa cccctcatc tacatcctga gaaacaagga tgtggtggg ctcttcagaa 420
 agttctggga acacatcaag tctctaaaca gaacaca 457

<210> 484
 <211> 972
 <212> DNA
 <213> Unknown (H38g333 nucleotide)

<220>
 <223> Synthetic construct

<400> 484
 atgtctttct tctttgtaga cttaagaccc atgaacaggt cagcaacaca catcgtgaca 60
 gagtttatcc tcttgggatt ccctgggtgc tgggaagattc agattttcct cttctcattg 120
 tttttggtga tttatgtctt gaccttgctg ggaatggag ccatcatcta tgcagtgaga 180
 tgcaaccac tactacacac ccccatgtac tttctgctgg gaaattttgc cttccttgag 240
 atctgggatg tgcctccac tattcctaac atgctagtca acattctctc caagaccaag 300
 gccatctcat tttctgggtg cttcctccag ttctatttct tcttttact gggaacaact 360
 gaatgtctct tttctggcagt aatggcttat gatcgatacc tggccatctg ccaccactg 420
 cagtaccctg ccatcatgac tgtaagggtc tgtggtgaagc tgggtgtctt ctgttggctt 480
 attggattcc ttggataccc aattcccatt ttctacatct cccaactccc cttctgtggt 540
 cctaatatca ttgatcactt cctgtgtgac atggacccat tgatggctct atcctgtgac 600
 ccagctccca taactgaatg tattttctat actcagagct cccttgcct ctttttact 660
 agtatgtaca ttcttcgatc ctatatacctg ttactaacag ctgtttttca ggtccctct 720
 gcagctggtc ggagaaaagc cttctctacc tgtggttctc atttggtgt ggtatctctt 780
 ttctatggga cagtcatggt aatgtatgta agtcctacat atgggatccc aactttattg 840
 cagaagatcc tcacactggt atattcagta acgactcctc tttttaatcc tctgatctat 900
 actcttcgta ataaggacat gaaactcgct ctgagaaatg tcctgtttgg aatgagaatt 960
 cgtcaaaatt cg 972

<210> 485
 <211> 945
 <212> DNA
 <213> Unknown (H38g334 nucleotide)

<220>
 <223> Synthetic construct

<400> 485
 atggccaaca tcaccaggat ggccaaccac actggaaagt tggatttcat cctcatggga 60
 ctcttcagac gatccaaaca tccagctcta cttagtgtgg tcatctttgt ggttttcctg 120
 aaggcgttgt ctggaaatgc tgcctgatc cttctgatac actgtgacgc ccacctccac 180
 agccccatgt actttttcat cagtcaattg tctctcatgg acatggcgta catttctgtc 240
 actgtgtccc agatgctcct ggaccaggtc atgggtgtga ataaggctc agccccctgag 300
 tgtgggatgc agatgttctt ctatctgaca ctaggaggt cggaattttt ccttctagcc 360
 accatggcct atgaccgcta cgtggccatc tgccatcctc tccgttaccc tgtcctcatg 420

aaccataggg	tctgtctttt	cctggcatcg	ggctgctggt	tcctgggctc	agtggatggc	480
ttcatgctca	ctcccatcac	catgagcttc	ccctctctgca	gacccctggga	gattcatcat	540
ttcttctgtg	aagtcctctg	tgtaacgatc	ctgtcctgct	cagacacctc	actctatgag	600
accctcatgt	acctatgctg	tgctcctcatg	ctcctcatcc	ctgtgacgat	catttcaagc	660
tcctatttac	tcctcctcct	caccgtccac	aggatgaact	cagcagaggg	ccggaaaaag	720
gcctttgcca	cctgtcctc	ccacctgact	gtgggtcatcc	tcttctatgg	ggctgccgtc	780
tacacctaca	tgctccccag	ctcctaccac	acccctgaga	aggacatgat	ggtatctgtc	840
ttctatacca	tcctcactcc	ggtgctgaac	cctttaatct	atagtcttag	gaataaggat	900
gtcatggggg	ctctgaagaa	aatgttaact	gtgagattcg	tcctt		945

<210> 486

<211> 759

<212> DNA

<213> Unknown (H38g335 nucleotide)

<220>

<223> Synthetic construct

<400> 486

agccacctct	ccgtcattga	cacattatac	atctccacca	ttgtgcccaa	gatgctggta	60
gattatctca	tgggcgaggg	gaccatctct	ttcatcgctt	gcactgctca	gtgctttctc	120
tacatgggct	ttatgggggc	tgaattcttc	ctgctggggc	tcattggccta	tgaccgctac	180
gtggccatct	gcaacccact	gcgtatcct	gtcctcatca	gctggcgggg	ctgctgggatg	240
atcctggcca	gctcttggtt	cgttgggggt	ttggacagtt	ttctcctcac	ccccattacc	300
atgagtctcc	cgttctgtgc	ctctcaccac	atcaatcact	ttttctgtga	ggcaccacc	360
atgctgaggg	tggcctgtgg	ggacaaaacc	acctatgaaa	cagtgatgta	tgtgtgctgc	420
gttgaatgc	tgctgatccc	cttctcggtg	gtgactgcat	cctacaccag	gattctcatc	480
acagtgcac	agatgacatc	ggctgaaggg	aggaagaagg	cctttgccac	ctgctcttca	540
cacatgatgg	tggtagacatt	gttctatggg	gctgccttgt	atacgtatac	gcttccccaa	600
tcttaccaca	ccccaatcaa	agataaggtc	ttctctgcct	tttataccat	cctcacaccc	660
ttattaaacc	ctctcatcta	cagtctgagg	aacagggatg	tgatgggtgc	cttgaagaga	720
gttgtggcaa	gatgttaggg	gacatgtggt	gtgatgagg			759

<210> 487

<211> 857

<212> DNA

<213> Unknown (H38g336 nucleotide)

<220>

<223> Synthetic construct

<400> 487

gtttttctccc	gcacccgggt	tcgcctcaat	tgcaaacgca	tattctggct	aacgccagtc	60
ttttttttgt	ccccctcatg	cccattctct	atcgagtggt	ctaagagtgc	agtcagcttc	120
gtgtcacaga	gcaggcgcat	tagatttttg	ggctgtgaca	ttcaaacggg	atgtgttcct	180
gggcccctgg	gggaactgaa	gcccttctct	ttgggtttat	gtcttatgat	cgctatgtag	240
ctatctgtca	ccctttacat	tatcctatgc	ttatgagcaa	gaagatctgc	tgccctcatgg	300
ttgcatgtgc	atgggccagt	ggttctatca	atgctttcat	acatacattg	tatgtgtttc	360
agcttccatt	ctgtaggtct	cggctcatta	accacttttt	ctgtgaagtt	ccagctctac	420
tatcattggt	gtgtcaggac	acctcccagt	atgagtatac	agtcctcctg	agtggaactta	480
ttatcttgct	actaccatc	ctagccattc	tggcttccta	tgctcgtgtg	cttattgtgg	540
tattccagat	gagctcagga	aaaggacagg	caaaagctgt	ttccacttgt	tcctcccacc	600
tgattgtggc	aagcctgttc	tatgcaacca	ctctctttac	ctacacaagg	ccacactcct	660
tgcggtcccc	ttcacgggat	aaggcgggtg	cagtatttta	caccattgtc	acacctctac	720
tgaacccatt	tatctacagc	ctgagaaata	aggaagtgc	gggggcagtg	aggagactgt	780
tgggatattg	gatatgctgt	agaaaatatg	acttcagatc	tctgtattga	ttgagcatta	840
acaacataaa	aagctgt					857

<210> 488

<211> 812

<212> DNA

<213> Unknown (H38g337 nucleotide)

<220>

<223> Synthetic construct

<400> 488

agaagggaca	ttttctattt	tgccttcatt	tgtagctatt	catgactgac	tctccgttct	60
tttgtctact	tgttcatccg	tccatccatc	catccatcca	tccactcagc	cattcttttg	120
ttcaacagtg	atttactgaa	ttccttacta	tgactcttct	atatttgaca	tgccacacga	180
tgttcagcaa	tgactttctac	tcaagagcta	gttttttagtt	tcacactgct	tttctcttgt	240
tctttatctt	ttgcttttgt	agctcagaac	agaaaaatct	atagaaaaga	tcttgctacc	300
aggctatggg	accctcttgt	ccatggcgat	atcttactgt	ctttgtgtct	ttgggctgag	360
caatcctgca	gcatgggtga	tgctcaataa	tgctcatgga	acaaaatggt	gtgggttcctc	420
ttccaggaag	tgctgccatc	tctcttttga	ttgagaatag	gtttacctag	gtgattacat	480
cactaacatt	gtattcctgt	gatttcttcc	tcatgatagg	acagatttta	ctaaaaagtc	540
aaaaattatt	tattacatta	tgccggtcct	cttacttttc	atgccagatt	aaattttctt	600
ggtccttcaa	tgcccacttc	taatatcaat	aaacaagtaa	cctttcccca	acctactgaa	660
gtcgccatgt	ggaattgggc	attctttctg	ttgattccat	atcatccctt	tcattcttct	720
gtctgcccgt	ttgtccatcc	atztatccat	ccacttagct	attcgttcgt	tcaacaatga	780
tttagtgaat	acctacttac	tgtgacccta	tt			812

<210> 489

<211> 931

<212> DNA

<213> Unknown (H38g338 nucleotide)

<220>

<223> Synthetic construct

<400> 489

atgtcattag	ctgaaggaaa	tcagagttct	ggagccgtat	ttaccctctt	gggctttctca	60
gaatatgcag	acctccaggt	tcctctgttc	ctggctcttc	tgaccatcta	cacaatcact	120
gtattgggaa	acctgggcat	gatcatgac	atcaggatca	accccaact	ccacaccgc	180
atgtactttt	tcctcagcca	cttgtccttt	gttgatttct	gttattccac	cacagttaca	240
cccaaaactgc	tggaagaact	ggttgtggaa	gacagaacca	tctccttcac	aggatgcac	300
atgcaattct	tcctggcggt	tatatgtgca	gtggcgagaaa	cattcatgct	ggcagtgatg	360
gcctatgatt	gatacgtggc	ggtgtgtaac	cctttgtctct	acacagttgt	cagggtccag	420
aaactctgtg	catcattagt	ggcagggccc	tacacatggg	gtataatctc	ttctctgaca	480
ctcacctatt	tcctcttgte	attatccttc	tgtgggtcta	acatcatcaa	taattttgtc	540
tgtgagcact	ctgtcatcat	ctctgtctcc	tgctctgacc	cctacatcag	ccaaatgctt	600
tgttttgtca	ttgcaatatt	caatgaggtg	agcagcttgg	gagtcacctc	cactacctat	660
attttcatct	ttattgctgt	cataaaaatg	ccttctgctg	ttgggcacca	aaaagctttc	720
tctacctgtg	cttcccacct	gactgccatc	actattttcc	acgggactgt	cctgttcctt	780
tattgtgtac	ccaactccaa	aaactcatgg	ctcatagtca	aagtaggttc	tgtgttttat	840
acagtcatca	tccccacgtt	gaacccttta	acctacagcc	tcaggaacaa	agacgtgaaa	900
gagagtgttc	gaaagttaat	gaatcactca	a			931

<210> 490

<211> 651

<212> DNA

<213> Unknown (H38g339 nucleotide)

<220>

<223> Synthetic construct

<400> 490

ttcttgggtcc	tttttgcatt	tatagaagac	atgttccctga	ctgtgatggc	ctatgactgc	60
tttatagcca	tctgtcatcc	tctgcaactac	ccagtcacgc	tgaatccctca	cctctgtgtc	120
ttcttcattt	tggtgtcctt	tttcttagc	ctgttggatt	cccagctgca	tagctggatt	180
gtgtttacaat	tcaccatcat	caagaatgtg	gaagttctcta	attttgtctg	tgacccctct	240
caactttctca	aacttgccctg	ttctgacagc	gtcatcaata	gcatattcat	atatttcgat	300

aatactatgt	ttgggttttct	tcccatttca	gggatccttt	ggtcttacta	taaaatcgct	360
ccctacattc	tcaggatttc	atcgtcagat	gggaagtata	aagccttcgc	cacctgtggc	420
tctcacctgg	cagttgcttg	ctgattttat	ggaacaggca	ttggcatgta	cctgacttca	480
gctgtgtcac	cacccccag	gaatggtgtg	gtggcatcag	tgatgtacgc	tgtggtcacc	540
cccatgtga	acctttttat	ctacagcctg	agaaacaggg	acatacaaag	tgccctgcgg	600
aggctgcgcc	ccagaacagt	cgaatctcat	gatctgttcc	atcctttttc	t	651

<210> 491

<211> 933

<212> DNA

<213> Unknown (H38g340 nucleotide)

<220>

<223> Synthetic construct

<400> 491

atgggcaagg	aaaactgcac	cactgtggct	gagttcattc	tccttggact	atcagatgtc	60
cctgagttga	gagtcgtcct	cttcctgctg	ttccttctca	tctatggagt	cacgttggtta	120
gccaatctgg	gcatgactgc	actgattcag	gtcagctctc	ggctccacac	ccccgtgtac	180
tttttctca	gccacttgct	ctttgtagat	ttctgctact	cctcaataat	tgtgccaaag	240
atggttgcta	atatctttaa	caaggacaaa	gccatctcct	tcctagggtg	catggtgcaa	300
ttctacttgt	tttgcacatg	tggagtcact	gaggtcttcc	tgctggccgt	gatggcctat	360
gaccgctttg	tggccatctg	taacccctcg	ctgtacatgg	tgaccatgtc	tcagaagctg	420
cgtgtggagc	tgacctcttg	ctgctacttc	tgtgggacgg	tgtgttctct	gattcactcg	480
tccttagctc	ttaggatcct	cttctataga	tctaagtga	ttaaccactt	cttctgtgat	540
ctacccctc	tcctaagtct	tgcttgctct	gatgtcactg	tgaatgagac	actgctgttc	600
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tgtgcctccc	acctcacagc	catcactgtc	tcccatggaa	caatccttta	catttattgc	780
aggccgagtt	caggcaacag	tggagatggt	gacaaagtgg	ccaccgtgtt	ctacacagtt	840
gtgattccca	tgctgaaccc	cctgatctac	agcctgagaa	ataaggatgt	gaacaaagct	900
ctcagaaaag	tgatgggctc	caaaattcac	tcc			933

<210> 492

<211> 963

<212> DNA

<213> Unknown (H38g341 nucleotide)

<220>

<223> Synthetic construct

<400> 492

atgtttctga	cagagagaaa	tacgacatct	gaggccacat	tcactctctt	gggcttctca	60
gattacctgg	aactgcaaat	tcccctcttc	tttgtatttc	tggcagtcta	cggcttcagt	120
gtggtagggg	atcttgggat	gatagtgatc	atcaaaatta	acccaaaatt	gcataccccc	180
atgtattttt	tcctcaacca	cctctccttt	gtggatttct	gctattcctc	catcattgct	240
cccatgatgc	tggtgaacct	ggtttagtaa	gatagaacca	tttcattctc	aggatgtttg	300
gtgcaattct	ttttcttttg	cacctttgta	gtgactgaat	taattctatt	tgcggtgatg	360
gcctatgacc	actttgtggc	catttgcaat	cctctgctct	acacagttgc	catctcccag	420
aaactctgtg	ccatgctggg	ggttgatttg	tatgcatggg	gagtcgcatg	ttccctgaca	480
ctcgcgtgct	ctgctttaaa	gttatctttt	catggtttca	acacaatcaa	tcatttcttc	540
tgtgagttat	cctccctgat	atcactctct	taccctgact	cttatctcag	ccagttgctt	600
cttttctactg	ttgccacttt	taatgagata	agcacactac	tcatcattct	gacatcttat	660
gcattcatca	ttgtcaccac	cttgaagatg	ccttcagcca	gtgggcaccg	caaagtcttc	720
tccacctgtg	cctccacact	gactgccatc	accatcttcc	atggcaccat	cctcttcttc	780
tactgtgtac	ccaactccaa	aaactccagg	cacacagtca	aagtggcctc	tgtgttttac	840
accgtggtga	tccccttggt	gaatccctcg	atctacagtc	tgagaaataa	agatgttaag	900
gatgcaatcc	gaaaaataat	caatacaaaa	tattttcata	ttaaacatag	gcattggtat	960
cca						963

<210> 493

<211> 303
 <212> DNA
 <213> Unknown (H38g342 nucleotide)

<220>

<223> Synthetic construct

<400> 493

tgttgcccac	tccaccacca	ttacctgcct	agacagtcac	tggatcagct	cacatactta	60
attgctttga	ttttcaattt	tctctttgtt	tttggcctcc	agagtccctt	tattttctta	120
aaggcatgac	agtgccttcc	aaaggatata	cactatattt	tcgttaaggc	gagaagggct	180
tcaggttatc	taacctacca	tattgctgga	aatagaagtt	aaaccgtttt	tttcctagtc	240
tgtaactgcc	actattatgg	tgatgatata	ggctaagtct	gaatatttta	tgtgaacata	300
tta						303

<210> 494

<211> 957

<212> DNA

<213> Unknown (H38g343 nucleotide)

<220>

<223> Synthetic construct

<400> 494

atgcctgtgg	ggaaacttgt	cttcaaccag	tctgagccca	ctgagtttgt	gttccgtgcg	60
ttcaccacag	ccactgaatt	ccaggttctt	ctcttccttc	tcttctcctt	cctctacttg	120
atgatcctct	gtggcaacac	agccatcatc	tgggtggtgt	gcacacacag	caccctccgc	180
accccgatgt	atttcttctt	gtccaacctg	tctttcctgg	aactctgcta	caccaccgtg	240
gtagtaccct	tgatgctttc	caacattttg	ggggcccaga	agcccatctt	gttggtcgga	300
tgtggggccc	aaatgttctt	ctttgtcacc	ctcggcagca	cggactgttt	cctcttggcg	360
atcatggcct	atgaccgcta	tgtggctatc	tgccaccgcg	tgcactacac	cctcatcatg	420
acccgcgagc	tggtcacgca	gatgctgggt	ggggccctgg	gcctggccct	cttcccctcc	480
ctgcagctca	cgcctttaat	cttcaccctg	cccttttgcg	gccaccacca	ggaaatcaac	540
cacttctctt	gcgatgtgcc	tcccgtctct	cgcctggcct	gcgctgacat	ccgcgtgcac	600
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cgggccttct	ccacctgctc	cttccacctc	accgtggctc	tgctgcagta	tggctgtctg	780
agcctcgtgt	acctgcgtcc	tcggctccagc	acctcagagg	atgaggacag	ccaaatcgcg	840
ttggtctaca	cctttgtcac	ccctttactc	aaccttttgc	tttacagcct	taggaacaag	900
gatgtcaaag	gtgctctgag	gagtgccatt	atccgtaaaag	cagcctctga	cgccaac	957

<210> 495

<211> 624

<212> DNA

<213> Unknown (H38g344 nucleotide)

<220>

<223> Synthetic construct

<400> 495

atggagctgg	agaatggcac	tgtgaagact	gggttctttc	tcctgggatt	cagcgaccat	60
ctggaacttc	agagtctcct	ttttgcagaa	tttttttcca	tctactctgt	tactctgatg	120
gggaaccttg	gaatgatttt	attaatcaca	atcagttccc	acttgcacac	tcctatgtac	180
tttttctctt	gtgtgttgtc	cttcatagat	gcatgctact	cttctgtcat	tgctcccaaa	240
ttacttgtga	acttgggttc	tgaaaagaag	accatttctt	acaatggctg	tgttgcacag	300
ttatatttct	tctgctcttt	agttgacaca	gaatctttcc	tcttggctgc	catggcttaa	360
gaccggtaca	tagcaatctg	taaccgcgtg	ctctatacag	tgattatgtc	caagaaggtt	420
tgttgccagc	ttgcaattgg	agcatttttg	gggggcacta	tgagctcaat	tattcatacc	480
acgaacactt	tcacatctgc	attctgctcc	agagatatta	accatttctt	ttgtgatata	540
tcccactctt	tctctctgtc	ctgcactgac	acatacatgc	atgacatcat	tctgggtgtc	600
tttgccagtt	ttgtggaagc	aatc				624

<210> 496
 <211> 963
 <212> DNA
 <213> Unknown (H38g345 nucleotide)

<220>
 <223> Synthetic construct

<400> 496
 cacacagagc cacggaatct cacagggtgc tcagaattcc tcctcctggg actctcagag 60
 gatccagaac tgcagcctgt cctccctggg ctgtccctgt ccatgtatct gctcacggtg 120
 ctgaggaacc tgctcatcat cctggctgtc agctctgact cccacctcca caccctcatg 180
 tacttcttcc tctccaaccc gtcattgggt gacatcgctt tcacctcggc cacagttccc 240
 aagatgattg tggacatgca gtgcgcatagc agtcattctt tatgcaagct gcctgacaca 300
 gatgtctttc tttgcccttt ttgcatgcat agaagatcat gctcctgatt gtgatggcct 360
 atgaccgatt tgtagccgtc tgtcactccc cacactaccc agtcattcat aatcctcggc 420
 tcgggtgtctt cttegttttg gtgtcctttt tccttagcct gttggattcc cagctgcaca 480
 gttggactgt gttacaattc accttcttca agaattgtga aatctctaata tttgtctgtg 540
 acccatctca acttctcaac cttgcctgtt ctgacagcgt catcgatagc atattcatat 600
 atttagatag tactatgttt cgttttcttc cgatttcagg gatccttttg tcttactcta 660
 acattgtccc ctccattcta agaatttcat catcagatgg gaagtctaaa gccttctcca 720
 cctgtcgtc tcacctggca gttgtttgct tattttatgg aacaggcatt ggcgtgtacc 780
 tgacttcagc tgtggcacca cccccaggag tgggtgtgtg gtgtcagtga tgtacactgt 840
 ggtcaccccc atgtgaacc ctttcatcta ctgctgaga aacagggaca ttcaaagcgc 900
 cctgtggagg ctgcgcagca gaacagtcga atctcatgat ctgttccatc ctttttcttg 960
 tgt 963

<210> 497
 <211> 932
 <212> DNA
 <213> Unknown (H38g346 nucleotide)

<220>
 <223> Synthetic construct

<400> 497
 gaaaagaatc tcattcttat gaatgggttt atgaacttca ctgattaccc agagttggaa 60
 atgcccttgt tcttagtggt tctcagttgc ttcctggcca ttattttgag aaatatggaa 120
 tgggtcattc tgaccaagt gaatgtgcat ctcttcaccc tatatacttc ttcctaacia 180
 atgtcaccct ttgggatacc tcagtcatca tgcctcagat cctggccatt ctggccacag 240
 gcaagacaac catttccfat ggccgctaata aaaagcaatg aggtcctttt tcttcatttg 300
 tgtaggaact tagtgtttcc tgccaacagc aatgaccata agcagccac tgccccacac 360
 tacaagccat gaacttcaag acatgttggg gttttttttt ggtggggatt tgttgttga 420
 catgctgggt tttgatgggt aacgtgggtga atgcctacac ctgaggacta tcaggagcca 480
 ctttcaacac catctgcaca tttgcccgct tcttctgtga tgacaattag atcaaattct 540
 gtcacatcct gccctgctg aagctcattt gaaatacttc aggaaacagc aagataatta 600
 ttgtgatctt tgacagcttt tatgattata gctggcacta gggtcacct gatctcttac 660
 ctgctaataca tcagggtctt gaggatgaaa tcacgagtg gcaaagccaa taattttatc 720
 catccacttg tgctccccc ctaactgcta tgaccttctt ttgggatccc catcttcaga 780
 catgtgaagt acctcagata aatcactgac agaagacaag ttggcatcat gacttgcacc 840
 atctttattc ctatgctaga acttttgatc caaagtctaa agaaggatat acaagttgcc 900
 ttcaaaaagg ccataggtaa cttctgggtt tt 932

<210> 498
 <211> 1005
 <212> DNA
 <213> Unknown (H38g347 nucleotide)

<220>
 <223> Synthetic construct

<400> 498

tctacagacc	cacagaatct	aacagatgtc	tctatatctc	tcctccgaga	acctcagagg	60
atccagaatg	gcagctgggc	cttgcctggg	tggtcctgtc	catgtgcctg	gtaacgggtgc	120
tggggaacct	gtcctatcat	ctggccgtca	gccctgactc	ccacctccac	acccccatgt	180
acttcttcct	ctccaacctg	tccttgccctg	acatcggttt	cacctccacc	acggtagcca	240
agatgattgt	ggacatccaa	tctcacagca	gagtcattct	ctatgcaggc	tgcttgactc	300
agatgtctcc	ctttgccatt	tttggagtca	tggaagagag	acacgctcct	gagtgtgatg	360
gcctctgacc	gctttgtagc	catctgtcac	cctctatatc	attcagccat	catgaacccg	420
tgtttctgtg	gctttctagt	tttgttgtct	tttttttttt	tttctgtcct	ttagatgccc	480
agctgcacaa	cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
tcttctgtga	cccttctcaa	ctcccccatc	ttgcattgtg	tgacaccttc	accaataaca	600
taatcatgta	tttccctgct	gccatatttg	gttttcttcc	catctcggtt	tcccttttct	660
cttactataa	aattgtttcc	tccattctga	gggtttcatc	atcaggtggg	aagtattagg	720
ccttctcttc	ctgttggtct	cacctgtcag	ttgtttgctg	attttatgga	acaggcggtg	780
gaggtacctc	agttgagatg	tgctcatctc	cccagggaag	gttgacgtgg	cctcagtgat	840
gtacatgggtg	gtcaccctca	tgctgaaccc	ctttgtctac	agcctgagaa	acagggatat	900
taaaagtgtc	ctgcgggtgc	cgcacggcag	cacggtctaa	tctcaatata	ttcttatctg	960
ttccattcct	tttgtagtgt	aggttaaaaa	ggcagcaagg	tcaaaa		1005

<210> 499

<211> 975

<212> DNA

<213> Unknown (H38g348 nucleotide)

<220>

<223> Synthetic construct

<400> 499

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accatcactg	aattcattct	cctgggattt	ttcaagcagg	atgagcatca	aaacctcttc	120
tttgtgcttt	tcttggggat	gtacctgggc	actgtgattg	ggaacgggct	catcattgtg	180
gctatcagct	tggtacgta	ccttcatacc	cccatgtatc	tcttccttgc	caatctatcc	240
tttgctgata	tttccctccat	ttccaactca	gtccccaaaa	tgctgggtgaa	tattcaaacc	300
aagagtcaat	ccatctctta	tgagagctgc	atcacacaga	tgtacttttc	tattgtgttt	360
gtcgtcattg	acaatttgct	cttggggacc	atggcctatg	accactttgt	ggcgtatctg	420
cacctctctg	attatacaat	tctcatgcgg	cccagggttcg	gcattttgct	cacagtcctc	480
tcattggttc	tcagtaatat	tattgctctg	acacacaccc	ttctgtctcat	ccaattgctc	540
ttctgttaac	acaacactct	cccacacttc	ttctgtgact	tgccccctct	gctcaaactg	600
tctgtttcag	atacattgat	caatgagctt	gtgttggtta	ttgtgggttt	atcagttatc	660
atcttccctt	ttacactcag	cttcttttcc	tatgtctgca	tcacagagac	tgctctgaga	720
gtatcttcca	cacagggaaa	gtggaaagcc	ttctccactt	gtggctctca	cctgacagtt	780
gtattactgt	tctacggaac	cattgttaggc	gtgtactttt	ttccctcttc	cactcaccct	840
gaggacactg	ataagattgg	tgctgtccta	ttcactgtgg	tgacacccat	gataaaccct	900
ttcatctaca	gcttgaggaa	taaggatatg	aaagggtgcc	tgagaaagct	catcaataga	960
aaaatttctt	ccctt					975

<210> 500

<211> 768

<212> DNA

<213> Unknown (H38g349 nucleotide)

<220>

<223> Synthetic construct

<400> 500

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cccaaaactgt	tagagatttt	ggttggtggaa	gacagaacta	tctccttcaa	aggatgcatg	120
gtacaatttt	tctttgggtg	tgcatgttga	atcacagaaa	tggtcatgtt	agcgggtgatg	180
gcttatgact	tggttatggc	tggttgtaac	ccctgtctct	acacagtggc	tatgtctcct	240
aagctctgtg	ctctcctggg	agctggaact	tacacatggg	gtggactctg	ttccctgaca	300

ctcacttatt	ctcttttggg	gttatcctac	tgtggatcta	acatcataaa	tcactttggc	360
tgtgagtact	ctgccattct	ttctctatcc	tgtctctgac	cctacttcaa	ccagatggcg	420
tgttttagtca	tttctatatt	cagtgaagct	tgtagcctcc	tggccatcct	tgccttctat	480
gtcttcatag	ttgccactgt	catcaagatg	ctttctacgg	gtggacccca	aaaggccatc	540
tccacctgtg	cctccacact	gaccacgctc	tccattttcc	atgggggtcat	cctgctcctt	600
tactgtgtgc	ccaactccaa	aagctcatgg	ctcctgggtca	aagtgggtac	tgtacttttt	660
acagtcataa	tccctatgct	gaatcccctg	atctacagcc	ttaggaacaa	agatgtaaaa	720
gggaccgtca	ggaagttgat	aaactcccaa	tcaccttttc	actcaaaa		768

<210> 501

<211> 951

<212> DNA

<213> Unknown (H38g350 nucleotide)

<220>

<223> Synthetic construct

<400> 501

atggcagaga	gtggcaccac	gggtgacagaa	ttttttctga	gggggttccg	gttgaaggca	60
gagctgcaga	taggtctctt	ctttgtgttt	ctggtcattt	ttctcatcac	catggggggc	120
aacctgggca	tgattgtgct	aatttaattc	agactgacct	tgggtccag	actcccatgt	180
acttcttct	cagtcattct	tccttcctgg	acatttgcta	ctcttctgtt	attggctctc	240
agttgcttga	gactttggga	ctgataagat	gatcatcacc	tatgagcgt	gtgccagcca	300
attcttctt	ttcacactct	gtgctagcat	tgagtgtttc	cttttggtg	tgatggctta	360
tgaccggta	ctggctgtgt	gtaacccct	cctctatgcc	atagtcatga	caccaaagac	420
ccgctggcg	ctgctggccg	gggcatattc	tggtgccata	gtcaattctg	tgatctgcac	480
tggtgcacc	ttctctatct	ccttctctaa	gtccaaccat	gtagacttct	ttttctgtga	540
cctccaccc	ctgctgaagc	ttgcctgtag	tgaaccagg	ccacgggaat	gggtaatcta	600
cctctcagct	tttctggtca	tcacaaccag	catttcagtg	attcttacat	cgtacttgtt	660
catcattcag	tctgttctga	agattcgtac	agcaggtgga	aagccaagac	cttctccacc	720
tgtgttctc	acatgactgc	attgactctc	ttctttggaa	cactcatatt	catatacctg	780
aaaggcaaca	tgggcgaatc	ccttgaggaa	gacaagatcg	tgtcaatatt	ttacactgtg	840
gtcatcccca	tgctaaatcc	aatgatctac	agcctgagaa	acaaagacat	gaaagaggct	900
ctgaagaaa	gtttcaacag	gataagggtt	tcccaagcag	agtaactctt	g	951

<210> 502

<211> 939

<212> DNA

<213> Unknown (H38g351 nucleotide)

<220>

<223> Synthetic construct

<400> 502

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taccagaac	tgcaagtccc	actcttctct	gtttttctgg	ccatctacaa	tgtcactgtg	120
ctaggaata	ttgggttgat	tgtgatcatc	aaaatcaacc	ccaaactgca	taccccatg	180
tactttttcc	tcagccaact	ctcctttgtg	gatttctgct	attcctccat	cattgctccc	240
aagatgttgg	tgaaccttgt	tgtcaaagac	agaaccattt	catttttagg	atgcgtagta	300
caattctttt	tcttctgtac	ctttgtggtc	actgaatcct	ttttattagc	tgtgatggcc	360
tatgaccgct	tcgtggccat	ttgcaaccct	ctgctctaca	cagttgacat	gtcccagaaa	420
ctctgcgtgc	tgctggttgt	gggatccctat	gcctggggag	tctcatgttc	cttgggaactg	480
acgtgctctg	ctttaaagtt	atgttttcat	ggtttcaaca	caatcaatca	cttcttctgt	540
gagttctcct	cactactctc	cctttcttgc	tctgatactt	acatcaacca	gtggctgcta	600
ttctttcttg	ccacctttta	tgaatcagc	acactactca	tcgttctcac	atcttatgcg	660
ttcattgttg	taaccatcct	caagatgcgt	tcagtcatgt	ggcgccgcaa	agccttctcc	720
acctgtgcct	cccacctgac	tgccatcacc	atcttccatg	gcaccatcct	cttcttttac	780
tgtgtgccca	actccaaaaa	ctccaggcac	acagtcaaag	tggcctctgt	gttttacacc	840
gtgggtatcc	ccatgttgaa	tcccctgatc	tacagtctga	gaaataaaga	tgtcaaggat	900
acagtcaccg	agatactgga	caccaaagtc	ttctctttac			939

<210> 503
 <211> 932
 <212> DNA
 <213> Unknown (H38g352 nucleotide)

<220>

<223> Synthetic construct

<400> 503
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 ctccagtgga gggttcctct cttcctcata tttttgagtt tctatcttgc cactatgtta 120
 gggaacacag gcatgatcct cctgatccgt ggcatcgtc ggctccacac cccgatgtac 180
 ttcttctctca gccaccttct cttgggtggac atctgctact cgtccgccat catccctcag 240
 atgctggctg tgctgtggga gcacggcaca accatctccc aggtcgcgtg tgcagctcag 300
 ttcttctctct tcaccttctt tgctccatc gactgctacc ttctggccat catgcctatg 360
 accgctacac ggccgtgtgc agccctgct ttatgtcacc atcataaccg agaaggaccg 420
 ctgggctag tcactggggc ttacgttgct ggttttttca gtgcctttgt tgcacggtca 480
 cagccttcac tctctccttt tgtggaaaca atgagatcaa cttcatttct tgtgacctcc 540
 ctctcttatt aaaactctcc tgtggggaca gctacactca ggaagtgtgt attattgtgt 600
 ttgctctttt cgtcatgcct gcctgtatct tgggtatctt ggtatcctac ctgtttatca 660
 ttgtggccat cctgcagatc cactctgctg gaggccgggc caagaccttc tccacctgcg 720
 cctccacact cactgccgtc gctcttttct ttggcaccct catcttcatg tacctgcgag 780
 acaacacagg ccagtcctcc gagggagacc gagtggtgtc tgtgctctac acggtggtga 840
 cccaatgct gaatcccctt atctatagcc tgagaaacaa ggaggtaaaa gaggccacta 900
 ggaaagccct gagcaaatca aagcctgcta ga 932

<210> 504

<211> 762

<212> DNA

<213> Unknown (H38g353 nucleotide)

<220>

<223> Synthetic construct

<400> 504
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 gtcaccatgc tgagtatat ctggttcaat gtgagggaaa tcagctttaa tgcctgcttg 120
 tcccacatgt tctttattaa attcttcact gtcattggaat cctcagtgtt gttggccatg 180
 gcttttgcac gttttgtggc cgtctctaata ccccttaggt atgccatgat tttaactgac 240
 tccagaatag ctcaaattgg agtggcaagt gtcacaggg ggctcctaata gctgacacca 300
 atggtagcac ttcttataag actttcttac tgccacagcc aagtactcca ccactcctac 360
 tgctaccacc ctgatgtgat gaagctctca tgcacagaca ccagaatcaa cagtgcagtt 420
 gggctgactg ccattgtctc tactgttggg ttagacttac ttctcatcct cttttcttat 480
 gttttgatca ttaggactgt ccttagcgtt gcttcccag aagagaggaa ggaaaccttc 540
 agtacatgtg tctccacat tgtggctttt gctatatatt acattccatt gatcagctcg 600
 tccattgttc acagatttgg gaaacaagcc ccagcctatg tacatactat gattgctaac 660
 acctacctgc tgatctcccc tttgatgaac cctgtcatct acagtgtgaa aaccaaacag 720
 atacgtagag ctgtgataaa aattctccat tccaaagaaa ca 762

<210> 505

<211> 565

<212> DNA

<213> Unknown (H38g354 nucleotide)

<220>

<223> Synthetic construct

<400> 505
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 ccagagatga aagtgacctt atttgctgta ttcttggctg tttatatcat taatttctca 120
 gcaaatcttg gaatgatagt tttaatcaga atggattacc aacttcacac accaatgtat 180

ttcttctca	gtcatctgtc	tttctgtgat	ctctgctatt	ctactgcaac	tgggccaag	240
atgctggtag	atctacttgc	caagaacaag	tcaataccct	tctatggctg	tgctctgcaa	300
ttcttgggtct	tctgtatctt	tgcagattct	gagtgtctac	tgctgtcagt	gatggccttt	360
gatcgggtaca	aggccatcat	caacccccctg	ctctatacag	tcaacatgtc	tagcagagtg	420
tgctatctac	tcttgactgg	ggtttatctg	gtgggaatag	cagatgcttt	gatacatatg	480
acactggcct	tccgcctatg	cttctgtggg	tctaatagaga	ttaatcattt	cttctgtgat	540
atccccctct	ctcttattac	tctct				565

<210> 506

<211> 978

<212> DNA

<213> Unknown (H38g355 nucleotide)

<220>

<223> Synthetic construct

<400> 506

ctcaatttca	ttatcttctt	caggtgaacc	agctatatgt	agcctatggc	caaaagaaat	60
ctcagcactg	tgacagagtt	cattcttcta	gtcttcacag	atcaccctga	actggcagtt	120
ccactcttcc	tagtggttct	cagtttctat	cttgctcactt	ttctggggaa	tggggggatg	180
atcattctaa	tccaagtga	tgcccaactc	cacacccccg	tgtacttctt	cctgagccac	240
cttgctttcc	tggatgcctg	ctgtgcctca	gtaatcaccc	ctcagattct	ggccacactg	300
gccacagaca	agacagttat	ctcctatggc	tgccgtgctg	tgacagttctc	tttcttcacc	360
atatgtgcag	gcacagagtg	ttacctgctg	tcagtgtatg	cctatgaccg	ctttgttgcc	420
attagcaatc	cactgcactg	taacatgacc	atgactccag	gtacctgcag	ggtctttttg	480
gccagtgcct	tcatctgtgg	ggtgtcaggg	gccattctgc	ataccacgtg	caccttcacc	540
ctctccttct	gttgtgacaa	tcagatcaac	ttcttcttct	gtgacctccc	acccctgctg	600
aagctgcctc	gcagcagcat	gacacaaact	gagattgtca	ttctcctttg	tgcaaaatgc	660
atgttcctag	ccaatgtcat	ggttatcctg	atctgctaca	tgctcattat	cagagccatt	720
ttgaggggtga	agtcggcagg	tgggtaagcc	aagaccttct	ccacctgcac	ctccccatctc	780
accactgttg	tctcttctct	tgggacactt	gccttcatgt	accagagaag	taactccgcc	840
aaatcctcag	aggaagacaa	gatagtgtct	gtcttttaca	ctgtaatcat	ccctatgttg	900
aacctcttga	tctacagtct	gaggaacaaa	gatgtaaaa	ctgcatttgg	aaaactcggt	960
ggtaaattcc	aatttcca					978

<210> 507

<211> 983

<212> DNA

<213> Unknown (H38g356 nucleotide)

<220>

<223> Synthetic construct

<400> 507

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attggcatcc	cagggtctga	ggcggttcat	ggctggctcg	ccatccccctt	ctcctccatg	120
tacactgtgg	ccctccctgg	gaactgcctg	atcctcctgg	ctgtgaagag	gaaccccagc	180
ctgcaccagc	ccatgtgcta	cttctctgtc	atgtgtggcg	tccccaaagc	gggcctcacc	240
ttgtccacac	tgcccatcac	cttggtctgt	ctctgggttg	accaccggct	catgggcttc	300
aatgcctgcc	tggtccagat	gttcttctct	cactcctctg	tggtggagtc	ctcagtgtct	360
ctggccatat	cctttgacca	ctttgtggcc	atctccaacc	ccctgcacta	tgacagtgtc	420
ctcacaata	gtgtcatcat	caggattggg	ctggccattg	tggtctcaagt	tacctgtgtc	480
ctcttctctg	gccatttccg	gttaagagtc	ttaaatttctg	ccctgggtgat	aacatcccat	540
ccactcgtt	ctgtttccac	cctgatgtaa	tgaggcgggc	ctgtgcggac	atcacgatca	600
atatatgcta	tggggtctac	gtgggtgttt	ctacaggggg	cttagactcg	ctgctcatct	660
ttctgtccta	taccttcac	ctgcacacag	tcatgggtct	ggctgtctcc	agggagcgca	720
tctgggccct	caacacctgc	gtttcccaca	ttccggctgt	ctttgtcttc	tttattccag	780
gtatcacctg	gtccatgac	caccattttg	ggaggcacct	gccccacatt	gtacatgtct	840
ttgttacct	tgtgtacctg	gtgatgcctt	ctgtgtctca	ccccatcatt	tacagtatga	900
agtccaagcc	catcaggag	gccatcctca	ggatgctgat	ggggagaagc	caaggctgat	960
gaaattacaa	aatattatag	ggt				983

<210> 508
 <211> 933
 <212> DNA
 <213> Unknown (H38g357 nucleotide)

<220>
 <223> Synthetic construct

<400> 508
 atgggcaagg aaaactgcac cactgtggct gagttcattc tccttggact atcagatgtc 60
 cctgagttga gactctgcct cttcctgctg ttccttctca tctatggagt cacgttgta 120
 gccaacctgg gcatgattgc actgattcag gtcagctctc ggctccacac ccccatgtac 180
 ttttctctca gccacttgct ctctgtagat ttctgctact cctcaataat tgtgcaaaa 240
 atgttggcta atatctttaa caaggacaaa gccatctcct tcctaggggtg catgggtgcaa 300
 ttctacttgt ttgcaacttg tgtggctact gaggtcttcc tgctggccgt gatggcctat 360
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 ctgggtggcca ctttgaatga gagtggtacc atcatgatca tcctcacctc ctacctgcta 660
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 tgtgcttccc acctcacagc tatcactgtc ttccatggaa cagtccttct catttattgc 780
 aggccagtt caggcaatag tggagatgct gacaaagtgg ccaccgtgtt ctacacagtc 840
 gtgattccta tgctgaactc tgtgatctac agcctgagaa ataaagatgt gaaagaagct 900
 ctcagaaaag tgatgggctc caaaattcac tcc 933

<210> 509
 <211> 621
 <212> DNA
 <213> Unknown (H38g358 nucleotide)

<220>
 <223> Synthetic construct

<400> 509
 cccctctgc gatgggggtc ctaagagcca gcgagggaag aggggctggc tctcagttcc 60
 cgcctttttt ttttttctca gtgttttaga cgcccagctg cacaacttga ttgccttaca 120
 aatgacctgc ttccaggatg cggaaattcc taatttcttc tgtgacctt ctcaactccc 180
 ccactctgca tgttgtaga ccttcaccaa taacataatc atgtatttcc ctgctgtcat 240
 atttggtttt cttcccatct ctgggaccct tttctcttac tataaaattg tttcctccat 300
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 gtcagttgtt tgctgatttt acggaacggg cgttggagga tacttcagtt cagatgtgtc 420
 atcttccccg agaaaggctg cagtggcctc agtgatgtac acgggtgatca ccccatgctg 480
 aacccttcca tctacagcct gagaaacagg catattaaaa gtgtcctgcg gcggccgcac 540
 agcagaccg tccaatctcc gtgtcttctt aactgttcca ttccttttgt agtgtgggtt 600
 aacaaaggca gcaaggtaaa a 621

<210> 510
 <211> 633
 <212> DNA
 <213> Unknown (H38g359 nucleotide)

<220>
 <223> Synthetic construct

<400> 510
 atttgactga aattgatctt tggaaatcct agatagtaat agattttcag atgtgtctat 60
 gattattttg tgggactgtc aacccttgct ttatgacacc atcacaaactc tcaagatgtc 120
 tggcagaagc tgggtactgc atattgtaga gggtttgaca aatgtaatcc aatgtatata 180
 cttcacctgc tcactctcct tttgtgcctt catctatagg tttcactctc tgtgacctcc 240

attgctgctg	accctgaatt	gggtgatagc	ttcctccagc	agctgctgat	ttttcacttt	300
gctctgtata	tgattctgac	cagactagtt	ttgatcctgt	tctctgactt	gttcacacgc	360
aaggccatct	aaacacctgc	aatcagggtc	tctaggcaaa	gattcctcaa	cctttttcta	420
cctttgcctc	atgcagaact	gcagttcggg	tgattgttga	gactacagct	ttgatctatg	480
tgtgcagcag	taggcaagtc	ccttacaggg	gagagggccg	tgaccatgtt	ttagactgta	540
gtgaacacca	ggctgaccat	tccaatttta	tagcctgagg	aaaaaaaggc	aaaggaggcc	600
ctgaggaaag	gtcttaataa	agccaagttg	ttc			633

<210> 511

<211> 945

<212> DNA

<213> Unknown (H38g360 nucleotide)

<220>

<223> Synthetic construct

<400> 511

atgagttcct	gcaacttcac	acatgccacc	tttgtgctta	ttggtatccc	aggattagag	60
aaagccatt	tctgggttgg	cttccccctc	ctttccatgt	atgtagtggc	aatgttttga	120
aactgcatcg	tggtcttcat	cgtaaggacg	gaacgcagcc	tgacgctcc	gatgtacctc	180
tttctctgca	tgcttgacgc	cattgacctg	gccttatcca	catccaccat	gcctaagatc	240
cttgcccttt	tctggtttga	ttcccgagag	attagctttg	aggcctgtct	taccagatg	300
ttctttattc	atgccctctc	agccattgaa	tccaccatcc	tgctggccat	ggcctttgac	360
cgttatgtgg	ccatctgcca	cccactgcgc	catgtgcag	tgctcaacaa	tacagtaaca	420
gcccagattg	gcacgtggc	tgtggtccgc	ggatccctct	ttttttccc	actgcctctg	480
ctgatcaagc	ggctggcctt	ctgccactcc	aatgtcctct	cgcactccta	ttgtgtccac	540
caggatgtaa	tgaagtggc	ctatgcagac	actttgccc	atgtggtata	tggtcttact	600
gccattctgc	tggtcatggg	cgtggacgta	atgttcatct	ccttgtccta	ttttctgata	660
atacgaacgg	ttctgcaact	gccttccaag	tcagagcggg	ccaaggcctt	tggaacctgt	720
gtgtcacaca	ttggtgtggg	actcgccctc	tatgtgccac	ttattggcct	ctcagtggta	780
caccgctttg	gaaacagcct	tcattccatt	gtgcgtgttg	tcatgggtga	catctacctg	840
ctgctgcctc	ctgtcatcaa	tcccatcatc	tatggtgcca	aaaccaaa	gatcagaaca	900
cgggtgctgg	ctatgttcaa	gatcagctgt	gacaaggact	tgacg		945

<210> 512

<211> 834

<212> DNA

<213> Unknown (H38g361 nucleotide)

<220>

<223> Synthetic construct

<400> 512

atgtatgcct	tgccaccct	gggtaacctg	accattgtcc	tcattcattcg	tgtggagagg	60
cgactgcatg	agcccatgta	cctcttcctg	gccatgcttt	ccactattga	cctagtccctc	120
tcctctatca	ccatgcccaa	gatggccagt	cttttcctga	tgggcatcca	ggagatcgag	180
ttcaacattt	gcctggccca	gatgttcctt	atccatgctc	tgtagccgt	ggagtcagct	240
gtcctgctgg	ccatggcttt	tgaccgcttt	gtggccattt	gccaccatt	gcgcatgct	300
tctgtgctga	caggtgtac	tgtggccaag	attggactat	ctgccctgac	cagggggttt	360
gtattcttct	tccactgcc	cttcactctc	aagtggttgt	cctactgcca	aacacatact	420
gtcacacact	ccttctgtct	gcaccaagat	attatgaagc	tgctctgtac	tgacaccagg	480
gtcaatgtgg	tttatggact	cttcactc	ctctcagtc	tggtgtgga	ctctctcttc	540
attggcttct	catatctct	catctgtgg	gctgttttgg	agctgtcctc	tcggagggca	600
gcactcaagg	ctttcaacac	ctgcactctc	cacctctgtg	ctgttctggg	cttctatgta	660
cccctcattg	ggctctcggt	ggtgcatagg	ctgggtgggc	ccacctccct	cctcatgtg	720
gttatggcta	atacctactt	gctgctacca	cctgtagtca	accccttgt	ctatggagcc	780
aagaccaaag	agatctgttc	aagggtcctc	tgtatgttct	cacaaggtgg	caag	834

<210> 513

<211> 957

<212> DNA

<213> Unknown (H38g362 nucleotide)

<220>

<223> Synthetic construct

<400> 513

atgctggggtc	cagcttacaa	ccacacaatg	gaaacccctg	cctccttctt	ccttgtgggt	60
atcccaggac	tgcaatcttc	acatcttttg	ctggctatct	cactgagtgc	catgtacatc	120
acagccctgt	taggaaacac	cctcatcgtg	actgcaatct	ggatggattc	cactcggcat	180
gagcccatgt	attgtcttct	gtgtgttctg	gctgctgtgg	acattgttat	ggcctcctcc	240
gtggtaccca	agatggtgag	catcttctgc	tcgggagaca	gctccatcag	ctttagtgtc	300
tgtttcactc	agatgttttt	tgtccactta	gccacagctg	tggagacggg	gctgctgctg	360
accatggctt	ttgaccgcta	tgtagccatc	tgcaagcctc	tacactacaa	gagaattctc	420
acgcctcaag	tgatgctggg	aatgagtatg	gccgtcacca	tcagagctgt	cacattcatg	480
actccactga	gttggtgat	gaatcatcta	cctttctgtg	gctccaatgt	ggttgtccac	540
tcctactgta	agcacatagc	tttgccagg	ttagcatgtg	ctgacccgt	gcccagcagt	600
ctctacagtc	tgattggttc	ctctcttatg	gtgggctctg	atgtggcctt	cattgctgcc	660
tcctatatct	taattctcag	ggcagtat	gatctctcct	caaagactgc	tcagttgaaa	720
gcattaagca	catgtggctc	ccatgtgggg	gttatggctt	tgtactatct	acctgggatg	780
gcatacatct	atgcggcctg	gttggggcag	gatatagtgc	ccttgccacac	ccaagtgtctg	840
ctagctgacc	tgtacgtgat	catcccagcc	actttaaatc	ccatcatcta	tggcatgagg	900
accaaacaat	tgctggaggg	aatatggagt	tatctgatgc	acttcctctt	tgaccac	957

<210> 514

<211> 966

<212> DNA

<213> Unknown (H38g363 nucleotide)

<220>

<223> Synthetic construct

<400> 514

atgaatgaga	caaatcattc	ttgggtgaca	gaatttgtgt	tgctgggact	gtctagtcca	60
agggagctcc	aacctttctt	gtttcttata	ttttcactac	tttatctagc	aattctgttg	120
ggcaactttc	tcatactcct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	caaacctgtc	atztatagac	gtatgtgttg	cctcttctgc	tacctctaaa	240
atgattgcag	actttctggt	tgagcacaag	actatttctt	ttgatcccca	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatgggtg	tcctagtttc	catggcctat	360
gaccgttatg	ttgctatatg	caaacctccc	cactacatga	caatcatgag	ctgctgtgta	420
tgtgttgctg	tcgtcctcat	ttcctgggtt	gtgggcttca	tccataccac	cagccagttg	480
gcattcacgt	taatctgcca	ttttgtggtc	ctaataagg	agatagtttt	tttctgtgac	540
cttcctctag	cgacgaagtt	agcctgcata	gacacttatg	ttgtcagcct	actaatagtt	600
gcagatagtg	gctttctttc	tctgagttcc	tttctcctct	tggttgtctc	ctacactgta	660
atacttgta	cagttaggaa	tcgctcctct	gtaagcatgg	tgaaggccca	ctccacattg	720
actgtcaca	tcactgtggt	cactttatct	tttgatcgt	gtattttcat	ctatgtgtgg	780
cccttcagca	gttactcagt	tgacaaagtc	ccttgctgtat	tctacaccat	cttcacgtct	840
attttaaac	ctgtaatcta	catgctaaga	aacaagaag	tgaaggcagc	tatgtcaaaa	900
ctgaagagtc	ggtatcagaa	gcttggtcag	gtttctgtag	tcataagaaa	cgttcttttc	960
ctagaa						966

<210> 515

<211> 966

<212> DNA

<213> Unknown (H38g364 nucleotide)

<220>

<223> Synthetic construct

<400> 515

atgctggggtc	cagcttataa	ccacacaatg	gaaacccctg	cctccttctt	ccttgtgggt	60
atcccaggac	tgcaatcttc	acatcttttg	ctggctatct	cactgagtgc	catgtacatc	120

atagccctgt	taggaaacac	catcatcgtg	actgcaatct	ggatggattc	cactcggcat	180
gagcccatgt	attgctttct	gtgtgttctg	gctgctgtgg	acattgttat	ggcctcctcg	240
gtggtacca	agatgggtgag	catcttctgc	tcaggagaca	gtcfaatcag	ctttagtgtc	300
tgtttcactc	agatgttttt	tgccactta	gccacagctg	tggagacggg	gctgctgctg	360
accatggctt	tgaccgcta	tgtagccatc	tgcaagcctc	tacactacaa	gagaattctc	420
acgcctcaag	tgatgctggg	aatgagtatg	gccatcacca	tcagagctat	catagccata	480
actccactga	gttggatggg	gagtcattct	cctttctgtg	gctccaatgt	ggttgtccac	540
tcctactgtg	agcacatagc	tttggccagg	ttagcatgtg	ctgaccccg	gccagcag	600
ctctacagtc	tgattggttc	ctctcttatg	gtgggctctg	atgtggcctt	cattgctg	660
tcctatatct	taattctcaa	ggcagtat	ggtctctcct	caaagactgc	tcagttgaaa	720
gcattaagca	catgtggctc	ccatgtgggg	gttatggcct	tgtactatct	acctgggatg	780
gcattcatct	atgctggcctg	gttggggcag	gatgtagtgc	ccttgacac	ccaagtctg	840
ctagctgacc	tgtagctgat	catccagcc	accttaaatc	ccatcatcta	tggcatgagg	900
accaaacaac	tgctgggagag	aatatggagt	tatctgatgc	atgtcctctt	tgaccattcc	960
aacctg						966

<210> 516

<211> 942

<212> DNA

<213> Unknown (H38g365 nucleotide)

<220>

<223> Synthetic construct

<400> 516

atggagggt	tcaactattc	cagagtatct	gaattcatgt	tacttggact	tactgattct	60
cctgaactcc	agatattctt	ttctgtgggt	ttttctgtct	tctattta	gaccatgttg	120
ggcaactgcc	tgattttgct	cactgtccta	tcacctcac	accttctc	tcgcatgtac	180
ttctgtctca	gcaacatgtc	tcattgacat	gtgctgtcc	tcctttgcca	caccaaagat	240
gattatggac	ttttttgtc	tgctgaagac	catctctttt	gaaggctgca	tttctcagat	300
ctttttttta	cacctcttca	atgggactga	gattgtgctg	ttgatctcca	tgtcttttga	360
caggtatatt	gccatatgta	aacctctcca	ctattcaaca	attatgagcc	aaagagtgtg	420
tggttagctt	gtggcagttt	cttgttggac	agtgggcttt	ctacatacaa	tgagccaatt	480
agtttttccc	tctatttgcc	cttctgtgtt	cccaatgttg	tagacagttt	tttctgtgat	540
cttcttttgg	tcateccagt	agcttgtata	gatatttatg	ttcttgggac	ctccatgatt	600
tcaaccagt	gtgtgattgc	tcttataagt	tttctgtctt	tgctcacctc	ctacatcatt	660
gttcttaata	ttgtcagggg	ctactcctcc	acaggatcct	ccaaggctct	ttctacctgt	720
acagcgcatt	ttattgttgt	gttaatgttc	tttgggacct	gtattttcat	ttatgtgtgg	780
ccttcacaaa	acttctcgtg	agacaaaatt	ctctccgttt	tctataccat	cttactccc	840
tttctgaatc	cacttatcta	tactttgaga	aaccaggaag	tgaagacagc	aatgaagaag	900
aaactgaata	ttcagtattt	cagtcttggg	aaaactgctc	cg		942

<210> 517

<211> 952

<212> DNA

<213> Unknown (H38g366 nucleotide)

<220>

<223> Synthetic construct

<400> 517

atgctcactt	ttcataatgt	ctgctcagta	cccagctcct	tctggctcac	tggcatccca	60
gggtggaggt	ccctacacgt	ctggctctcc	atcccctttg	gctccatgta	cctgggtggct	120
gtggtgggga	atgtgaccat	cctggctgtg	gtaaagatag	aacgcagcct	gcaccagccc	180
atgtactttt	tcttgtgcat	gttggctgcc	attgacctgg	ttctgtctac	ttccactata	240
cccaaacttc	tgggaatctt	ctgggtccgt	gcttgtgaca	ttggcctgga	cgctgcttg	300
ggccaaatgt	tccttatcca	ctgctttgcc	actgttgagt	caggcatctt	ccttgccatg	360
gcttttgatc	gctacgtggc	ccatctgcaa	cccactacgt	catagcatgg	tgctcactta	420
tacagtgggt	ggctgcttgg	ggcttgttcc	tctctccggg	ggtgttctct	acattggacc	480
tctgcctctg	atgatccgcc	tgctggctgcc	cctttataaa	acccatgtta	tctccactc	540
ctactgtgag	cacatggctg	tagttgcctt	gacatgtggc	gacagcaggg	tcaataatgt	600

ctatgggctg agcatcggct ttctgggtgtt gatcctggac tcagtggcta ttgctgcatc	660
ctatgtgatg attttcaggg cctgatggg gttagccact cctgaggcta ggcttaaaac	720
cctggggaca tgcgcttctc acctctgtgc catcctgatc ttttatgttc ccattgctgt	780
ttcttccttg attcaccgat ttggtcagtg tgtgcctcct ccagtcacaca ctctgctggc	840
caacttctat ctctcattc ctccaatcct caatcccatt gtctatgctg ttcgcaccaa	900
gcagatccga gagagccttc tccaaatacc aaggatagaa atgaagatta ga	952

<210> 518

<211> 301

<212> DNA

<213> Unknown (H38g367 nucleotide)

<220>

<223> Synthetic construct

<400> 518

cagatgctga cagattggtg gggacctaata aggaccacaa gttacgtgaa ctcaccattc	60
aattccttgt ctctctgtag ttatgtgcca ctatataatt tctacaatta ttttataaatt	120
atatgccatc ctttgttaata tttgttaatac atgaacctat atctcctcct taatcttact	180
tttaactctg agggataaatt cattcatttt tggcatcatg tatactctca tcctaaaaaat	240
tccaaggatg aaaaaaaaaa accttcagat aattcccctc attggttgcg gccttgctga	300
a	301

<210> 519

<211> 506

<212> DNA

<213> Unknown (H38g368 nucleotide)

<220>

<223> Synthetic construct

<400> 519

aatagttagt ccaagcattt cttactctta aaattgtgtt caatgtttgc agtcactttc	60
ctatccctga tattatcagg aaagggcctg caatttcctt tctacttctc tgagtcaact	120
gcaaagtctc agatgttttc acagtgtgaga caagagaaca agaagcacca atgaaaacca	180
cggggttcta tggaggcatc atggtgtggt gagtagaagc atgctactct agctgtatct	240
cactgggttc aaatcctgac tatacggcat atggtgcatt aacagcccgc tgaccacaag	300
aatttctatg ctggtaaaaat aggtttataa taatgccagt caatctaaag atgctttaag	360
tgaagactat ttggtgtttt tcaaggactc aataatcatt aactgtgac acgatctttc	420
ccttacctac tttcaataag taaataaatt acattttatta aacaaaagaa atttaattct	480
gcttttctga aacaacacaa ttctat	506

<210> 520

<211> 837

<212> DNA

<213> Unknown (H38g369 nucleotide)

<220>

<223> Synthetic construct

<400> 520

ctccctccc tgtttttttag agtttttgta attttggttt gtttactac tctttgttaa	60
gctatgcatt ctctttctaa ttattctact tgttaaatat ttattaaaaa caaaaatagc	120
aatgacatat tttacatatt tatctaatta taagctcaaa gcatgaaata gtattgactt	180
ccacatacat atgttttgtt acgtgtatat tatgaataaa ttagttcatc tcaaatatga	240
aactttaaca tctttaccat ttttttgga tagtctagga ttttagacac tctttaattt	300
tgttttacct tttatgtcac atattcttca ttaatagtta ttaatatgtt gtattttcta	360
gctgttcttg caaaaagtag ttttatttta tgtttcaaca gtctcagcgt caactgtgac	420
actttctgtg tttggctttc ttgttttgga attgtttatac ttgatgtgca tcccattgca	480
cattgttatg tttctcaaaa gattatttaa atgttatgtg tttttatgat cactcgtttt	540
ttgcttcatg catgcattat tgccttaaac attaaaaaat acttggtttg atgtgctttt	600

tatctttata	tgtgaaaaat	ctttgctggc	taatatgtct	tttgtcacia	ttgtttcctc	660
cttaattctc	ttaacgaatt	aagagattat	ttcattttct	tctgtcattt	tatgtggtag	720
aatacatctg	aatctgtcct	catttttctt	acatagggtt	ttcattttct	ttttctgctt	780
gaaattgccca	acatatatct	aaatgttgac	ctacttagta	ttatactgac	tttggtga	837

<210> 521

<211> 461

<212> DNA

<213> Unknown (H38g370 nucleotide)

<220>

<223> Synthetic construct

<400> 521

tgcacatgt	gtgtttggct	cttagcttga	gacaggcaaa	tccacataca	ctcacattcc	60
aacaagccaa	agcaagtcac	ccaccccat	gcttctggga	caaggatgta	cattcctcct	120
gggcgtgggg	gtgcgggtac	cgcaagggga	ataaattttt	cctgagctac	gatacactct	180
cccacaaaa	gtcatacacc	catttagata	acaacttttc	ttgagtagtt	cagatatcat	240
caatgatcca	catattgata	aacatgactc	gacactaata	acactgtgag	cattttacac	300
tattttctat	aaactccact	atgctccatt	tattctcaga	aattctctct	atgatatact	360
tcatgggcac	aaagaagaat	gagtgaagc	cacgcaaaaa	ggactgtgaa	agccactaaa	420
aagggctgga	ataaatggga	caaatcatca	tactcttcta	t		461

<210> 522

<211> 554

<212> DNA

<213> Unknown (H38g371 nucleotide)

<220>

<223> Synthetic construct

<400> 522

cctgtcacc	cccgttcccc	ccaccacct	ctctttcccc	cttacatcta	cccaaaaact	60
ttttccccac	catctttccg	caaaaccttc	tctcctcct	gttcaccacc	gtttttcccc	120
ctccacctac	ccccaacatt	ttttccccac	cgtcttttcc	tcactgtctt	ttttgcaaca	180
ccttctcctg	ctcgccatcc	tcttttcccc	ttggcactaa	ccacctctct	tactcctcca	240
tctaccccaa	aactattttc	cccttccctac	cgtctccagcc	acactgcagt	ctccgtcgct	300
gccaccaacc	gcagcgaggc	gagctgtggt	gccgcagcca	cagcctccag	catgcagcgg	360
tggtctagccc	ttgtcctggt	cctctaagcc	gggaacggag	cagccccgcg	cgagacacg	420
catgagccta	gaacggcctg	acacctcttc	agcaccattt	atatactgag	gttatgcata	480
tgaggttctt	ggactacatg	ttccaggatt	gggtaagaga	aaacgcagag	gcctactctg	540
attggacttt	gtta					554

<210> 523

<211> 424

<212> DNA

<213> Unknown (H38g372 nucleotide)

<220>

<223> Synthetic construct

<400> 523

tatatagaaa	tggaacaacta	ttttctaaca	taactataac	gatatttact	atttttccat	60
tttataatct	ctactcaata	ttttggtatt	aaaaaattca	tcctaacttc	tttgttggtc	120
tattgttttt	gatgttcagc	attactaaat	ttttgactta	tggtttgaaa	tggtctgtca	180
ttcctgattg	ctgacccctg	tatcaacatg	cctgatattaa	cccttaacaa	attctattct	240
tacaaaatag	ctgaagtggg	ttggagggtt	atttttacca	tttcttttat	ttgctgtccc	300
ttttgataaa	attatttttc	ttagttaaaa	aatgtattta	aataagtaaa	taatatctgt	360
gctagtgggt	actcgggtgga	catttcagag	gtgtgtccat	actttatgta	ttttatcact	420
ggtt						424

<210> 524
 <211> 246
 <212> DNA
 <213> Unknown (H38g373 nucleotide)

<220>
 <223> Synthetic construct

<400> 524
 aatgtattta ggtaatttct tgactttctgc agggactctg atatacacag agcgtacctg 60
 tgtatactgt ccagtttagct cagattctca gttttgggca ttttctaagg gagggcaatg 120
 aacatccctga taggtttaac taaggtttta aaatgtccaa ttttatgtgt ggtttttaac 180
 cacacctgca tcctaattac gaccttggtt gttatagctt ataggtttag gcaatctgga 240
 tatagt 246

<210> 525
 <211> 619
 <212> DNA
 <213> Unknown (H38g374 nucleotide)

<220>
 <223> Synthetic construct

<400> 525
 gaaattatat tgattgggat ttctctcaaa ctaatctagt tgtattcacc attattaaaa 60
 ttaagtgaca ctcaattgga ctaagtagca ataaaaatat gagacttcct agtgattttt 120
 ttttatccca agccatttac tactgatggg ccttgatgtg tgtgcttgaa aacaaaacat 180
 atgcaagtgt tagactgggt tgaagatttg ggtggtgaaa gttagctaata tagatgtcag 240
 tgctctatct agaagccaat cttggaaaata tgtgataatg ccctttttaa atagctgaaa 300
 agaaattatt ttgtgtttgt ttccacttca ttcttgtttg gttgtatagc atttaagtga 360
 aaggagattt tttatcccta tactagtatt tgcatttacc atcttttaata gatggagaga 420
 aaagttagtt gtcttacttt gatatgtttg gcataggacc tatgacactt ttgatgtttt 480
 tggtcacagt tctgtcacta gaatgctagc aattagatat atgcaatgag taacctactt 540
 taatacaatg gtttgaagta ccacaggcag taactcctaa acaccaaata acagtgtttt 600
 aatttgtaac atgttaaag 619

<210> 526
 <211> 939
 <212> DNA
 <213> Unknown (H38g375 nucleotide)

<220>
 <223> Synthetic construct

<400> 526
 atgagaaatt tgagtggagg ccatgtcgag gagtttgtct tgggtgggttt ccctaccacg 60
 cctccccctc agctgtcctt ctttgtcctt ttttttgcaa tttaccttct gacattgttg 120
 gagaatgcac ttattgtctt cacaatatgg cttgctccaa gccttcacg tcccatgtac 180
 tttttccttg gccatctctc ttctctggag ctatggtaca tcaatgtcac cattcctcgg 240
 ctcttggcag cctttcttac ccaggatggt agagtctcct acgtagggtg catgacccaa 300
 ctgtacttct ttattgcctt agcctgtact gaatgtgtgc tgttggcagt tatggcctat 360
 gatcgctacc tggccatctg tggacccctc ctttacccta gtctcatgcc ttccagtctg 420
 gccactcgcc ttgctgtctc ctcttggggc agtggcttct tcagctccat gatgaagctt 480
 ctttttattt cccaattgtc ctactgtgga cccaacatta tcaaccactt tttctgtgat 540
 atttccccac tactcaacct cacctgctct gacaaggagc aagcagagct agtagacttc 600
 cttctggccc tggatgatgat tctactccct ctattggctg tggtttcatc atacactgcc 660
 atcattgcag ccatoctgag gatccctacg tccaggggac gccacaaagc cttttccact 720
 tgtgcccgtc atctggcagt ggttgttacc tactactcct ccactctctt cacctatgca 780
 cggccccggg ccatgtacac cttcaaccac aacaagatta tctctgtgct ctacactatc 840
 attgtaccat tcttcaacct agccatctac tgccctgagga acaaggaggt gaaggaggcc 900
 ttcaggaaga cagtgatggg cagatgtcac tatcctagg 939

<210> 527
 <211> 965
 <212> DNA
 <213> Unknown (H38g376 nucleotide)

<220>
 <223> Synthetic construct

<400> 527
 cacacagagc cactgaatct cacagggtgtc tgagaattcc tcctcctggg actctcagag 60
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 acgggtgtga ggaacctgct cagcatcctg gctgtcagct ctgactccca cctccacacc 180
 cccatgtact tcttcctctc caacctgtgc tgggctgaca tcgggttacac ctccggccacg 240
 gttcccaaga tgattgtgga cagcagtcg catggcagag tcatctctca tgctggctgc 300
 ctgacacaga tgtctttctt ggtccttttt gcatgtatag aagacatgct cctgactgtg 360
 atggcctatg actgctttgt agccatctgt tgcctctgc actaccagc catcgtgaat 420
 cctcacctct gtgtcttctt cgttttggtg tcctttttcc ttagcctgtt ggattcccag 480
 ctgcacagtt ggattgtgtt acaattcacc atcatcaaga atgtggaaat ctctaatttt 540
 gtctgtgacc cctctcaact tctcaaaact gcctgttctg acagcgtcat caatagcata 600
 ttcatatatt ttgatagtag tatgtttggt tttcttccca ttccagggat ccttttgtct 660
 tactctaaaa ttgtcccctc cgttctaagg atgtcatcgt cagaaggga gtataaagcc 720
 ttctccacct gtggctctca cctagcagtt gtttgctgat ttgatggaac aggcattggc 780
 atgtacctga cttcagctgt ggcaccaccc cccaggaatg gtgtcgtgga gtcagggatg 840
 tacgctgtgg tcaccccat gctgaacctt ttcactaca gcctgagaaa caggcacaca 900
 caaagtgcgc tgcggaggct gcgcacagaa cagttgaatc tcatgatctc ttgcatcctt 960
 tttct 965

<210> 528
 <211> 557
 <212> DNA
 <213> Unknown (H38g377 nucleotide)

<220>
 <223> Synthetic construct

<400> 528
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 gaaacctatg atttgtccca gatttttctt tttcccttgc tcttcatatc tatcagtgat 120
 actaattcta aactaacctt aacgaactgc atctgtgcc ctctctcacc tctcctccct 180
 cactttcagt gcattgactg aggtacacc atgtgaatta ttaccatgga atgctaacag 240
 aattattgct tccaatggta ccatgccata atcctcctt catatgggtg ccaataaatt 300
 tttaaaatat ttatttgtat ctgctacttc tcagggttaa agcttcccag catgttgaag 360
 atggaatgca aacagctctg catgcatgcc ctttgcctcat gcagctccta ttgtccatcc 420
 cccactctta cccactcttg ctggataatt cctttttatt ctttaagactt catccaagaa 480
 gcaagctctc atatttcctt catatacttc tgtcatagcc ctttacatat gttaatcatc 540
 tgttaccttt tctcttg 557

<210> 529
 <211> 1007
 <212> DNA
 <213> Unknown (H38g378 nucleotide)

<220>
 <223> Synthetic construct

<400> 529
 tctagagacc cacagaatct aacagatgtc tctatatctc tcctcctaga agctcagagg 60
 atccagaacg gcagccggc ctcactgggc tgttcctgtc cagctgcctg gtcattggcg 120
 tggggaacct gctcatcacc ctggccatca gccctgactc ccacctccac acccccatgt 180
 actttctctt ctccaacctg tccttgctgt acatcagttt cacctccacc acagtcccca 240

agatgactgt	ggacatccaa	tctcacagca	gagtcacctc	ctatgcagge	tgcttgactc	300
agatgtctct	ctttgccatt	tttgaggca	tggaagacag	acatactcct	gagtgtgatg	360
gcctatgacc	agttttagc	caaagtgcac	cctctatata	attcagccat	catgaacccg	420
tgtttctgtg	gctttctact	tttggtgtct	tttttttttc	cctcagtcct	ttagatgccc	480
agctgtacaa	tttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
tcttctgtga	cccttctcaa	ctccccatc	ttgcatgttg	tgacaccttc	aacaataaca	600
taatcctgta	tttccctgat	gccatatttg	gttttcttcc	catctcgggg	acacttttct	660
cttacgataa	aattgtttcc	tccattctga	gggtttcctc	atcagggtgg	aagtataaag	720
ccttctccac	ctatgggtct	cacctgtcag	atgtttcctg	attttatgga	acaggcggtg	780
gagggtagct	cagttcagat	gtgtcatctt	ccccgagaaa	gactgcagtg	gcctcagtg	840
tgtacgcagt	ggtcaccccc	atgatgaacc	ccttcatcta	cagtcagaga	aacagggata	900
tgaaaagtgt	cctgcgggcg	ccgcacggca	gcacgttcta	atctcaatac	cttcttatct	960
gttccattcc	ttttgcagtg	tgggtcgaaa	aaggctgcat	gatgaaa		1007

<210> 530

<211> 471

<212> DNA

<213> Unknown (H38g379 nucleotide)

<220>

<223> Synthetic construct

<400> 530

tttttaaaaa	tgagattaaa	ggaattaatg	taagatagaa	ccataatgga	ttattggagg	60
gaaggtaggc	acatttaggg	gatgttcttg	gcctttccgt	ttggctgacc	tatcccaaaa	120
cttttctctt	gggtctctat	cagagacatg	gcagtaacct	ggatggacca	taggcacgag	180
tccctgtagc	cattccctcc	gaagctgcag	cctttttcat	cctgccatgt	atctgagtta	240
tgacagtgcc	ttgacacctt	cactaaatca	tatataactt	gaatccgggg	actcaagggg	300
ttcaaccatc	tttgttttct	tctccattac	tgctactgtg	ctagagccca	agtctcctga	360
aatgcgcctt	ggagccttgc	tcaaagatgt	caacccaaca	tgctgatcag	gtagctatct	420
tgtctgaagc	tggtagtcca	tgacaggctc	tgacatgtgc	tgagcttgct	c	471

<210> 531

<211> 974

<212> DNA

<213> Unknown (H38g380 nucleotide)

<220>

<223> Synthetic construct

<400> 531

atgaagatca	accagacaat	cctgaaggaa	ttcattcttg	ttggcttttc	tgtgtaccca	60
catgtacaga	catttctttt	tgtgggtctc	ttttgtctct	accttctcac	ccttgccagg	120
aatctgacca	tcatgggtct	aacttgagtg	gacagggtcc	tccacacccc	tatgtatctc	180
ttccttagtg	cactctcctt	ctctgagacc	tgctatacac	tgaccatcgt	ccccagatg	240
ctggaagatc	tactggccaa	ggacagaagc	atttcagtca	caggttgtag	cttacagatg	300
tgcttcttct	tgggacttgg	tggcacaac	tgtatcattc	tcactttgat	gggatatgac	360
cgcttctctg	ccatttgtaa	ccctctaaga	tatccactgc	ttatgaccaa	cattgtatgt	420
ggacaacttg	tggcctctgc	ttgcaactga	ggcttcttta	tctctcttac	agagactgca	480
ctgatattca	gggactcttt	ctgcagaccc	aaccttgcca	aacacttctt	ctgccatatt	540
ctggcagtta	ttaggctgtc	ttgtatagac	agtaaccaca	cagaattcat	tataacactg	600
atctcagtg	ctgggttggc	gggtaccctt	ctgctcatca	tcttgactga	tgtcttcatt	660
atttctactg	tcctcaggat	cccttcagct	gagggcaagc	agaaggcctt	caccacctgt	720
gcctcccacc	tcaccgtggt	tataatccac	tttggttttg	catctattgt	ttatttgaag	780
ccagaagcct	caggagatga	cacactcata	gcagtcctct	atactgtcat	taccccttct	840
ctcagcccca	tcatattcag	cctgaggaat	aaggacatga	aaaatgcttt	tagaagaatg	900
atgggaaaca	cagttgcctt	gaaaaaataa	tcttgggttg	ttgctgcttg	tttgaagaag	960
ggctcaatgt	cccc					974

<210> 532

<211> 939

<212> DNA

<213> Unknown (H38g381 nucleotide)

<220>

<223> Synthetic construct

<400> 532

atggggcaga	ccaacgtaac	ctcctggagg	gattttgtct	tcctgggctt	ctccagttct	60
ggggagttgc	agtccttct	ctttgecttg	ttcctctctc	tgatctagtg	cactctgacc	120
agcaatgtct	tcattatcat	agccatcagg	ctggatagcc	atctgcacac	ccccatgtac	180
ctcttccttt	ccttcctatc	cttctctgag	acctgctaca	ctttgggcat	catccctaga	240
atgctctctg	gcctggctgg	gggggaccag	gctatctcct	atgtgggctg	tgctgcccag	300
atgttctttt	ctgcctcatg	ggcctgtact	aactgcttcc	ttctggctgc	catgggcttt	360
gacagatatg	tggccatctg	tgctccactc	cactatgcca	gccacatgaa	tcctaccctc	420
tgtgcccagc	tggtcattac	ttccttcctg	actggatacc	tctttggact	gggaatgaca	480
ctagttattt	tcacactctc	attctgcagc	tcccatgaaa	tccagcactt	tttttgtgac	540
acgccacctg	tgctgagcct	agcctgtgga	gatacaggcc	cgagtgaagt	gaggatcttt	600
atcctcagtc	ttttggctct	cttggctctc	ttcttcttca	tcaccatctc	ctacgcctac	660
atcttggcag	caatactgag	gatccctctc	gctgaggggc	agaagaaggc	cttctccact	720
tgtgcctcgc	accttacagt	ggtcattatt	cattatggct	gtgcttcctt	cgtgtacctg	780
aggcccaaag	ccagctactc	tcttgagaga	gatcagctta	ttgccatgac	ctatactgta	840
gtgaccccc	tccttaatcc	cattgtttat	agtctaagga	ctagggctat	acagacagct	900
ctgaggaatg	ctttcagagg	gagattgctg	ggtaaagga			939

<210> 533

<211> 866

<212> DNA

<213> Unknown (H38g382 nucleotide)

<220>

<223> Synthetic construct

<400> 533

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gtgttctttg	ccatcaaact	ggatttctgc	ctgcacagct	ccttgatatt	cttcatcagt	120
gtcctctcct	tcctagagat	ctgggtatacc	accatcacca	tccccaagat	gttcttcaac	180
ctagccagtg	agcagaagac	cacctccctg	gatgggtgcc	tattgcagat	gtatttcttt	240
tactccctcg	gcatactga	ggtttgcttg	ctcaccacca	gggctatgga	cagataacctg	300
gccatctgta	atcacctttg	ctaccccaca	gtcacgacac	cttagctcta	cactcagggtg	360
attctaggtt	gttgcatctg	tggcttcttc	acgctgctcc	ctgagattgc	ttggatatcc	420
acactgccat	tttgtggtcc	aaatcaaate	cacaacattt	tctgtgacct	tgatcctatc	480
ctgaatctag	catgtgtaga	cactggccca	gttgttttta	tcaagggtgt	ggacattgta	540
catgctgtgg	agatcatcac	agctataatg	cttggtgactt	tggcttacgt	ccaaattatt	600
gcagtgatcc	taagaaactg	ctctgctgat	ggatgccaaa	aggcattttc	tacctatgct	660
ttccaccttg	ctattttctt	aatctttttt	ggaagtgtag	ccctgatgta	cctgctcttc	720
tctgccaagt	actccttttt	ctggggacaca	accatcagcc	taatgtttgc	agtgtgtgta	780
ccgacacaat	catctgtagt	ctgaggaata	aagagataaa	ggaagcaata	aaaaagcaca	840
tgtgccaatc	aatgatatgc	acacat				866

<210> 534

<211> 954

<212> DNA

<213> Unknown (H38g383 nucleotide)

<220>

<223> Synthetic construct

<400> 534

atggagagcc	ccaatcgaac	caccattcag	gagtttatct	tctccgcttt	cccttattcc	60
tgggttaagt	ctgttgtctg	ctttgttcca	ctgctcttca	tctatgcttt	cattgttgtt	120
ggaaacctgg	tcatcatcac	agtgttcag	ttgaatactc	acctccacac	tcccatgtat	180

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acttttatca gtgctctttc tttcctggag atttggata ccacagccac aatcccaaag      240
atgctgtcta gcctgcttag tgagaggagc atttccttca atggttgtct cctgcagatg      300
tatttcttcc attccaccgg catctgtgag gtgtgtctct tgacagttaa ggcctttgac      360
cactacctgg ccatatgcag cctcttcat tatccctcta tcatgacccc caagctatgt      420
acccaactga ctttaagtgt ctgtgtttgt ggctttatca cacccttcc tgagattgcc      480
tggatctcta cactgccatt ttgtggttcg aatcaccttg aacatatctt ctgtgacttc      540
ctcccagtgc tgcgtctggc ctgcacagac acacgagcca tcgtcatgat tcaggtagtg      600
gatgtcattc atgcagtgga gattattaca gctgtgatgc tcatcttcat gtcctacgat      660
gggtattgtg ctgtaattct acgtattcat tcagctggag gccgcccgcac agcattttcc      720
acgtgtgtct ctcacttcat tgtcttttcg ctctcttttg gcagtgtgac tctcatgtac      780
ctacgcttct ctgccaccta ctctttgttc tgggatatag ccattgtctt ggcctttgca      840
gttttgtctc cttcttcaa ccccattatc tatagcctga ggaataaaga aataaaagaa      900
gctataaaaa agcacatagg tcaagctaag atattttttt ccgtaagacc aggg          954

```

<210> 535

<211> 386

<212> DNA

<213> Unknown (H38g384 nucleotide)

<220>

<223> Synthetic construct

<400> 535

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ctactgaaac tctcctgctc agacacacac ctcaatgagg tcataatcct tagtgagggg      60
gccctgggtca tgatcacccc atttctttgc atcctggctt cttatatgca catcacctgc      120
actgtcctga aggtcccatc cacaaaggga aggtggaaag ccttctccac ctgtggttct      180
cacctggctg tggttctcct cttctacagc accatcattg ctgtgtattt taaccctctg      240
tcctcccact cagctgagaa agacactatg gctactgtgt tgtatacagt agtgactccc      300
atgctaaacc ctttatctac agcctgagga acagggtactt gaaaggggct ctgaaaaaag      360
tagttggcag ggtgggtgttt tctgtc

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<210> 536

<211> 486

<212> DNA

<213> Unknown (H38g385 nucleotide)

<220>

<223> Synthetic construct

<400> 536

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ctgtctcatca tcccagccat tgccactgac acccggctct ctgtgctcgt gcgctttttc      60
cttgccaacc tggccttcgt ggtcacttgc ttcacctcca ccaccatccc caagatgctg      120
gacgtgcaaa gagatccctt gtgtcatgtc aggatgcaaa gggattcctt atgctgggtg      180
cctgaccagc atgtcttctt tcatctgtta ggcaccaca gcttctgct gactgcaatg      240
gccaatgaac actgtgtggc catctgtcac tctctgaact ccacagggtc tgtgacacca      300
tagctctgtg gcctcctggt ggtggcctcc tggaccttcg cattcaggaa tgccctgacc      360
caccagtggt tactgaccgc cctctcactc tgcacctacg agtgggtcag ccatgtcttc      420
tgcaacctca gccagctgct gaagttggcc tgctcagacg ccactctcaa caatgtgacg      480
gtgcaa

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<210> 537

<211> 980

<212> DNA

<213> Unknown (H38g386 nucleotide)

<220>

<223> Synthetic construct

<400> 537

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atgttaaccc ctaataatgc ctgtccgtg cctacctctt tccggctcac tggcatccct      60
ggcctggaat cctgcacat ctggctctcc atccccttg gctccatgta cctggtagct      120

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gtgctgggga	acataacccat	cctggcagtg	gtaaggatgg	agtacagcct	gcatcagccc	180
atgtacttct	tcctgtgcat	gttggtgtgc	attgacttgg	tcctgtcaac	ctctaccatg	240
cccaaaactac	tggccatctt	ctggtttggt	gcccaaca	ttggtgttaa	tgccctgttg	300
gcccagatgt	tcttcattca	ttgctttgcc	actgttgagt	caggcatctt	ccttgccatg	360
gcttttgatc	actatgtggc	catctgtgac	ccactgcac	ataccttggt	gctcacccat	420
gctgtgggtg	gtcgtttggg	gctggctgcc	ctcctccggg	gggtaattcta	cattggacct	480
ctgcccttag	tgatttgtct	gaggttgccc	ctttaccaca	cccaaactcat	tgcccatctg	540
tactgtgagc	acatggctgt	ggtcaccttg	gcatgtgggt	tgacacaagg	gtcaacaact	600
tatatggaat	ggggattggc	tttctgggtat	taatcctgga	ttcattggcc	atcactgcct	660
cctatgtgat	gatttttcagg	gctgtaatgg	gcttggccac	ctctgaagcc	aggcttaaaa	720
ccttagggac	atgtggctct	cacatctgtg	ccatcctcgt	cttctacatc	cccatgtctg	780
tttctctct	cacacaccgc	tttggccatc	gtgtgcctcc	ccatatccat	atccatatcc	840
atatccatat	ccatatccat	atccttttgg	ccaacattta	cctcctcacc	ccacctatcc	900
tcaacccaat	agtctatgct	gtccgcacaa	agcagatccg	agaggctctt	ctccatatta	960
aggcaaggac	tcaaaccagg					980

<210> 538

<211> 967

<212> DNA

<213> Unknown (H38g387 nucleotide)

<220>

<223> Synthetic construct

<400> 538

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gagttggcga	gttctctctg	ctcagcatca	ccagtgactc	agagaagcag	caggccctct	120
tctggctctt	cctgtgtatg	cacttagtca	ctgaggctgg	aaacacaccc	atcatcctgg	180
gcatcggtc	caaccctcgc	ctgcacaccc	ccacgtactt	cttcacccat	ctctcctttg	240
tcaacatctg	cttcatcacc	aacctgatcc	ccaagctcct	ggccaacccat	gtggcaggaa	300
cagggtgat	cagatctct	tctcccag	gctgactca	gatgtacttc	ctcatctcct	360
ttgccaacgt	ggacaccttt	ctgctggcca	tcatggcact	ggaccactat	gtggccatct	420
gcagcgccct	gcggtaactgc	tccatcatca	cccccggtc	tgtcaggggc	tgcccggtgt	480
agcgtgagca	ggctccagcc	tcatctcct	ggccacacg	gtcatcatga	gcagactggc	540
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tgccctgctca	catacatgtc	aatcagcatg	tggttctgtg	ggccgtgtgc	ctgttctctg	660
ctccctgtgc	gtcctatctg	gtctcctaca	tccgcattgc	tgacagccatc	ctccggattc	720
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aggacaccat	agcaaccatc	atgtacactg	tggtgacctc	tatgtctaac	cccttcatct	900
acagtctgat	gaacaaggag	gtccaggagg	ccgtgagaag	gctcttcagt	aggggctcac	960
actcatc						967

<210> 539

<211> 603

<212> DNA

<213> Unknown (H38g388 nucleotide)

<220>

<223> Synthetic construct

<400> 539

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cccctacgac	actacataat	gtgggcaacg	cattgtcgca	ttatgtgtgc	gcatgggaat	120
tgttttctcc	attcgttgag	ccagttggcc	tttgccgtgc	acttaccctt	ctgtgggtccc	180
aatgagttcg	atagttttta	ttgtgacctt	cctagggtta	tcaaacttgc	ctgtacagat	240
acctacaggc	tagatattat	ggtcattgtc	aacagtgtgt	tgctcactgt	gtgttctttt	300
gttcttctaa	tcatctcata	cactatcatc	ctaattacca	tccagcatcg	ccctttagat	360
aagtcgtcca	aagctctgtc	cactttgact	gtcacatta	cagtagttct	ttgtttcttt	420
ggaccatgtg	tctttattta	tgccctggcca	ttcccatca	agtcattaga	taaattcctt	480
gctgtatttt	attctgtgat	caccctctc	ttgaacccaa	ttatatacac	actgagggaac	540

aaagacatga agacggcaat aagacagctg agaaaatggg atgcacattc tagtgtaaag 600
 ttt 603

<210> 540

<211> 935

<212> DNA

<213> Unknown (H38g389 nucleotide)

<220>

<223> Synthetic construct

<400> 540

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gtgggtggga	atgtgacat	cctggctgtg	gtaaagatag	aacgcagcct	gcaccagccc	180
atgtactttt	tcttgtgcat	gttggctgcc	attgacctgg	ttctgtctac	ttccactata	240
cccaaacttc	tgggaatctt	ctgggtcggg	gcttgtgaca	ttggcctgga	cgccctgcttg	300
ggccaaatgt	tccttatcca	ctgctttgcc	actgttgagt	caggcatctt	ccttgccatg	360
gcttttgcac	gctacgtggc	catctgcaac	ccactacgtc	atagcatggg	gctcacttat	420
acagtgggtg	gtcgtttggg	gcttgtttct	ctcctccggg	gtgttctcta	cattggacct	480
ctgcctctga	tgatccgcct	gcggctgccc	ctttataaaa	cccatgttat	ctccactcc	540
tactgtgagc	acatggctgt	agttgccttg	acatgtggcg	acagcaaggt	caataatgtc	600
tatgggatga	gcatcggctt	tctggtgttg	atcatggaat	cagtggatag	tgatgcatca	660
taggtgagga	gtatcagggc	cgtgatgggg	ttagccaatc	atgaggatag	gattagagac	720
catggggaca	ggcgaatata	acatatgtgc	catcatgata	ttataggatc	ccagtgatgt	780
atattccatg	agatcaccca	gatggtcagt	gtgtgcatca	tccagtccac	aatatgatgg	840
ccaggatata	tatcatcagt	catccaagca	tcaagcccag	tgtataggat	gatcgcacca	900
agcagagccg	agagagctat	atccaaagag	caaga			935

<210> 541

<211> 945

<212> DNA

<213> Unknown (H38g390 nucleotide)

<220>

<223> Synthetic construct

<400> 541

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cacagtactg	ctgaccttgt	cctcttctcc	gtggttatgg	cggtcttcac	agtggccctc	120
tgtgggaatg	tcctctcat	cttctctatc	tacatggacc	ctcaccttca	caccccatg	180
tacttcttcc	tcagccagct	ctccctcatg	gacctcatgt	tggctctgtac	caatgtgcca	240
aagatggcag	ccaacttcct	gtctggcagg	aagtccatct	cctttgtggg	ctgtggcata	300
caaattggcc	tctttgtctg	tcttgtggga	tctgaggggc	tcttgtctgg	actcatggct	360
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cacattctag	ggactgtgct	gcaaatgcac	tctgctcagg	cctggaaaaa	ggccctggcc	720
acctgctcct	cccacctgac	agctgtcacc	ctcttctatg	gggcagccat	gttcatctac	780
ctgaggccta	ggcactaccg	ggccccagc	catgacaagg	tggcctctat	cttctacacg	840
gtccttactc	ccatgctcaa	ccccctcatt	tacagcttga	ggaacaggga	ggtgatgggg	900
gcactgagga	aggggctgga	ccgctgcagg	atcggcagcc	agcac		945

<210> 542

<211> 975

<212> DNA

<213> Unknown (H38g391 nucleotide)

<220>

<223> Synthetic construct

<400> 542

atgggaagat	gggtgaacca	gtcctacaca	gatggcttct	tcctcttggg	catcttttcc	60
cacagccaga	ctgaccttgt	cctcttctct	gcagttatgg	tggtcttcac	agtggccctc	120
tgtgggaatg	tcctcctcat	cttccctcatc	tacctggacg	ctggacttca	cacccccatg	180
tactttctcc	tcagccagct	ctccctcatg	gacctcatgt	tggtctgtaa	cattgtgcca	240
aagatgcagc	caacttcctg	tctggcagaa	gtccatctcc	tttgtgggct	gtggcataca	300
aattggcttt	tttgtctctc	ttgtgggatc	tgaggggctc	ttgctgggac	tcattggctta	360
tgaccgctac	gtggccgtta	gccaccact	tcactatccc	atcctcatga	atcagagggt	420
ctgtctccag	attactggga	gctcctgggc	ctttgggata	atagatggag	tgattcagat	480
ggtaggcagc	atgggcttac	cttactgtgg	ctcaaggagc	gtggatcact	ttttctgtga	540
ggtacaagct	ttattgaagc	tggcctgtgc	agacacttcc	ctttttgaca	ccctcctctt	600
tgctgtctgt	gtcttcatgc	ttctccttcc	cttctccatc	atcatggcct	cctatgcttg	660
catcctaggg	gctgtgctcc	gaatacgtc	tgctcaggcc	tggaataaag	ccctggccac	720
ctgctcctcc	acctaacagc	tgtcaccctc	ttctatgggg	cagccatgtt	catgtacctg	780
aggcctaggc	gctaccgggc	ccctagccat	gacaagggtg	cctctatctt	ctacacagtc	840
cttactccca	tgctgaacct	cctcatttac	agcttgagga	atggggagggt	gatgggggca	900
ctgaggaagg	ggctggaccg	ctgcaggatt	ggcagccagc	actgaacccc	agagtcgggt	960
gcctgctgtg	ccccct					975

<210> 543

<211> 942

<212> DNA

<213> Unknown (H38g392 nucleotide)

<220>

<223> Synthetic construct

<400> 543

atgggggatg	tgaatcagtc	ggtggcctca	gacttcattc	tggtgggcct	cttcagtcac	60
tcaggatcac	gccagctcct	cttctccctg	gtggctgtca	tgtttgatcat	aggccttctg	120
ggcaacaccg	ttcttctctt	cttgatccgt	gtggactccc	ggctccacac	acccatgtac	180
ttctgtctca	gccagctctc	cctgtttgac	attggctgtc	ccatggtcac	catccccaag	240
atggcatcag	actttctgcg	gggagaagg	gccacctcct	atggagggtg	tgacagctcaa	300
atattcttcc	tcacactgat	gggtgtggct	gagggcgctc	tgttggctct	catgtcttat	360
gaccgttatg	ttgctgtgtg	ccagccctctg	cagtatcctg	tacttatgag	acgccaggta	420
tgtctgtgta	tgatgggctc	ctcctgggtg	gtagggtgtg	tcaacgcctc	catccagacc	480
ttcatcacc	tgcattttcc	ctactgtgcc	tcccgatttg	tggtatcactt	cttctgtgag	540
gtgccagccc	tactgaagct	ctcctgtgca	gatacctgtg	cctacgagat	ggcgctgtcc	600
acctcagggg	tgctgaccc	aatgctccct	ctttccctca	tcgccacctc	ctacggccac	660
gtgttgacag	ctgttctaag	catgcgctca	gaggaggcca	gacacaaggc	tgtcaccacc	720
tgctcctcgc	acatcacggg	agtggggctc	ttttatgggt	ccgccgtgtt	catgtacatg	780
gtgccttgcg	cctaccacag	tccacagcag	gataacgtgg	tttccctctt	ctatagcctt	840
gtcaccctca	cactcaaccc	ccttatctac	agcttgagga	atccggagggt	gtggatggct	900
ttggtaaaag	tgcttagcag	agctggactc	aggcaaatgt	gc		942

<210> 544

<211> 350

<212> DNA

<213> Unknown (H38g393 nucleotide)

<220>

<223> Synthetic construct

<400> 544

aatattaagg	gcattgctgg	tgccccatgtt	tattgaagtg	ttggatctat	tctttatcat	60
cctattctat	atctttatcc	cttcaggcag	ttctacaact	ctcctctcag	aggccccgta	120
caaagcattt	gggacatgtg	tctctcacat	agggtccatc	ttagccttct	acacaccttc	180
agtcattctc	tcagtcatgc	accgtgtggc	ccgctgtgct	gcgccacacg	tccacattct	240
cctcgccaat	ttctatctgc	tcttcccacc	catgggtcaat	cccatcatct	acggcggtta	300

gaccaagcag atccgtgaca gtcttgggag tattccccgag aaaggatgtg

350

<210> 545

<211> 948

<212> DNA

<213> Unknown (H38g394 nucleotide)

<220>

<223> Synthetic construct

<400> 545

atgcctagtc	agaactatag	catcatatct	gaatttaacc	tctttggctt	ctcagccttc	60
ccccagcacc	tcctgcccac	cttgttcctg	ctgtacctcc	tgatgttcc	gttcacattg	120
ctgggcaacc	ttctcatcat	ggccacaatc	tggattgaac	acagactcca	cacacccatg	180
tacctcttct	tgtgcaccct	ctccgtctct	gagattctgt	tcactgttgc	catcacccct	240
cgcagtctgg	ctgatctgct	ttccacccat	cattccatca	cctttgtggc	ttgtgccaac	300
cagatgttct	tctccttcat	gtttggcttc	actcactcct	tccttctcct	ggtcatgggc	360
tatgatcgct	atgtggccat	ctgccaccca	ctgcgttaca	atgtgctcat	gagcccccg	420
gactgtgccc	atcttgtggc	ctgtacctgg	gctggtggct	cagtcatggg	gatgatgggtg	480
acaacgatag	ttttccacct	cactttctgt	gggtctaata	tgatccacca	ttttttctgt	540
catgtgcttt	ccctcttgaa	gttggcctgt	gaaaacaaga	catcatctgt	catcatgggt	600
gtgatgctgg	tgtgtgtcac	agccctgata	ggctgtttat	tcctcatcat	cctctcctat	660
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tctacgtgtg	tatccacact	cactgtgggtg	gtcacgcact	atagttttgc	ctcctttatc	780
tacctcaagc	ccaagggcct	ccattctatg	tacagtgaag	ccttgatggc	caccacctat	840
actgtcttca	cccccttctc	tagcccaatc	attttcagcc	taaggaacaa	ggagctgaag	900
aatgccataa	ataaaaaactt	ttacagaaaa	ttctgtcctc	caagttcc		948

<210> 546

<211> 990

<212> DNA

<213> Unknown (H38g395 nucleotide)

<220>

<223> Synthetic construct

<400> 546

atgtgttctt	ttttcttgtg	ccaaacaggt	aaacaggcaa	aaatatcaat	gggagaagaa	60
aaccaaacct	ttgtgtccaa	gtttatcttc	ctgggtcttt	cacaggactt	gcagacccag	120
atcctgctat	ttatcctttt	cctcatcatt	tatctgctga	ccgtgcttgg	aaaccagctc	180
atcatcattc	tcacttctct	ggattctcgc	cttcacactc	ccatgtattt	ttttcttaga	240
aatctctcct	ttgcagatct	ctgtttctct	actagcattg	tcctcaagt	gttggttcac	300
ttcttggtaa	agaggaaaac	catttctttt	tatgggtgta	tgacacagat	aattgtcttt	360
cttctgggtg	ggtgtacaga	gtgtgcgctg	ctggcagtga	tgtcctatga	ccggtatgtg	420
gctgtctgca	agcccctgta	ctactctacc	atcatgacac	aacgggtgtg	tctctggctg	480
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catcttccct	actggggaca	gaatataatc	aatcactact	tttgtgaacc	tcctgccctc	600
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gttatccaga	tgagctctgg	ggaagggaga	ctcaaggctt	tttccacctg	tggctcccat	780
cttattgttg	ttgtcctctt	ctatgggtca	ggaatattca	cctacatgag	accaaactcc	840
aagactacaa	aagaactgga	taaaatgata	tctgtgttct	atacagcggt	gactccaatg	900
ttgaacccca	taatttatag	cttgaggaaac	aaagatgtca	aaggggctct	caggaaacta	960
gttgggagaa	agtgtctctc	tcataggcag				990

<210> 547

<211> 676

<212> DNA

<213> Unknown (H38g396 nucleotide)

<220>

<223> Synthetic construct

<400> 547

ggaaaggaaa	gagagacacg	ggtctggagg	ccgagagcgc	aagaccgggg	ggtgagcacc	60
cggcacgctg	cgagggtaac	aagctatcag	gaatgcgggg	tccgtggcgg	gggagtgttg	120
tgggcgcggg	tagggccgag	ccttttagac	cccagctgca	caacgtgatt	gcctacagaa	180
ggacctgctt	caaggatgtg	gaaattccga	atttcgctgt	gacctttctc	aattccccgt	240
cttgcatgtg	tggcaccttc	accaataaca	taatcatgta	ttccctgct	gccatatttg	300
gttttcttcc	catctcgggg	acccttttct	cttacgataa	aattgttttc	tccattctga	360
gggtttcatc	atcaggtggg	aagcataagg	ccttctccac	caggggggtc	cacctgtcag	420
ttgtttgctg	attttatgga	acaggcattg	gaggctacct	cagttcagat	gtgtcatctt	480
ccccgagaaa	ggctgcagtg	gcctcagtg	tgtaacgggt	ggccatcccc	atgctgaacc	540
ccttcaccta	cagcctgaga	aacagggtga	ttaaaagtgt	cctgcccac	cgcacggcag	600
cacggtctca	tctcaatata	ttcttatctg	ttccattcct	ttttagtggt	gggttaaaaa	660
aggcagcaag	gtcaaa					676

<210> 548

<211> 992

<212> DNA

<213> Unknown (H38g397 nucleotide)

<220>

<223> Synthetic construct

<400> 548

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ttcccttgcc	ccaggggagg	acagatcctc	ctcgttgtgc	tcttactgt	tgtttacctc	120
ctgacctca	tgggcaatgg	ttccatcaac	tgtgctgtgc	actgggtcag	agactccatg	180
cccccatgta	catcctgctc	gccaacttct	ccttccctga	gatctgttat	gtcacctcta	240
cagtccccaa	cgtgctggcc	aacttcctct	ctgacacaag	atcatctcgt	tctctggctg	300
cttccctcaa	ttctactttt	ttttctcctt	gggctctaca	gaatgctttt	tcctgggagc	360
tatggcattt	gacctatacc	ttgccatctg	ccggcctcta	cgctatccaa	ccattatgac	420
cagacgtctc	tgcaacattc	ttgtgggcag	ctgctgggta	cttggtttct	tgtggttctt	480
gattcctatc	agtgtcattt	ctcaaatgac	ctgtggatct	aggattattg	accacttccc	540
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tagctccacc	ttaagttctc	tacttctatt	tattcccttt	ctcttcatcg	tggggtgcta	660
tgtcttggtc	ctgagagctg	tgttgagggt	tccttcagca	tctggaagaa	gaaaggcttt	720
ctctacctgt	ggctcccacc	tggtgtagt	ttcactgttt	atggctcaat	gatgatcacg	780
tatgtgagcc	caacatctgg	gcatgaattc	ggaatgcaga	agactgtgac	tctgttctat	840
tctgtgggtc	ctccccttat	taatcctgtc	atatacagtc	tgaggaacaa	ggaaatgaaa	900
catgcaatga	ggaactacac	tgtaatgttt	tattttctag	aattcatagg	gctacaagag	960
atgtcaaaga	tgtattctat	ctctttaatt	tt			992

<210> 549

<211> 805

<212> DNA

<213> Unknown (H38g398 nucleotide)

<220>

<223> Synthetic construct

<400> 549

ttctcaagta	tatatgcttg	tatatatcag	atctctatct	caactatcta	tctaatactc	60
tatctatatt	taaattagta	gactggatta	tcaattgtta	tttgtattat	attttacagc	120
ctactcactt	tattctagca	gttcatttac	acttgtgaaa	tgaatcaatt	taaataagtaa	180
caaaatagga	acaatctgac	aacttttttag	ggatacttct	actcaggaat	atgtggcagg	240
agaaactgta	caatgtgatt	gataacaatc	ttcatttttg	aatattgcta	gcatggcttc	300
atcacaaatc	actctgtcat	ggacagtggt	cagcacttgg	ccatctgcca	cccactgcac	360
taccttatcc	tcatgactga	tgaaaataga	gatcgaatgt	ttatggggccc	gctgacagcc	420
tttccctaca	ccgatgccac	atctcagaac	atgcactatg	taaattttct	tattatcatt	480
ctcagtattt	tgtacatccc	tggaccatat	acgttgatcc	taagagctat	gcttcagctg	540

ctttcagcag	ctagccatca	aaatgccttt	tctatccgtg	ggctctcactt	aatagtgggtg	600
tctctgttct	gtgaaacat	atgatgatgt	gtgtgaatct	catatctgac	catttagtat	660
aaatgaagat	gacaaatcac	aatatcataa	tgatatcctc	cataaagact	ctagttttta	720
actttgtcaa	ttacacctta	ctcaatatga	acttaaaacc	tatcttcagt	ttttttttta	780
tggaatgagt	attagccaaa	gctca				805

<210> 550

<211> 933

<212> DNA

<213> Unknown (H38g399 nucleotide)

<220>

<223> Synthetic construct

<400> 550

atgaaaatct	tcaacagccc	cagcaactcc	agcaccttca	ctggetttcat	cctcctgggc	60
ttcccttgcc	ccagggaggg	gcagatcctc	ctctttgtgc	tcttcactgt	tgtttacctc	120
ctgacctca	tgggcaatgg	ttccatcatc	tggtgtgtgc	actgggatca	gagactccac	180
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ttcctatgtg	accagctcc	tcttctaact	ctcacttgca	aaaaaggccc	tgtgatagag	600
cttgtctttt	ctgtcttaag	tcctctgcct	gtctttatgc	tctttctctt	cattgtgggg	660
tcctatgctc	tggtcggtgag	agctgtgttg	agggtccctt	cagcagctgg	gagaagaaag	720
gctttctcca	cctgtgggtc	tcacctggct	gtggtttcac	tggtctacgg	ctcagtactg	780
gtcatgtatg	ggagcccacc	atctaagaat	gaagctggaa	agcagaagac	tgtgactctg	840
ttttattctg	ttgttaccac	actgcttaac	cctgtgatat	atagtcttag	gaacaaagat	900
atgagaaaag	ctctgaagaa	atgttgggga	aca			933

<210> 551

<211> 977

<212> DNA

<213> Unknown (H38g400 nucleotide)

<220>

<223> Synthetic construct

<400> 551

acagccctgg	aattcacaaa	caattcagag	acaagcacta	tgacggaatt	tggttctcctt	60
ggctttctctg	gttgtcagga	gatgcaaagt	ttcctcttct	ccctgttctt	tgtgatctat	120
gtattttacca	taataggaaa	tgggaccatt	gtctgtgtctg	tgagattgga	caaacggctt	180
cataccacca	tgtatattct	cctagggaac	tttgctttcc	ttgaaatccg	gtaagtact	240
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ggctgtttcc	tccagttcta	cttttttact	tcctttggta	caatagaagc	atacttctc	360
tgcatcatgg	catatgatcg	gtaccttgct	atctgcccgc	cattgacta	cccaaccatc	420
atgacccac	aactctgcta	catattgatg	tctttttgct	gggtgtttgg	attcctcagt	480
tactctgtct	ccactgtgca	actgtctcaa	ctgcctttct	gtgggcccac	catcatcaat	540
cactttttgt	gtgacatgga	cccactgatg	gctctgtcct	gtgcctcagc	tcctatcact	600
gagattatct	tctatatact	gagctccctc	attatcattc	tcactcttct	gtacatctgt	660
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aggccttttc	cacctgtgga	tctcatctga	cagtggtgtg	tttattcttt	ggggccctac	780
tggcaatgta	tgtgagcccc	acaactgata	acccagctgc	aatttagaag	attataactt	840
tggtctatct	tgtggtgacc	cccttcttaa	acccctgat	ttacagctta	cgaacaaaag	900
agatgaaggc	tgcggtgaag	aaagtcctga	ggatagaatg	agaataaagt	catctacatg	960
agaccaagca	aaccatt					977

<210> 552

<211> 945

<212> DNA

<213> Unknown (H38g401 nucleotide)

<220>

<223> Synthetic construct

<400> 552

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gataacttat	taatcttctc	tgctgtaagg	ctggacaccc	atctccacaa	ccccatgtat	180
aattttatca	gtatattttc	ctttctggag	atctgggtaca	ccacagccac	cattcccaag	240
atgctctcca	acctcatcag	tgaaaagaag	gccatctcaa	tgactggctg	catcttgacg	300
atgtattttc	tccactcact	tgaaaactca	gaggggatct	tgctgaccac	catggccatt	360
gacagatacg	ttgccatctg	caaccctctt	cgctatcaaa	tgatcatgac	cccccggtc	420
tgtgctcaac	tctctgcagg	ttcctgcctc	ttcggtttcc	ttatcctgct	tcccgagatt	480
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ttcagcgaca	cttatccacc	agttttggac	acagccattg	actgatgtt	tactgtactt	840
gtccattctt	tcaatcccat	catttatagc	ctgagaaaca	aggacatgaa	caatgcgatt	900
aaaaaactgt	tctgtcttca	aaaagtgttg	aacaagcctg	gaggt		945

<210> 553

<211> 921

<212> DNA

<213> Unknown (H38g402 nucleotide)

<220>

<223> Synthetic construct

<400> 553

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tgcttcttct	cattcatcct	ggttctctat	ctcctgacac	tgctagggaa	tgagagctatt	120
gtctgtgcag	tgaaattgga	caggcggtc	cacacacca	tgtacatcct	tctgggaaac	180
tttgcccttc	tagagatctg	gtacatttcc	tccactgtcc	caaacatgct	agtcaatatt	240
ctctctgaga	ttaaaacccat	ctccttctct	ggttgcttcc	tgcaattcta	tttctttttt	300
tcactgggta	caacagagtg	tttcttttta	tcagttatgg	cttatgatcg	gtacctggcc	360
atctgtcgtc	cattacacta	cccctccatc	atgactggga	agttctgtat	aattctgggtc	420
tgtgtatgct	gggtaggcgg	atttctctgc	tatccagtcc	ctattgttct	tatctcccaa	480
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aaccagcag	gaatgcagaa	gatcatcact	ctgggtatata	cagcaatgac	tccattctta	840
aatcccttta	tctatagtct	tcgaaacaaa	gacatgaaag	atgctctaaa	gagagtctctg	900
gggttaacag	ttagccaaaa	c				921

<210> 554

<211> 768

<212> DNA

<213> Unknown (H38g403 nucleotide)

<220>

<223> Synthetic construct

<400> 554

atgtataatt	ttatcagcat	tttctcattt	ctggagatct	ggtacacaa	tgccacaatt	60
cccaagatgc	tctccatcct	catcagcagg	cagaggacca	tctccatggt	tggtgcctc	120

ttgcagatgt	acttcttcca	ttcactggga	aattcagagg	ggattttgtt	gaccaccatg	180
gccattgata	ggtagcttgc	catctgtaac	cctctccgct	acccaaccat	catgaccccc	240
gggctctgtg	ttcagctctc	tgtgggggtcc	tgcattctttg	gctttcttgt	gttgctccca	300
gagattgcat	ggatttccac	actgcccttc	tgtggacca	accaaattcca	ccagatcttc	360
tgtgattttg	aacctgtgct	gcgcttggcc	tgtacagaca	cgtccatgat	tctgattgag	420
gatgtgatcc	atgctgtggc	cattgtattc	tctgtcctga	ttattgccct	ttcttatatc	480
agaatcatca	ctgtaatcct	gaggattccc	tctgttgaag	gccgccagaa	ggccttttct	540
acctgtgccg	cccattcttag	tgtctttctg	atgttctatg	gcagtgtatc	cctcatgtac	600
ctgcgtttct	ctgccacttt	cccaccgatt	ttggacacag	ctgttgcaact	gatgtttgca	660
gttcttgctc	cctttttcaa	ccctatcatc	tatagcttta	gaaataagga	catgaagatt	720
gcaattaaaa	agcttttctg	ccctcagaag	atggttaatt	tatctgta		768

<210> 555

<211> 960

<212> DNA

<213> Unknown (H38g404 nucleotide)

<220>

<223> Synthetic construct

<400> 555

agtctgggaa	gcatgaataa	ctcacagata	tctactgtga	cgcagtttgt	gttggtgggg	60
tttctgggtc	cctggaaaat	tcagatcatc	ttttctcaa	tgattttgtt	gggtctacatc	120
ttcactctga	ctgggaatat	ggccatcatc	tgtgcagtga	gggtgggacca	tcgactccat	180
acccctatgt	acgtgctcct	agccaaacttc	tccttcctag	agatctggta	tgtgacctgc	240
acagtcacca	acatgctggt	aaattttttc	tccaaaacta	agaccatata	attctctgga	300
tgtttcactc	agttccactt	cttcttttcc	ctgggcacaa	ctgaatgctt	cttcctctgt	360
gtcatggctt	atgatcggtg	cctggccatc	tgccaccac	tgcactatcc	ctccattatg	420
actggccagc	tctgtggcat	cttgggtgtc	ctttgttggc	tcattggttt	ccttggacat	480
tcaatttcca	ttttcttcat	ttttcaacta	cctttctgtg	gtcccaacat	cattgatcat	540
tttctgtgtg	atgtagacct	actgatggca	ttgtcctctg	cccctactca	catcataggg	600
catgtgttcc	attctgtgag	ctctcttttc	atcaacctca	ccatggtgta	catccttggg	660
tcctatacct	tgggtctcag	aactgtgctt	taggttcctt	cttcagctgg	atggcaaaag	720
gccatctcta	cctgtgggtc	acacttgggt	gttgtgtctc	tgttctatgg	agccataatg	780
ctgatgtatg	tgagtccac	acctggcaac	tcagttgcta	tgcataagct	catcacactg	840
atatattctg	tggtaacacc	tgtcttaaac	cccctcatct	acagcctacg	caacaaggac	900
atgaaatatg	ccctccatca	tgtcttctgt	ggaatgagaa	ttatccagag	atcatgaata	960

<210> 556

<211> 957

<212> DNA

<213> Unknown (H38g405 nucleotide)

<220>

<223> Synthetic construct

<400> 556

atggatccag	agaatcagac	aatggtgact	gagttttatt	tctctgattt	tcctcaatct	60
aagaatggca	gcctcttatt	cttcattcct	atgctcttta	tttatatatt	cattcttgtt	120
ggaaatttca	tgattttctt	tgtgtccaa	ccggaccccc	atctccataa	tcctatgtac	180
agttttatca	gtgtcttctc	cttcctggag	atttgggtaca	ccaccgtgac	tatccccaa	240
atgctctcca	accttctcag	tgaacagaaa	accatctctt	tcataggttg	cctcctgcag	300
atgtacttct	tccactcact	cggggtcaca	gaagccctag	tcctcacagt	gatggccatt	360
gacaggtgtg	tagccatctg	caacccccct	cgctatgcaa	tcactatgtc	cccttgactg	420
tgcattccagc	tctccactgg	ctcttgcaat	tttggcttcc	tcattgttact	gccagagatt	480
gtgtgcattt	ccactcttcc	attctgtggc	gccaaacaaa	ttcatcaact	cttttgtgac	540
tttgaacctg	tgtctgcagt	agcctgcaca	gatacgtaca	taattctggg	tgaagatgtg	600
atccgtgcta	tttccattct	gacctctgtc	tctgtcatca	cccttttcta	tttaagaatc	660
atcacgtgta	tcctgaggat	tccctctggg	gagagtgcgc	agaaggcttt	cttcacatgt	720
gcagcccaca	ttgctatttt	tttgcgtgtt	tttggcagtg	tgtcactcat	gtatctgcgc	780
ttctctgtca	cattcccacc	attactggac	aaggccattg	cactgatgtt	tgctgtcctt	840

gccctacttt tcaacccagt aatctatagt ctgaggaaca aagatatgaa aaacgccacc 900
aagaaaaatcc tctgttctca aaagatgttc aatgcctctg ggagctaata gagttca 957

<210> 557
<211> 951
<212> DNA
<213> Unknown (H38g406 nucleotide)

<220>
<223> Synthetic construct

<400> 557
atgacacagt tgacggccag tgggaatcag acaatgggtga ctgagttcct cttctctatg 60
ttcccgcatg cgcacagagg tggcctctta ttctttatc ccttgcttct catctacgga 120
tttatcctaa ctggaaacct aataatgttc attgtcatcc aggtgggcat ggccctgcac 180
acccctttgt atttctttat cagtgtcctc tccttcctgg agatctgcta taccacaacc 240
accatcccca agatgctgtc ctgcctaate agtgagcaga agagcatttc cgtggctggc 300
tgcctcctgc agatgtactt ttccactca cttggtatca cagaaagctg tgtcctgaca 360
gcaatggcca ttgacaggta catagctatc tgcaatccac tccgttacct aaccatcatg 420
attcccaaac ttgtatcca gctgacagtt ggatcctgct tttgtggctt cctccttggtg 480
cttctgaga ttgcatggat ttccaccttg cctttctgtg gctccaacca gatccaccag 540
atattctgtg atttcacacc tgtgctgagc ttggcctgca cagatacatt cctagtgggtc 600
attgtggatg ccatccatgc agcggaaatt gtgacctcct tcctgggtcat tgctctatcc 660
tacatccgga ttattatagt gattctggga atgcactcag ctgaagggtca tcacaaggcc 720
ttttccacct gtgctgctca ccttgctgtg ttcttgctat tttttggcag tgtggctgtc 780
atgtatttga gattctcagc cacctactca gtgttttggg acacagcaat tgctgtcact 840
ttgtttatcc ttgctccctt tttcaacccc atcatctata gcctgaaaaa caaggacatg 900
aaagaggcta ttggaaggct tttccactat cagaagaggg ctggttgggc t 951

<210> 558
<211> 831
<212> DNA
<213> Unknown (H38g407 nucleotide)

<220>
<223> Synthetic construct

<400> 558
atggctctaa ttggaaacct atccatgatt cttctcatct tcttggacac ccattctccac 60
acacccatgt atttcctact tagtcagctc tccctcattg acctaaatta catctccacc 120
attgttctta agatggcatc tgattttctg tctggtaaca agtctatctc cttcactggg 180
tgtgggattc agagtttctt cttctcggca ttagggaggtg cagaagcact acttttggca 240
tctatggcct atgatcgta cattgctatt tgctttcctc ttactatcc catccgcatg 300
agcaaaagaa tgtgtgtgct gatgataaca ggtcttggga tcataggctc gatcaatgct 360
tgtgtcaca ctgtatatgt actccatatt ccttatggc aatccagggc catcaatcat 420
ttcttctgtg atgtcccagc aatggtgact ctggcctgca tggacacctg ggtctatgag 480
ggcacagtgt ttttgagcac caccatcttt ctcgtgtttc ccttcattgc tatttcatgt 540
tcctatggcc gggttctcct tgctgtctac cacatgaaat ctgcagaagg gaggaagaaa 600
gcctacctga cctgcagcac ccacctcact gtagtaactt tctactatgc accttttgtc 660
tacacttate tacgtccaag atccctgcga tctccaacag aggacaaggt tctggctgtc 720
ttctacacca tcctcaccac aatgctcaac ccatcatct atagcctgag gaacaaggag 780
gtgatggggg ccctgacacg agtgagtcag agaactctgt ctgtgaaaat g 831

<210> 559
<211> 725
<212> DNA
<213> Unknown (H38g408 nucleotide)

<220>
<223> Synthetic construct

<400> 559
 atggatagag taaataattc tgcggtatct aaatttgtat tgattggact ttcaagctct 60
 tgggagatgc atctttttct tttttgggtc ttctctgtgt tctacatggg aattatcctg 120
 gaaaatctct tcatttgtgt cacagtaatt attgactctc atttaaattc cccagggtact 180
 gcctactggc caacatttat cttcttgatc tgggtcttct cctacagttc tgactttttc 240
 actaactgca gcatcatttc ttttccaaga tgcattgatac agatattttt catttgtgtc 300
 atgcgtaaaa attgagatgg tgctgctcat aaccatggca tagagcaggt acactgccaa 360
 tctgtaagcc tccccattac ctgaccacaa tgaaccccaa aatgtgtgtt tcctttgttg 420
 gaggcacccg ggatagtcag gataatccat gctgtatctc agtttgtttt tgccataaac 480
 ttgccttttt gtggccctaa tagagtaggt agttttcact gtgattttcc ttatgtcatg 540
 aaacttgctt gtgtagatac ttacaaacta gaggtttagt tcaactgctaa cagtgggctt 600
 atatccatag ctacctgttt cttattaata ataccctata ttttcatttc ggtaaccgtc 660
 tagaatcctt cttcaggaga cttatctaaa gcatttgtgt catgttagat cacatcacag 720
 taggg 725

<210> 560

<211> 936

<212> DNA

<213> Unknown (H38g409 nucleotide)

<220>

<223> Synthetic construct

<400> 560
 atggacacag ggaactggag ccaggtagca gaattcatca tcttgggctt ccccatctc 60
 cagggtgtcc agatttatct ctccctcttg ttgcttctca ttacatcat gactgtgttg 120
 ggaaacctgc tgatattcct ggtggtctgc ctggactccc ggcttcacac acccatgtac 180
 cactttgtca gcattctctc cttctcagag cttggctata cagctgccac catccctaag 240
 atgctggcaa acttggtcag tgagaaaaag accatttcat tctctgggtg tctcctgcag 300
 atctatttct ttcactccct tggagcgact gagtgctatc tcttgacagc tatggcctac 360
 gataggtatt tagccatctg ccggccctc cactacccaa cctcatgac cccaacactt 420
 tgtgcagaga ttgccattgg ctggtggttg ggaggcttgg ctgggccagt agttgaaatt 480
 tccttgattt cagccctccc attctgtggc cccaatcgca ttcagcacgt cttttgtgac 540
 ttccctcctg tgctgagttt ggcttgcaat gatacgtcta caaatgtcct agtagatttt 600
 gttataaatt cctgcaagat cctagccacc ttctgtctga tctctgtctc ctatgtgcag 660
 atcatctgca cagtgtcag aattccctca gctgccggca agaggaaggc catctccacg 720
 tgtgcctccc acctcactgt ggttctcatc ttctatggga gcaccccttc catgtatgtg 780
 cggtgaaga agagctactc actggactat gaccaggccc tggcagtggt ctactcagtg 840
 ctacacacct tctcaaccc cttcatctac agcttgacaa acaaggagat caaggaggct 900
 gtgaggaggc agctaaagag aattgggata ttggca 936

<210> 561

<211> 635

<212> DNA

<213> Unknown (H38g410 nucleotide)

<220>

<223> Synthetic construct

<400> 561
 gaattccttt ttataatta caatcaaaca tcaactgatt tcatcttatt ggggctgttc 60
 ccacaatcaa gaattggcct ttctgtattc accctcattt ttctcatttt cctaattggct 120
 ctaattggaa atctatccat gattcttctc atcttttttg acatccatct ccacacacct 180
 atgtatttcc tacttagtca gctctccctc attgacctaa attacatctc caccattgtt 240
 ccaaagatgg ttatgattt tctgtatgga aacaagtcta tctccttcac tggatgtggg 300
 attcagagtt tcttcttctt gacttttagca gttgcagaag ggctgtcctt gacatcaatg 360
 gcctatgata gttatgtggc catttgcttt cctctccact atcccatccg tataagcaaa 420
 agagtgtgtg tgatgatgat aacaggatct tggatgataa gctctatcaa ctcttgtgct 480
 cacacagtat atgcactctg tatcccatat tgcaagtcca gagccatcaa tcattttttc 540
 tgtgagggat cctctgagag gtacctggga gcatgcaagc ttggcgctgg gccgcggtg 600
 aaacggcgtg actggtaaaa ccctgggctg gccca 635

<210> 562
 <211> 789
 <212> DNA
 <213> Unknown (H38g411 nucleotide)

<220>
 <223> Synthetic construct

<400> 562
 atgttgggga attactctag cgccactgaa ttttttctct taggcttccc tggctcccaa 60
 gaagtatgcc gtatcctatt tgcgacctt ttcctcttgt atgcagtac agtgatggga 120
 aacgtgggca tcatcatcac tgtctgtgt gataaatgtc tgcagtcccc catttatatt 180
 ttcttgggcc acctctgtgt cctggagatc ctgatcacat ccaccgctgt cccttttatg 240
 ctctgggggt tgcgtcttcc aagcaccag atcatgtctt tgacagcctg tgctgcacag 300
 ctatatttat acctttcttt gggtagcttg gagttggcat taatgggagt gatggctgtg 360
 gaccgttatg tggctgtgtg taaccctttg aggtacaaca tcattatgaa cagcagcacc 420
 ttcatattgg tgataattgt gtcattgggt ttggggtttc tttctgaaat ctggccagtt 480
 tatggcaatt ttcagcttac tttctgcaaa tcaagtgtgt tagatcattt ttattgtgac 540
 cgaggacaat tgcacaagt atcctgtgag gacactcttt tcagagagtt tattcttttt 600
 ctaatggctg ttttcattat cattggttct ttgatcccta cgattgtctc ctacacctac 660
 atcatctcca ccaacctcaa gattccgtca gcctctggct ggaggaaatc cttttccacc 720
 tgtgcctccc acttcaccta tgttgtgatt ggctatggca gctgcttgtt tctctacgtg 780
 aaaccaag 789

<210> 563
 <211> 951
 <212> DNA
 <213> Unknown (H38g412 nucleotide)

<220>
 <223> Synthetic construct

<400> 563
 atggatcaat acaaccattc aagcctggct gaatttgtgt tccttggctt tgccagtgtg 60
 ggctatgtca ggggctggct ttttgtctg ctgctattgg catacctgtt caccatctgt 120
 ggtaacatgc tcatcttctc agtcatccga ctggatgcag ctctgcacac acctatgtac 180
 cactttgtca gtgttcttcc ctctctggag ttgtggtata cagctaccac tatccctaag 240
 atgttgtcta atattctcag tgagaagaaa accatttctt ttgcaggatg cctccttcag 300
 acctacttct tccactcctt gggagcgtct gaatgctacc ttcttacagc catggcctat 360
 gatagatacc tggccatttg tcggcccttc cactacccta taattatgac caccacactc 420
 tgtgccaaga tggctgctgc ttgttggact tgtggcttcc tgtgtcccat ttctgaggtc 480
 atccttgctt cccagctccc attttgtgct tacaatgaaa tccaacacat tttctgtgac 540
 tttccacctt tgcgtagctt ggcttgcaag gacacatctg ctaacattct ggtggacttt 600
 gccattaatg ctttcataat tcttatcact ttcttcttta tcatgatttc ttatgcaagg 660
 atcattgggg ctgtgctgaa gataaaaaca gcatcaggaa gaaagaaggc cttttctacc 720
 tgtgcctcac atcttgcgtg ggctctcatc ttctttggga gcatcatctt catgtatgtg 780
 cggctaaaga agagctatcc cctgacctt gaccgaacac ttgctatagt ttactccgta 840
 ctaacaccaa tgggtcaatcc aattatctac agtcttcgta acaaggaaat cattaaagct 900
 atcaagagga ccatcttcca gaaggagat aaagctagtc ttgctcatct t 951

<210> 564
 <211> 945
 <212> DNA
 <213> Unknown (H38g413 nucleotide)

<220>
 <223> Synthetic construct

<400> 564
 atgcaggggc taaaccacac ctccgtgtct gaattcatcc tcgttggctt ctctgccttc 60

ccccacctcc	agctgatgct	cttcctgctg	ttcctgctga	tgtacctgtt	cacgctgctg	120
ggcaacctgc	tcatcatggc	cactgtcttg	agcgagcgca	gcctccacat	gcccattgtac	180
ctcttctctg	gtgccctctc	catcacccag	atcctctaca	ccgtggccat	catcccgcgc	240
atgctggccg	acctgctgtc	cacccagcgc	tccatcgctt	tcctggcctg	tgccagtcag	300
atgttcttct	ccttcagctt	cggcttcacc	cactccttcc	tgctcactgt	catggggtac	360
gaccgctacg	tggccatctg	ccacccctg	cgttacaacg	tgctcatgag	cctgcggggc	420
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tcggccattt	tccacctcgc	cttctgtgga	cacaaggaga	tccaccattt	cttctgccac	540
gtgccacctc	tgttgaagtt	ggcctgtgga	gatgatgtgc	tggtgggtgc	caaaggcgtg	600
ggcttgggtg	gtatcacggc	cctgctgggc	tgttttctcc	tcattcctct	ctcctatgcc	660
ttcactgtgg	ccgccattct	gaagatccct	tctgctgaag	gtcggaacaa	ggccttctcc	720
acctgtgcct	ctcacctcac	tgtgggtggtc	gtgcactatg	gctttgcctc	cgctatttac	780
ctgaagccca	aaggctccca	gtctccggaa	ggagacacct	tgatgggcat	cacctacag	840
gtcctcacac	ccttctctcag	ccccatcatc	ttcagcctca	ggaacaagga	gctgaaggtc	900
gccatgaaga	agacttgctt	caccaaactc	tttccacaga	actgc		945

<210> 565

<211> 958

<212> DNA

<213> Unknown (H38g414 nucleotide)

<220>

<223> Synthetic construct

<400> 565

cacacagagc	cacggcatct	cacagggtgc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagcctgt	cctcgctggg	ctgtcccat	ccatgtatct	ggtcacagt	120
ctgaggaacc	tgctcgctcat	cctggctgtc	agctctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaaccc	gtgctgggct	gacatcggtt	tcacttcggc	cacggttccc	240
aagatgactg	tggacatgca	gtcacatctc	agagtcattc	cttatgagag	ctgcctgaca	300
cggatgtctt	tcttggtcct	ttttgcatgt	atagaagaca	tgctcctgac	tgtgatggcc	360
taggactgct	ttgtagccat	ctgtcgccct	ctgcaactacg	cagtcactgt	gaatcctcac	420
ctctgtgtct	tcttagtttt	gggtgctctt	ttccttagcc	tggtggattc	ccagctgcac	480
agttagattg	ttacaattca	ccttcttcaa	gaatgtggaa	atctctcatt	ttgtctgtga	540
gccatctcaa	cttctcaacc	ttgcctgttc	tgacagcgtc	atcaatagca	tattcatgta	600
tttcaatagt	actatgtttg	gttttcttcc	catttcaggg	atccttttgt	cttactataa	660
aattgttccc	tccattctaa	ggatttctac	gtcagatggg	aagtataaag	ccttctccac	720
ctgtggctct	cacctggcag	ttgtttgctt	attttatgga	acaggcattg	gcatgtacct	780
gacttcagct	gtggcaccac	cccccaggaa	tggtgtgggtg	gcgtcagtga	tgtacgctgt	840
ggtcaccccc	atgctgaacc	ctttcatcta	cagcctgaga	aacagggaca	ttcaaagcgc	900
cctgtggagg	ctgcgcagca	gaacagtcga	atctcatgat	ctgttccatc	ctttttct	958

<210> 566

<211> 470

<212> DNA

<213> Unknown (H38g415 nucleotide)

<220>

<223> Synthetic construct

<400> 566

gtctccccc	tgtgggaatg	tgtgtcatga	cagcggctct	cccacttctt	atgctctgga	60
gactcagttt	tctgtctggg	tcacagtgtg	ggctgctgca	cactacttct	ttcacagagt	120
ttgcggcttc	tttcagtttt	cctgtttaagt	tcctgtgctg	cttcttggaa	aaaagtccac	180
agcatgaatc	tctacacacc	atcttgtctt	tctaagtggg	agaatcacgt	taacaatgcc	240
ttcaacctgc	catcatggaa	aaaaagttaa	agtgtggtca	ccatgttcta	agggcccgcc	300
atgatcacgt	acttgaggtc	tgactcctag	tataacctac	agtgggaaaa	cagttgggtgc	360
tgttctacag	cattgtctct	gccttcataa	aacctatcat	ctccagcctc	aggaacaagg	420
atgtaaaagg	ggcttcttgg	aaagtactta	gagtcaaagg	gacagctcaa		470

<210> 567

<211> 862
 <212> DNA
 <213> Unknown (H38g416 nucleotide)

<220>
 <223> Synthetic construct

<400> 567
 atggaaaatt acaatcaaac atcaactgat ttcattcttat tggggctgtt tccaccatca 60
 agaattgacc ttttcttctt cattctcttt gttctcattt tcttgatggc tctaattgga 120
 aacctatcca tgattcttct catcttcttg gacaccatc tccacacacc catgtatttc 180
 ctgcttagtc agctctccct cattgacctt aattacatct ctacgattgt tcctaagatg 240
 gcttctgatt ttctgtatgg aaacaagtct atctccttca ttgggtgtgg gattcagagt 300
 ttcttcttca tgacttttgc aggtgcagaa gcgctgtctc tgacatcaat ggcctatgat 360
 cgttatgtgg ccatttgctt tctctccac tatcccatcc gtatgagcaa aagaatgtat 420
 gtgctgatga taacaggatc ttggatgata ggctccatca actcttgtgc tcacacagta 480
 tatgcattcc gtatcccata ttgcaagtcc agagccatca atcatttttt ctgtgatgtt 540
 ccagctatgc tgacattagc cgttacagac acctgggtct atgagtacac agtggtttttg 600
 agcagcacca tctttcttgt gtttcccttc actggcattg cgtgttccta tggctgggtt 660
 ctcttctgtg tctaccgcat gcaactctga gaaggaggaa aaaggcctat tcgacctgca 720
 gcacccacct cactgtagta actttctact atgcaccctt acgttatacc tatctatgtc 780
 caagatccct gtttatttct gacagaggac aaggttgggg gggggggggg acaccatcct 840
 cacctcaatg ctcaacccca tc 862

<210> 568
 <211> 930
 <212> DNA
 <213> Unknown (H38g417 nucleotide)

<220>
 <223> Synthetic construct

<400> 568
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 gggaatatgt gtatgattat cctgattaca acagacatc agcttcacac acccatgtat 180
 tttttcctct gcaacctctc ctttggtgac ctgggctact cctcagccat tgccccagg 240
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 ttgctttttt ttgtagggtt tgtggatgct gagtgctatg tctggcagc catggcctat 360
 ggtcgttttg tggccatttg tcgacctc cactatagca ccttcatgtc caagcaggtc 420
 tgcttggtgc tcatgctggg ctcttacctg gctgggtctag tgagtttagt agcccacact 480
 accctcacct tcagcctgag ttactgtggt tccaatatca tcaatcattt cttctgcgaa 540
 atcccaccac tcttgccctt ctcttgctca gacacctaca tcagtgaat cttgctcttc 600
 agtctgtgtg gcttcattga attcagcacc atcctcatca tcttcatctc ctataccttt 660
 atccttggtg caatcatcag aatgcgttca gctgaaggcc gccttaaggc tttctccacc 720
 tgcggtctc accttactgg catcaccctc ttctatggca cagtcattgt tatgtacctg 780
 aggccaacat ccagctactc cctggaccaa gacaagtggg cctctgtgtt ctacacggtt 840
 atcatcccca tgttaaatcc cttgatctac agtttgcgga acaaggatgt gaaagctgct 900
 ttcaaaaagc taattggaaa aaaatctcaa 930

<210> 569
 <211> 1005
 <212> DNA
 <213> Unknown (H38g418 nucleotide)

<220>
 <223> Synthetic construct

<400> 569
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tggggaacct	gctcatcatc	ctggccgtca	gtcctgactc	ccacctccac	acccccatgt	180
acttcttcc	ctccaacct	tccttgctg	acatcggttt	cacctccacc	acggtcccca	240
agatgattgt	ggacatccga	tctcacagca	gagtcattct	ctatgcaggc	tgcttgactc	300
agacgtctct	ctttgccatt	tttggaggca	tggaagagag	acatgctcct	gagtgtgatg	360
gcctatgacc	agtttgtagc	catctgtcac	cctctatatc	attcagccgt	catgaacct	420
tgtttctgtg	gctttctagt	tttgttgact	tttttttttc	tcagtctttt	agacgcccag	480
ctgcacaact	tgattgcctt	acaaatgacc	tgcttcaagg	atgtggaaat	tcctaatttc	540
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atcatgtatt	tccctgctgc	catatttggt	tttcttccca	tctcggggac	ccttttctct	660
tactataaaa	ttgtttcctc	cattctgagg	gtttcatcat	cagggtggaa	gtataaggcc	720
ttctccacct	gtgggtctca	cctgtcgggt	gtttgctgat	tttatggaac	aggcattgga	780
gggtacctca	gttcagatgt	gtcatcttcc	ccgagaaagg	ctgcggtggc	ctcagtgatg	840
tacacgggtg	tcaccccat	gctgaacccc	ttcatctaca	gcctgagaaa	cagggatatt	900
aaaagtgtcc	tgcggtggct	gcacggcagc	tctgtcta	ctcaacatct	tcttatctgt	960
tgcattcctt	ttgtagtgtg	ggttaaaaaa	ggcagcaggg	tcaaa		1005

<210> 570

<211> 907

<212> DNA

<213> Unknown (H38g419 nucleotide)

<220>

<223> Synthetic construct

<400> 570

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gggaacattc	tcattcattgt	cctggtacag	ttagattctg	gactgttcac	gcccattgtac	180
ttatttatca	gtgtcctctc	ctttgtagag	gtgtggtatg	tcagcaccac	agtgtcccatg	240
ctgctgcaca	ccttgctcca	agggtgttca	cccgtctcat	cagctgtatg	ctttattcag	300
ctatgtcttt	cattccttag	ggatgactga	gtgctacctg	ctgggtgtca	tggtactgga	360
tagctacctt	atcatctgcc	accactcca	ctaccacgca	ctcatgagca	gacagggtaca	420
gttacgacta	gctggggcca	gttgggtggc	tggcttctca	gctgcacttg	tgccagccac	480
cctcatcgcc	actctgccct	tctgcttgaa	agagggtggc	cattactttt	gtgacttggc	540
accactaatg	cggttggcat	gtgtggacac	aagctggcat	gctagggccc	atggcacagt	600
gattggtgtg	gccactgggt	gcaactttgt	gctcattttg	ggactctatg	gaggtatcct	660
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ctcccacgta	actgtggtgg	cactattcta	tgcttctgcc	ttcacagtat	atgtgggctc	780
acctgggagt	cgacctgaga	gcacagacaa	gcttgttgcc	ttggtttatg	cccttattac	840
ccctttcctc	aatcctatca	tctatagcct	tcgcaacaag	gaggtgaaga	aggctttaag	900
gagagtc						907

<210> 571

<211> 1006

<212> DNA

<213> Unknown (H38g420 nucleotide)

<220>

<223> Synthetic construct

<400> 571

ccaacgaaga	gagagaacca	cacagtgata	agggagtgtg	ttttccaggg	tttctccagc	60
tttcatgaac	acaagcttac	cctctttgtg	gtattttctta	ccttggtgtct	tttaaccctg	120
gctggcaatg	tcataattgt	gacaattatc	agcattgatc	gtcaccttca	cacccccatg	180
tacttctttg	ttagtatgct	ttccacttca	gagactgtct	acacattagt	cattgtacca	240
cggatgctct	ccagtctctt	aagtctaagc	caacctatct	ctttgggtgg	ctgtgccacc	300
cagatgtttt	ttttattacc	ttggccatca	acaactgctt	tctgtctaca	gcaatggggt	360
atgatcgcta	tgtggccatc	tgtaaccctt	tgaggtagat	gatcatcatg	aacaagaaag	420
tgtgtgtcca	gctggtagtg	gggtcctgca	gtgttgggct	gcttgtggcc	atagttcaga	480
tttcatctgt	gttcaggctg	cctttttgtg	ataaacagg	ggccatttat	ttctgtgata	540
tccacccagt	tatgaaactt	tctgtgtgtg	ataccactct	acatgacctt	attaattttg	600

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ttgttagttc cctgggttatt gtggtgcccg tgggtttggt cttcatctcc tacatcctca 660
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gtgcctccca cctcactgtg gttatcatcc actatggctg tgcctccatt gcctacctca 780
agcccaagtc agagaacacc agggatcagg accagctaatt ttcagtgaca tacaccgtct 840
ttactccact acttaatcct gttgtgtaca ctttgaggaa caaggaggtc aagaatgccc 900
ttcacgtgac tattggcaaa aaaccttttg cctagaatct tcatcagttt gacatatagt 960
cagtcatagt ctgggtattt ttttaagctc gagaaaattg aatcct 1006

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<210> 572

<211> 945

<212> DNA

<213> Unknown (H38g421 nucleotide)

<220>

<223> Synthetic construct

<400> 572

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atgtccataa ccaaagcctg gaacagctca tcagtgacca tgttcaccc cctgggattc 60
acagaccatc cagaactcca ggcctctctc tttgtgacct tctgggcat ctatcttacc 120
accctggcct ggaacctggc cctcattttt ctgatcagag gtgacacca tctgcacaca 180
cccattgact tcttcttaag caacttatct ttcattgaca tctgctactc tctgtctgtg 240
gtccccaata tgctcactga cttcttcttg gagcagaaga ccatatcatt tgtgggctgt 300
gctgctcagt tttttttctt tgtggcatg ggtctgtctg agtgccctct cctgactgct 360
atggcatacg accgatatgc agccatctcc agcccccttc tctacccac tatcatgacc 420
cagggcctct gtacacgcag ggtgggttgg gcataatgtt gtggcttctc gagctccctg 480
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ttctgcgacc tcccaccagt cctggctctg tcttgctctg acaccttctc cagtcaagtg 600
gtgaatttcc tcgtggtggt cactgtcgga ggaacatcgt tctccaact ccttatctcc 660
tatggttaca tagtgtctgc ggtcctgaag atcccttcag cagagggccg atggaaagcc 720
tgcaacacgt gtgcctcgca tctgatgggt gtgactctgc tgtttgggac agcccttttc 780
gtgtacttgc gacccagctc cagctacttg ctaggcaggg acaagggtgt gtctgttttc 840
tattcatttg tgatcccat gctgaaccct ctcatttaca gtttgaggaa caaagagatc 900
aaggatgccc tgtggaaggt gttggaagg aagaaagtgt tttct 945

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<210> 573

<211> 949

<212> DNA

<213> Unknown (H38g422 nucleotide)

<220>

<223> Synthetic construct

<400> 573

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atgccttgaa agatggagtc aataaacaca aacttcactg tcaactgaatt tgtgttctctg 60
gggttgctct ctgaacccaa gatacagctt attcttttta ttatgttctt gttctattta 120
tcaacgggtg ctggaaatgt tataatcate actattatct agatggaacc tctctccaa 180
accccatgt acttcttct cactaattta tctttcttg acatttgcta cacatccacc 240
aatgtccccc aaatgctgtc caacatggcg gggaaaaaga acaccatctc attctccagc 300
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tggtttatga cagatatgta gccatttgct atcctcttca ttataccttc attatggacc 420
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ttatcaatgt tctcacgttg agtttgccct actgtgggcc taatatctct aatcactttt 540
tctgtgaggt actttctgtc ctgaggttgg cttgcaccaa cactcattc acagagctgg 600
ttgtttttat cttcagtatc atcattgtct tcatcccttt cctcctcatt gttgttctct 660
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tatccacctg tacctcccat ttgacagtgg taaccttatt tatgggactg ccatcttcat 780
ggacatgaga ccacagtcga ggtcctcctg ggctggcgcc aagatcattg cggttttcta 840
cacggtggtc acacccatgc ttaacccctt gatttacagc ctgaggaacc aagatgtgaa 900
aggagctcga aggagagcta ttgcaaagca gaggatgtga cagctgtta 949

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<210> 574

<211> 1022
 <212> DNA
 <213> Unknown (H38g423 nucleotide)

<220>
 <223> Synthetic construct

<400> 574
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 aggcggcagc acaaacttgt cttctttgtt gtcttcctaa ctttgtacct gctgactctc 120
 tctggcaatg tgattatcat gaccattatt cgcctggacc atcatcttca caccctcatg 180
 tactttctcc tgtgcatgct atccatctct gagacctgct acactgtggc catcattccc 240
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 tatgaccgct atgtggccat ctgcaacccc ctaaggattt cagtcacatc gggtaagagg 420
 gcctgtatcc aactggcctc tggatcactg gggattggcc ttggcatggc cattgtccaa 480
 gtaacatctg tgtttggcct gccattctgt gatgcctttg tcatctccca cttcttctgt 540
 gatgtgagac acctgctgaa gctggcctgc acagacacca ctgtcaatga gataatcaac 600
 tttgttgtca gcgtctgtgt ccttgttcta cctatgggcc tggctcttat ctctatgtc 660
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 acctgcgctt cccacctcac agtgggtcatc atccactatg gctgtgcctc catcatctac 780
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 catcactccc ctactgaacc ctgttgtgta cagcctgaag aacaaggagg tcaaagatgc 900
 tctgcacaga gccgtggggc aaaaaactct gtctccttaa tgaagagagg ttgtgaaggc 960
 ttttcctttg cgtttataaa tatgtactaa tttttaatgc tctttcaata atgcccttat 1020
 gt 1022

<210> 575
 <211> 938
 <212> DNA
 <213> Unknown (H38g424 nucleotide)

<220>
 <223> Synthetic construct

<400> 575
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 atagggttcc caggcattca tgagtggcag cactggctct ccctgccctt agctcttggt 120
 gccaatctcc tcatcataat caccattcaa catgagacca tgctacatga acccatgtac 180
 catttgctgg gcatattagc agtgggtggc attggcctgg ccaccaccat catgcccag 240
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 gatagatata tggccatttg ttatcccctt cagtacactt ccatagttac tgaagctttt 420
 gtcacaaag ccacactgtc agtagtgctc aggaatggcc tgttgaccat ccagtgcca 480
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 aacttggggg tcacaagtct ggctgtgat gacaccata ttaacagggt ttaccagctg 600
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 attattcact cagtgtgaa gctgaactct gctaaagcaa catctaaggc cctgaatacc 720
 tgcagctccc acctatcct cattctcttt ttctacacag ctattattgt agtatctgtc 780
 accacctggc aggaagaagg gctcccgcga tccctgttct cctcaatgtg ctgcatattg 840
 tcatcccctc agcccttaac cccatagtat atgcccttag gacctaggag ctgagagcgg 900
 gcttcagaa gctgcttggt ttgggcgagt atgtgtcc 938

<210> 576
 <211> 945
 <212> DNA
 <213> Unknown (H38g425 nucleotide)

<220>
 <223> Synthetic construct

<400> 576

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ccagtgtctag	agaagatcct	gtttggggta	ttccttgcca	tctacctaat	cacactggca	120
ggcaacctgt	gcatgatcct	gctgatcagg	accaattccc	acctgcaaac	acccatgtat	180
ttcttccttg	gccacctctc	ctttgtagac	atttgctatt	cttccaatgt	tactccaaat	240
atgctgcaca	atttcctctc	agaacagaag	accatctcct	acgctggatg	cttcacacag	300
tgtcttctct	tcategccct	ggtgatcact	gagttttaca	tccttgcttc	aatggcattg	360
gatcgctatg	tagccatttg	cagccctttg	cattacagtt	ccaggatgtc	caagaacatc	420
tgtgtctgtc	tggtcactat	cccttacatg	tatgggtttc	ttagtgggtt	ctctcagtca	480
ctgctaacct	ttcacttatc	cttctgtggc	tcccttgaaa	tcaatcattt	ctactgcgct	540
gatectcttc	ttatcatgct	ggcctgctct	gacaccctgt	tcaaaaagat	ggcaatgttt	600
gtagttgcag	gctttaatct	ctcaagctct	ctcttcacca	ttcttctgtc	ctatcttttc	660
atttttgcag	cgatcttcag	gatccgttct	gctgaaggca	ggcacaaaag	cttttctacg	720
tgtgcttccc	acctgacaat	agtcactttg	ttttatggaa	ccctcttctg	catgtacgta	780
aggcctccat	cagagaagtc	tgtagaggag	tccaaaataa	ctgcagtctt	ttatactttt	840
ttgagcccaa	tgctgaacct	attgatctat	agcctacgga	acacagatgt	aatccttgcc	900
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<210> 577

<211> 771

<212> DNA

<213> Unknown (H38g426 nucleotide)

<220>

<223> Synthetic construct

<400> 577

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gtccagatgt	tctttgtaca	tgcactgact	gccatggaat	caggtgtgct	tttggccatg	180
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tgtgcacaca	tggcagtggg	agaactgggtg	gtgggttaaca	cacaggccac	caacttatat	420
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ggactcattg	cccatgctgt	gctgcagcta	cctaccgggg	aggcccatgc	caaggccttt	540
ggtacatgta	gttctcacat	ctgtgtcatt	ctggccttct	acataacctgg	tctcttctcc	600
tacctgcac	accgcttttg	tcatacact	gtcccaaaag	ctgtgcacat	ccttctctcc	660
aacatctact	tgctgtgtgc	acctgccctc	aacccctca	tctatggggc	cgcaccaag	720
cagatcagag	accgactcct	ggaaaccttc	acattcagaa	aaagcccgtt	g	771

<210> 578

<211> 1074

<212> DNA

<213> Unknown (H38g427 nucleotide)

<220>

<223> Synthetic construct

<400> 578

gtgagcatga	gcttcttaat	aagaagtgat	tcaacactac	acactccaat	gtgcttgttc	60
ctcagtcate	tctcctttgt	agatctctat	tatgccacca	atgccactcc	tccgatgctg	120
gttaactttt	ttttccaag	agaaaaaccg	tttcctttat	tggttgcttt	atccaatttc	180
accttttcat	tgactgggtg	atcacagatt	atcatatgct	cacagtgatg	gtgtatgacc	240
actacatggc	catctgcaag	cctttgttat	atggaagcaa	aatgtccagg	tgtgtctgcc	300
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aaaatgcatt	atatgcacat	ttaattccac	tataaatttt	tgaatggacg	gttggagagg	480
aagggagaaa	tacatattaa	cggagagaa	accaccaga	aagtatatac	aatgggagaa	540
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tctcagtatg	aagcatctcc	cagggtctgac	tctgatgtaa	aattggagat	caaccacttt	660

tattatgcag	aaccacccct	cttagtcctc	gcctgcttgg	atacttatgt	caaagaaact	720
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ttctccacct	gcgggtccct	tgtgactgcc	gtcactgtct	ttcaaggaac	gctgtttcac	900
atgtgcctga	ggcccccttc	tgaggcatct	gtagaacagg	ggaaaattgt	agctgctttt	960
tatatctttg	tgagtcctac	gttaaaccce	ttgatctacc	gtctgaggaa	taaaaatgtt	1020
aaaagaacaa	taaggggaagt	tatccaaaag	aaactgtttg	ctaagtaagg	taga	1074

<210> 579

<211> 937

<212> DNA

<213> Unknown (H38g428 nucleotide)

<220>

<223> Synthetic construct

<400> 579

atgtttggtg	ctaattctcac	caccttccat	cccactctat	tcattctcct	tggtcatccca	60
ggactggagc	aataccacat	ctggctttcc	attcctttct	accttatgta	catcactgca	120
gtcttgggaa	atggagccct	catectagtt	gtcctcagtg	aacacaccct	ccatgtcttc	180
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ccaatggcat	cggttttggt	agatgttgca	ttcattgggt	tttcctacac	tttgatcctc	660
caggctgtgt	ttagacttcc	ttcccaggag	tcccagcaca	aagctcttaa	cacctgtggt	720
tctacattgg	agttgttctc	ctcttcttca	tcccatcatt	ttttactttc	ctgacccacc	780
gctttggcaa	gaatatcccc	catcatgtcc	acatacttct	ggcaaatctc	tacttgcttg	840
ttcccccatg	cttaacccca	ttatctacgg	agagaagacc	aagcaaatca	gggacagtat	900
ggctcatatg	ttatctgtgg	tggggaagtc	ttgagac			937

<210> 580

<211> 941

<212> DNA

<213> Unknown (H38g429 nucleotide)

<220>

<223> Synthetic construct

<400> 580

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ctcatcacc	tgactgggaa	atttgggatg	attttcctaa	tcagattcac	tcctcagctc	180
caaaccaca	tgtatttttt	ccttactcat	ttagcatgtg	tggtatattt	ttactccact	240
aatgtctctc	cacagagctt	gttaatttct	tatctgagaa	gaagaccatt	tcctacgctg	300
gggtgtctggc	ccagtgtttt	gtctttgtga	ctctgtcctc	tactgagtat	tacatgcttg	360
gtgccatggc	ctatgactgc	tacatggcaa	tctgcaatcc	cctacattac	agcagcaaaa	420
tgtccagagc	agtttgcatc	tgcttgggtg	ctttcccta	cttctggggg	tctatgggtg	480
gcacgatgca	agtaatactg	acctctcggt	tgctcttttt	tggaaccaac	accatcaacc	540
atttctactg	tactgacca	cccctcttaa	tggtgacatc	ttctgacact	tacataaaaac	600
aaactgcctt	gtttgtgtca	gcagggatta	acctcacagt	ttccctgctc	atcattctca	660
tctcctacat	tttcatttct	atcaccatta	tgaggatccg	ttccagtga	gggcagctca	720
aagccttctc	cacctgtggc	tcccacctga	cagctgtcac	tatgttctat	gggtccctat	780
tctgcatgta	cctgagacca	acaaatgagc	tgtctgttga	gcaagggaaa	atgggagtgg	840
tgttttgtat	ttttgtgagt	cccatgctga	acccgtttat	ctaccgcctg	agaaacaagg	900
atgtgaaaca	ggccttgaaa	agagtgttta	tgagaaacct	t		941

<210> 581

<211> 958
 <212> DNA
 <213> Unknown (H38g430 nucleotide)

<220>

<223> Synthetic construct

<400> 581

atgagtccttc	tattctgaga	ctaagatatg	agaaacttta	caccactgtc	tggatttatt	60
atcctgggat	tcacggatca	cccagaatta	cagtgtcttc	tttttgtgtt	gtttcttctc	120
atctatatgt	tcaccgttgt	tggaatctt	ggcatgattc	tattaatcaa	gattgactca	180
catctccata	ctccaatgta	ctttttcctc	agtaacttgt	gccttggtga	cttctgttat	240
tcttctgtca	ttgcccctaa	tatgctgata	aatttctggg	tggagaaccc	agtcatttca	300
tttaaatgaat	gtgccactca	attcttcttt	tttggctcct	ttgctggcat	tgagggtttt	360
ctgttggctg	tcattggccta	tgactgttat	gtggccatct	gcaagcctct	gctttataca	420
gtcctgatgt	cacccacact	cagtggcctc	ctgggtgttag	ccacatatct	tttgggcttt	480
gtaaatgctg	ccattcacac	tggtctcacc	ttccagctgt	cattctgccca	ctccaatctc	540
attaactatt	ttttttgtga	tattccaccc	ctcctgaaac	tcttgttctg	atacacacat	600
caatgagggt	gtcatttttg	cctttgccag	ttttaatgaa	ttgagctgtc	tcctactgat	660
tcttgtttcc	tgtctctaca	tccttgctgc	catcttgaag	atccactctg	cagaagggag	720
gcacaaggcc	ttctccacct	gtgcttccca	cttggcggtg	gtcactatct	tctttgggac	780
aatcctgttc	atgtatctct	gcgtcccagc	tccagctact	caatggatca	agacaaagtg	840
gtgtctgtct	tacacagtag	tcattcccat	gttgaatcct	ttcatctata	gtttgagaaa	900
caaggaagtc	aaagcttctt	taagtaaaat	gtttaaaaca	gtctcttata	tctctact	958

<210> 582

<211> 897

<212> DNA

<213> Unknown (H38g431 nucleotide)

<220>

<223> Synthetic construct

<400> 582

atgggattac	caggcattca	tgagtggcag	cactggctct	ccctgcccct	gactctgctc	60
tacctcttag	ctcttgggtc	caacctcctc	atcataatca	ccattcaaca	tgagaccgtg	120
ctacatgaac	ccatgtacca	tttgcctggc	atattagcag	tggtggacat	tggcctggcc	180
accaccatca	tgcccagat	cctggccatc	ttctggtttg	atgccaaagg	cattagcctc	240
cccattgtgt	ttgctcagat	ctatgccatc	cactgcttct	tctgcataga	gtcaggcatc	300
tttctctgca	tggcagtaga	cagatacata	gccatctgtc	gccctcttca	gtaccctctc	360
atagtcacta	aagcttttgt	cttcaaagcc	acagggttca	tcattgctcag	gaatggcctg	420
ttgaccatcc	cagtgcctat	actggctgcc	cagagacact	actgttccag	gaatgaaatc	480
gagcactgcc	tctgtcttaa	cttgggggtt	atcagcctgg	cttgtgatga	catcactgtg	540
aacaaatttt	accaactgat	gctagcatgg	gtcttggttg	ggagtgatat	ggctctggta	600
ttttcttctc	atgctgtaat	ccttactctc	gtgctgaggc	tgaactcagc	agaagcaatg	660
tccaaggctc	tgagcacttg	tagctccac	ctcatctcca	tcctcttcca	cacaggtatc	720
attgtgctgt	ctgtcacaca	ccttgacag	aaaaagattc	cccttattcc	tgtgttccct	780
aatgtgctgc	acaatgtcat	ccccctgca	ctcaaccccc	tggcctgtgc	actcaggatg	840
cacaaactca	gactgggctt	tcagagactg	cttggactgg	gtcaggacgt	gtccaag	897

<210> 583

<211> 951

<212> DNA

<213> Unknown (H38g432 nucleotide)

<220>

<223> Synthetic construct

<400> 583

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ctcttaggac	tttccgacaa	tccagatcta	caaggagtcc	tctttgcatt	gtttctgttg	120

atctatatgg	caaacatggt	gggcaatttg	gggatgattg	tattgattaa	gattgatctc	180
tgtctccaca	cccccatgta	tttctttctc	agtagcctct	cttttgtaga	tgctctttac	240
tcttcttccg	tacttcccaa	gatgctggtg	aacctcatgg	ctgagaataa	ggccatttct	300
tttcatggat	gtgctgcccc	gttctacttc	tttggtcctc	tcctggggac	tgagtgtctc	360
ctgttgggca	tgatggcata	tgaccgctat	gcagccattt	ggaacccctc	gctctacca	420
gttctcggtg	ctgggagaat	ttgctttttg	ctaatagcta	cctccttctt	agcagggttg	480
ggaaatgcag	ccatacatac	agggatgact	tttaggttgt	ccttttggtg	ttctaatagg	540
atcaaccatt	tctactgtga	caccccgcca	ctgctcaaac	tctcttgctc	tgataccac	600
ttcaatggca	ttgtgatcat	ggcattctca	agttttattg	tcatacagctg	tgttatgatt	660
gtcctcatat	cctacctgtg	tatcttcatt	gccgtcttga	agatgccttc	gttagagggc	720
aggcacaag	ccttctccac	ctgtgcctct	tacctcatgg	ctgtcaccat	attcttttga	780
acaatcctct	tcatgtactt	gcgccctaca	tctagctact	caatggagca	agacaagggt	840
gtctctgtct	ttatacagt	aataatccct	gtgctaaatc	ccctcatcta	tagtttaaaa	900
aataaggatg	taaaaaaggc	cctaaagaag	atcttatgga	aacacatctt	g	951

<210> 584

<211> 951

<212> DNA

<213> Unknown (H38g433 nucleotide)

<220>

<223> Synthetic construct

<400> 584

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gggttggagg	cttatcacat	ttggctgtca	atacctcttt	gcctcattta	catcactgca	120
gtcctgggaa	acagcatcct	gatagtggtt	attgtcatgg	aacgtaacct	tcatgtgccc	180
atgtatttct	tcctctcaat	gctggccgct	atggacatcc	tgctgtctac	caccactgtg	240
cccaaggccc	tagccatctt	ttggcttcaa	gcacataaca	ttgcttttga	tgctgtgtgc	300
accaaggctt	tctttgtcca	tatgatgttt	gtgggggag	cagctatcct	gttagccatg	360
gcctttgatc	gctttgtggc	cattttgtgc	ccactgagat	atacaacagt	gctaacatgg	420
cctgtttgtg	ggaggattgc	tctggccgct	atcacccgaa	gcttctgcat	catcttccca	480
gtcatattct	tgctgaagcg	gctgcccttc	tgccaaacca	acattgttcc	tcactcctac	540
tgtgagcata	ttggagtggc	tcgttttagc	tgtgtgaca	tcactgttaa	catttgggtat	600
ggctttctcag	tgcccattgt	catggtcac	ttggatgtta	tcctcatcgc	tgtgtcttac	660
tcactgatcc	tccgagcagt	gtttcggttg	ccctcccagg	atgctcggca	caaggccctc	720
agcacttggt	gctcccacct	ctgtgtcatc	cttatgtttt	atgttccatc	cttctttacc	780
ttattgacct	atcatttttg	gcgtaatat	cctcaacatg	tccatatctt	gctggccaat	840
ctttatgtgg	cagtgccacc	aatgctgaac	cccattgtct	atgggtgtgaa	gactaagcag	900
atacgtgagg	gtgtagccca	ccggttcttt	gacatcaaga	cttgggtgctg	t	951

<210> 585

<211> 915

<212> DNA

<213> Unknown (H38g434 nucleotide)

<220>

<223> Synthetic construct

<400> 585

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ggaatgcagc	tgggcctctt	cgtgggtgtt	ctgggcgtgt	actctctcac	tgtggtagga	120
aatgacaccc	tcactgtgtt	gatctgtaat	gactcctgcc	tccacacacc	catgtatttt	180
gtcgtgggaa	atctgtcggt	tctggatctc	tgggtattct	ctgtctacac	cccaaagatc	240
ctagtgcact	gcactctctg	agacaaaagc	atctcctttg	ctggctgcct	gtgtcagttc	300
ttcttctctg	cagggctggc	ctatagttag	tgctacctgc	tggctgccgt	ggcttatgac	360
cgctacgtgg	ccatctccaa	gccctgtctt	tatgcccagg	ccatgtccat	aaagctgtgt	420
gcattgctgg	tagcagtctc	atattgtggt	ggctttatta	actcttcaat	catcaccaag	480
aaaacgtttt	cctttaactt	ctgccgtgaa	aacatcatgt	atgacttttt	ctgtgatttg	540
cttcccttgg	tggagctggc	ctgtggcgag	aagggcggct	ataaaaattat	gatgtacttc	600
ctgctggcct	ccaatgtcat	ctgccccgca	gtgctcatcc	tggcctccta	cctctttatc	660

atcaccagt	g	tcttgaggat	ctcctcctcc	aagggctacc	tcaaagcctt	ctccacatgc	720
tctcccacc	g	tgacctctgt	cactttatac	tatggctcca	ttctctacat	ctacgctctc	780
cccagatcta	g	ctattctttt	tgatatggac	aaaatagttt	ctacatttta	cactgtggta	840
ttccccatgt	t	gaatctcat	gatctacagc	ctaaggaata	aggatgtgaa	agaggctctg	900
aaaaaacttc	t	ccca					915

<210> 586

<211> 942

<212> DNA

<213> Unknown (H38g435 nucleotide)

<220>

<223> Synthetic construct

<400> 586

atgcttccct	ctaatacac	ctcaacacat	ccagctgtct	ttttgttgg	aggaattcct	60
ggtttggaa	acctgcatgc	ctggatctcc	atccccctct	gctttgctta	tactctggcc	120
ctgctaggca	actgtaccct	tctcttcatt	atccgggctg	atgcagccct	ccatgaaccc	180
atgtacctct	ttctggccat	gttggcaacc	attgacttgg	ttctttcttc	tacaacgctg	240
cccaaaatgc	ttgccatatt	ctggttcagg	gatcaggaga	tcaacttctt	tgctgtctg	300
gtccagatgt	tcttccctca	ctccttctcc	atcatggagt	cagcagtgtc	gctggccatg	360
gcctttgacc	gctatgtggc	catctgcaag	ccattgcact	acacgacgg	cctgactggg	420
tccctcatca	ccaagattgg	catggctgct	gtggcccggg	ctgtgacact	aatgactcca	480
ctccccctcc	tgctcagacg	cttccactac	tgccgaggcc	cagtgtattg	ccattgtctac	540
tgtgaacaca	tggctgtgg	aaggctggcg	tgtggggaca	ctagcttcaa	caatatctat	600
ggcattgtctg	tggccatgtt	tagtgtgtg	ttggacctgc	tctttgttat	cctgtcttat	660
gtcttcatcc	ttcaggcagt	tctccagctt	gcctctcagg	aggcccgtca	caaggcattt	720
gggacatgtg	tgtctcacat	aggtgccatc	ctgtccacct	acactccagt	agtcattctc	780
tcagtcatgc	accgtgtagc	ccgccatgct	gcccctcgtg	tccacatact	ccttgctatt	840
ttctatctcc	ttttcccacc	catggtcaat	cctatcata	atggagtcaa	gaccaagcag	900
attcgtgagt	atgtgctcag	tctattccag	agaaagaaca	tg		942

<210> 587

<211> 937

<212> DNA

<213> Unknown (H38g436 nucleotide)

<220>

<223> Synthetic construct

<400> 587

atgttaaaga	aaaaccatac	agccgtgact	gagtttgttc	tcttgggact	gacagatcgg	60
gctgagctgc	agtcctctct	ttttgtggta	tttctagtca	tctaccttat	cacagtaatc	120
ggcaatgtga	gcatgatctt	gttaatcaga	agtgactcga	cactacacac	tccaatgtac	180
ttcttctca	gtcacctctc	ctttgttagat	ctctgttata	ccaccaatgt	tactcctcag	240
atgctgggta	actttttatc	caagagaaaa	accatttcct	tcacgggctg	ctttatccaa	300
tttcactttt	tcattgcact	gggtgattaca	gattattata	tgctcacagt	gatggcttat	360
gaccgctaca	tggccatctg	caagcccttg	ttatatggaa	gcaaaatgac	caggtgtgtc	420
tgctctgtgc	tcgctgtctg	tccctatatt	tatggctttg	caaatggtct	aagcacagac	480
caccctgatg	cttcgtctgt	ccttctgtgg	acccaatgac	atcaaccact	tttactgtgc	540
ggaccacccc	ctcttagtcc	tcgctgtctc	agatacttat	gtcaaagaga	ccgccatgtt	600
ggtggtggct	ggttccaacc	tcatttgctc	tctcaccgtc	atcctcattt	cctacacttt	660
catcttcaat	gccattctgc	gtatccacac	tgctgagggg	aggcgcaagg	ccttctccac	720
ctgcgggtct	catgtgaccg	ctgtcactgt	cttctatggg	acactgttct	gcatgtacct	780
gaggccccct	tctgagacat	ctatacaaca	ggggaaaatt	gtagctgttt	tttatatctt	840
tgtgagtcgg	atgttaaacc	cattgatcta	cagcctgagg	aataaagacg	ttaaaagaag	900
tataaggaaa	gttattcaaa	agaaactgtt	tgctaag			937

<210> 588

<211> 942

<212> DNA

<213> Unknown (H38g437 nucleotide)

<220>

<223> Synthetic construct

<400> 588

atgtcagcct ccaatatcac cttaacacat ccaactgcct tcttgttggt ggggattcca	60
ggcctggaac acctgcacat ctggatctcc atcccccttct gcttagcata tacactggcc	120
ctgcttggaa actgcactct ccttctcatc atccaggctg atgcagccct ccatgaaccc	180
atgtacctct ttctggccat gttggcagcc atcgacctgg tcctttcttc ctcagcactg	240
cccaaaatgc ttgccatatt ctggttcagg gatcgaggaga taaacttctt tgcctgtctg	300
gcccagatgt tcttccttca ctccctctcc atcatggagt cagcagtgct gctggccatg	360
gcctttgacc gctatgtggc tatctgcaag ccactgcact acaccaaggt cctgactggg	420
tcctctcatca ccaagattgg catggctgct gtggcccggg ctgtgacact aatgactcca	480
ctccccctcc tgctgagatg tttccactac tgccgaggcc cagtgatcgc tcaactgctac	540
tgtgaacaca tggctgtggt gaggctggcg tgtggggaca ctagtctcaa caatatctat	600
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ttctatctgc tcttcccacc catggtcaat cccataatct atggtgtcaa gaccaagcaa	900
atccgtgaga gcatcttggg agtattccca agaaaggata tg	942

<210> 589

<211> 936

<212> DNA

<213> Unknown (H38g438 nucleotide)

<220>

<223> Synthetic construct

<400> 589

atgtcagcct ccagtatcac ctcaacacat ccaacttcct tcttgttgat ggggattcca	60
ggcctggagc acctgcacat ctggatctcc atcccccttct cagcatatac actggccctg	120
cttggaact gcacctcct tctcatcacc caggctgatg cagccctcca tgagcccata	180
tacctcttcc tggccatggt ggcagccatc gacctggctc ttctctcttc agcattgccc	240
aaaatgcttg ccatattctg gttcagggat cgggagatca acttttttgc ctgtctggtc	300
cagatgttct tccttctacc ctctctccatc atggagtcag cagtgtctgct ggccatggcc	360
tttgaccgct atgtggccat ctgcaagcca ctgcactaca ccacggctct gactgggtcc	420
ctcatcacca agattggcat ggctgtctg gcccgggctg tgacactaat gactccactc	480
cccttctctg tgagatgttt ccactactgc cgaggcccag tgattgcccg ctgtactgt	540
gaacacatgg ctgtggtcag gctggctgtg ggaacactag cttcaacaat atctatggca	600
ttgctgtggc catgtttatt ggagtgttg atctattctt tatcatccta tcttatatct	660
ttatccttca ggcagttcta caactctcct ctgaggaggc ccgctacaaa gcatttggga	720
catgtgtctc tcacataggt gccatcttag ccttctacac accttcagtc atctcttcag	780
tcatgcaccg tgtggcccgc tgtgtctgcgc cacacgtcca cattctcttc gccaatctct	840
atctgctctt cccacccatg gtcaatccca tcactacagg cgtaaagacc aagcagatcc	900
gtgacagtct tgggagtatt cccgagaaag gatgtg	936

<210> 590

<211> 955

<212> DNA

<213> Unknown (H38g439 nucleotide)

<220>

<223> Synthetic construct

<400> 590

atgacaaccc acaactccac tggtagcagc cactcactct tcattctgct gagcattcct	60
ggcttagaag accagcacac atggatgtct ctcccccttct ttatttctta ccttgttgct	120
ttccttggga acagcctcat catcttcac atcatcactg aatgcagcct ccacgaaccc	180

atgtacacctt	tcctctgcat	gctggctgtg	gctgacctta	tcctgtctac	taccactgtg	240
cccaaggccc	tagccatatt	ttggttctat	gctggagcaa	tatcccttgg	tggtgtgtt	300
acccaaatct	tctttatcca	tgtacacctc	atcgaggaat	caggaattct	gttggcgatg	360
gcacttgacc	gctatgtggc	catctgtgat	ccactgcact	ataccacagt	gctcagtcgt	420
gcaaaaatca	caaagattgg	cttggctgtg	gtcctgagaa	gcttctgtgt	gatcatgcc	480
gatgtgttcc	tggtaaagcg	gctgcctttc	tgccatagca	atctgctgcc	acatacctac	540
tgtgagcaca	tggtgtgtgc	caagtttgct	tgtgctgata	ttcatgtcaa	tggttggtat	600
ggcttgtctg	tccttctcta	tactgtagt	ctagatgcct	tgcttatctt	agtgtcctaa	660
agcttcatcc	tgtatacagg	cttccacctc	ccctcccaa	ggagctcggc	aaaaggctct	720
gggcacatgt	ggctcccacc	tcagagtcac	ttccatgttc	tacttgccctg	gtatttttac	780
cataattacc	cagcggtttg	ggcaccatgt	tcctctccat	acacacattc	tgctgggtaa	840
tgtctgggtg	ttggctcctc	ccatgctgaa	ccccatcatt	tatgggatca	acaccaggca	900
gattcaagag	tgtgtgctca	gtcttttgtc	ctcacagagg	aatgatgct	agatt	955

<210> 591

<211> 939

<212> DNA

<213> Unknown (H38g440 nucleotide)

<220>

<223> Synthetic construct

<400> 591

atgaattggg	taaagacag	catcatacag	gagtttatcc	tgctgggttt	ctcagatcga	60
ccttggtcgg	agtttccact	ccttggtggtc	ttcttgattt	cttacctgt	gaccatcttt	120
ggcaatctga	ccattattct	agtgtcacgc	ctggacacca	aacttcatac	ccccatgtat	180
ttttttctta	ccaatctatc	actcctggat	ctttgttaca	ccacatgtac	agtcccacaa	240
atgctagtaa	atttatgcag	catcaggaaa	gtaatcagtt	atcgtggctg	tgtagcccag	300
cttttcatat	ttctggcctt	gggggctact	gaatatcttc	tcctggccgt	catgtccttt	360
gataggtttg	tagctatttg	tcggcctctc	cattactcag	ttatcatgca	ccagagactc	420
tgccctcagt	tggtcagctg	atcctgggtt	actgggttta	gtaactcagt	gtggttgtct	480
accctgactc	tcagctgccc	actctgtgac	ccctatgtga	tagatcactt	tctctgtgaa	540
gtccctgcac	tgctcaagtt	atcttgtgtt	gagacaacag	caaatgaggc	tgaactattc	600
cttgtcagtg	agctcttcca	tctaataccc	ctgacactca	tccttatatc	atatgtcttt	660
attgtccgag	cagtattgag	gatacagctc	gctgaaggct	gacaaaaagc	atttgggaca	720
tgtggttccc	atctaattgt	ggtgtctctt	ttttatagta	cagccgtctc	tgtgtacctg	780
caaccacctt	cgcccagctc	caaggaccaa	ggaaagatgg	ttctctctct	ctatggaatc	840
attgcaccca	tgctgaatcc	ccttatatat	acacttagga	acaaggaggt	aaaggaaggc	900
tttaaaaggt	tggttgcaag	agtcttctta	atcaagaaa			939

<210> 592

<211> 997

<212> DNA

<213> Unknown (H38g441 nucleotide)

<220>

<223> Synthetic construct

<400> 592

atggaaaaat	ccaatgtcag	ctcagtgat	ggttttatct	tggtgggttt	ctctgatcgt	60
cccaagctgg	agatgggtgct	ctttacagta	aattttatcc	tgtattcagt	ggctgtgctg	120
ggaaattcaa	ccataatcct	tgtgtgtata	ttagactctc	aacttcatac	cccaatgtac	180
ttctttcttg	caaactcttc	ctttctagat	ctctgcttca	gtactagtgt	catcccacaa	240
atgctggtaa	acctctgggg	ccctgacaag	actattagct	gtgctggctg	tggtgtccag	300
cttttctctt	tcctttctgt	caggggaatt	gagtgcatcc	ttctggctgt	catggcctat	360
gacagctatg	ctgcagctctg	caaaccgttg	cgctatctgg	tcattatgca	cctccagctg	420
tgtctaggac	tgatggctgc	agcctggggg	agtggtactg	tcaatgccgt	tgctcatgtca	480
ccactaacia	tgaccctctc	cagaagtggc	cgccgcccag	ttaaccattt	cctctgtgaa	540
agccagcact	gatcaagatg	gcttgttttg	atgttcgtgc	agtggaatg	ctggcttttg	600
cttttgccgt	tctcattgtc	ctactgcccc	tcactcttat	tcttgtctcc	tacggctaca	660
ttgctgcagc	tgtgctaagc	atcaagtcag	ctgccaggca	atggaaggcc	ttccatacct	720

gtagctctca	cctcacagt	gtctccctgt	tttatgggag	catcatctat	atgtatatgc	780
agccaggaaa	cagttcttcc	caagaccaag	gcaagtttct	cactctcttc	tacaacctgg	840
tgactcctat	gttgaatctg	ctcatctata	ctttaaggaa	taaggagggtg	aaaggagcac	900
tgaagaaggt	tttggggagg	caataatgaa	ctggagaaat	atgataagtt	gtgaagtctt	960
aggcaaaata	tcttttccaa	atacatttat	tttgtgc			997

<210> 593

<211> 950

<212> DNA

<213> Unknown (H38g442 nucleotide)

<220>

<223> Synthetic construct

<400> 593

caagtagttc	atacaggctt	ttctccctag	ctatacgtct	tcaccctgct	gggaaatggg	60
gcatcctggg	gctcatctgg	ctggactcca	gactgcacac	ccccatgtac	ttctttctct	120
cacacctggc	catcattgat	atttcgtatg	cttccaacaa	tgcccccaag	atgctgacaa	180
accttggcct	gaacaagaga	aaaacaatct	cctttgtccc	atgcacaatg	cagacctttt	240
tatacatggc	ttttgctcac	actgagtgtc	tcactcttgg	aatgatgtcc	tacgatcggt	300
acatggctgt	ctgccaccct	ctgcaatatt	ctgtcatcat	gagatgggga	gtgtgcacag	360
tcctggctgt	cacttcttgg	gcatgtggtt	ccttctggcc	ctgggccatg	tggttctcat	420
cctgaggctg	cccttctgtg	ggccccatga	aatcaaccac	ttcttctgtg	aaatcctgtc	480
tgctctcaag	ttggcctgtg	ctgacacctg	gctcaaccag	gtggtcacat	ttgttctctc	540
agtgttcac	ctgggtgggg	cgctctgcct	ggtgctggtc	tcctactcgc	gcatcctggc	600
ggccatcttg	aggaatcagt	ctggggaggg	gcgagaaag	ggcttctcca	cctgtacttc	660
ccacctttgc	atggtgggac	tcttctttgg	cagcgccatt	gtcacgtaca	tggcccccaa	720
gtcccgccat	cctgaggagc	agcagaaagt	tctttccctg	ttttacagcc	ttttcaatcc	780
aatgctgaac	ccccctgata	tatagcctaa	ggaatgcaga	ggtcaagggc	gccctgagga	840
gtgcactgag	gaaggagagg	ctgacgtgag	acatctcaaa	gggaaccatg	gggagggagc	900
cttgcctcct	gcaaaatata	gaagttggct	tttttttttg	tcttctgcta		950

<210> 594

<211> 711

<212> DNA

<213> Unknown (H38g443 nucleotide)

<220>

<223> Synthetic construct

<400> 594

cagatgctga	cagattgggtg	gggacctaat	aggaccacaa	gttacgtgaa	ctcaccattc	60
aattccttgt	ctctctgtag	ttatgtgcca	ctatataatt	tctacaatta	ttttataatt	120
atatgccatc	ctttgttaata	tttggttaatc	atgaacctat	atctcctcct	taatcttact	180
ttaatacttg	agtataaatt	cattcatttt	tgatcatcatg	tatactctca	tcctaaaatt	240
cccaagggtat	gaaaaaaaaa	aaccttcagg	ataattccct	ccatgtgttg	ctagctatgc	300
tgaaaacagt	ttttctagat	gctacaattg	aagaaatgtc	tgtatttgtg	ttaatacaat	360
gtaaatgtcc	taatatgcct	tatcagtaat	tttacctgct	atggctacat	tgaggtgcac	420
taagaatgaa	tactagtaat	taaattagaa	gcaagctgag	aaatcagtat	catcatcatc	480
atcatagggtg	tcatttcatt	atagattcaa	tcttctatgg	aatcattgtg	taaatgctct	540
tgaagatgggt	aacaactcct	cccaagacca	agaaatgatt	ctttatcttg	ttttacacta	600
tactaactcc	aagtctcaaa	cttctagttt	atctgttaag	aataaagata	taaaggatat	660
ttcaaggaga	atactaagat	tggcagggaa	tcttcaaaaa	tgaaaggaaa	c	711

<210> 595

<211> 765

<212> DNA

<213> Unknown (H38g444 nucleotide)

<220>

<223> Synthetic construct

<400> 595

atgtatttcc	tactgagtca	gctctccctc	attgacctaa	attacatctc	caccattgtt	60
cctaagatgg	catctgattt	tctgcatgga	aacaagtcta	tctccttcac	tgggtgtggg	120
attcatagtt	tcttcttcac	gacttttagcc	gttgtagaag	cgctactcct	gatatcaatg	180
gcctatgttc	gttgcatgac	tatttgcttt	cctctccact	atctcatgcg	catgagcaaa	240
agagtgtgtg	tgctgatgat	aacaggatct	tggatcatag	gctcgatcaa	tgcttgtgct	300
cacactgtat	atatactcca	tattccttat	tgcccatcta	gggttatcaa	tcatttcttc	360
tgtgatgtcc	cagcaatggg	gactctggcc	tgcatggaca	cctgggtcta	tgagggcaca	420
gtgcttttga	gcgccaccat	ctttctcgtg	tttcccttca	ttgctatttc	atgttcctat	480
ggacgggttc	tccttgctgt	ctaccacatg	aaatctgcag	aaggggaagaa	gaaggcctac	540
ctgacctgca	gcacccacct	cactgtagtg	actttctact	atgcaccctt	tgcttacacc	600
tatctacgcc	caagatccct	gcgatctccg	acagaggaca	aggttctggc	tgtcttctac	660
accatcctca	tcctaatgct	caaccccatc	atctacagcc	tgagaaacaa	ggaggtgatg	720
ggggccctga	cacgagtgat	tcagaaaatc	ttttcagtga	aaata		765

<210> 596

<211> 960

<212> DNA

<213> Unknown (H38g445 nucleotide)

<220>

<223> Synthetic construct

<400> 596

ctgtcatgac	caaccagagc	tgcccagaaa	cagttcatct	tactgggttt	ctcaggcaga	60
cccaggctgg	agcatgtcct	ctttgtgttt	gtccctcatct	tctaccttgt	gaccttagtg	120
ggcaacatca	tcattatctt	gatctccac	ctggaccctt	gcctccacat	gcccattgtac	180
ttcttccctca	ctaaactgtc	tttccatagat	ctctgcttca	ccaccagttc	tatccccccag	240
ctgcttttca	atctaggcag	cccaggcaag	actatcagcc	acacgggctg	tgccatccag	300
ctcttcatgt	tcctgggcct	gggtggcaag	agtgtattct	cttggcagcc	gtggccctatg	360
accgcttcat	tgcaatctgc	aagccccttc	actattctgt	cattatgcac	cctcagctgt	420
gctggaagtt	ggtgtctgtg	gcccgggggt	gttggaactcc	tcagttctct	agttatgtct	480
cctgtgacta	tgaagctgcc	acgatgtgga	agatgtgaagt	tgaaacattt	cctgtgtgag	540
atgccagctc	taataaaaaat	cacctgtgtg	gacacagtgg	ctatggagag	cactgttttc	600
accttatcgg	tagtaattgt	cctgatgcct	ttgtgtctta	tcctcatctc	ttatagctac	660
attgccctag	cagtgtctgag	aatcaagtca	gccgcaggaa	gaaggaaggc	cttcaatatg	720
tgccgggtccc	acctcacctg	ggtctccttg	ttttatggga	atattatcta	tatgtatatg	780
caaccatgaa	ataattcttc	tcaggaccaaa	gggaagttcc	ttaccctttt	ctacaactta	840
atgaccccca	tgttaaacct	tgtcatctat	acactgagaa	acaaggatgt	aaaagggtgca	900
ctgaagaggc	ttgtgtctag	aaaacacagt	gacagtgcct	gctcttgaga	ctgcttcttt	960

<210> 597

<211> 377

<212> DNA

<213> Unknown (H38g446 nucleotide)

<220>

<223> Synthetic construct

<400> 597

atggaaaatt	acaatcaaac	atcaactgct	ttcatcttgt	tgggattgtc	gccaccacca	60
aaaattggcc	atttcatctt	cattctcatt	aatttcgttt	tcctaattggc	tctaattgga	120
aacctatcca	tgattcttct	catcttcttg	gacatccatc	tcacacacac	catgtatttc	180
ctacttagtc	agctctccct	cattgacctc	aattatattt	ccaccattgt	tcctaagatg	240
gtttatgatt	tttcatgtat	ggaaacaagt	ctatctcctt	cactgggtgt	gggattcaga	300
gtttcttctt	cctgacttta	gcagggtgcag	aagcgctgct	cctgacatca	atggccctatg	360
atcggttatgt	ggctatt					377

<210> 598

<211> 979

<212> DNA

<213> Unknown (H38g447 nucleotide)

<220>

<223> Synthetic construct

<400> 598

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atggaaagag ctaacgacag caccttctct ggattcatcc tectgggctt ctccaacagg      60
cctcagctgg aaacagctct ctttgtggtc atcttgatca tctactttct gagctttctg      120
ggcaatggca ccattatact tttatccatt gtagatcctc gcctccatac ccctatgtat      180
ttcttcctct ccaatctctc ttttatggat ctttgtttga ccacttgtag tgteccctcag      240
acactgggtca actttaaggg gaaggacaag accatcacct atgggtggctg cgtgaccag      300
ctattcattg ccttgggact cggggggagt ggagtgtgtc ttattgtctg ccatggccta      360
tgaccgctat gcagccgtct gccgcccact ccactacatg gtgagcatgc atccccaaact      420
ttgcttgtag ttggttgtaa ccacttggct cacagggttt ggcaattctg tgatacagac      480
agcattgacc atgactctcc cctctgtga taaaaaccaa gtggatcatt tcttctgtga      540
agttccagtg atgctgaaac tgctctgcac caacacctcc atcaacgagg ctgaaatctt      600
tgctgtcagt gtcttctctt tgggtgggtcc tctctcactc atcttagcat cctatgggtca      660
cattactcat gcagtcctga agataaagtc agctcaaggg aggcagaagg cttttggaac      720
ctgtggttct cacttcctgg tagtgatcat tttctttggg acactcatct ccatgtacct      780
ccagcctccc tccagttatt cacaggatgt gaacaaaagc attgcactct tctatactct      840
ggtgactcct ctactgaatc ccctaattta cactctgagg aacaaggaag tcaaaggggc      900
aactaagaag actagtgggg aggaccatag atgcatgaga aagttaacgc aggggtttgca      960
gttccaaaca tttgtgcac

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<210> 599

<211> 936

<212> DNA

<213> Unknown (H38g448 nucleotide)

<220>

<223> Synthetic construct

<400> 599

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atggaaaatt acaatcaaac atcaactgat ttcattctat tggggctgtt tccaccatca      60
ataattgacc ttttctctct cattctcatt gttttcattt tcctgatggc tctaattgga      120
aacctgtcca tgattcttct catcttcttg gacaccatc tccacacacc catgtatttc      180
ctactgagtc agctctccct cattgacctt aattacatct ccaccattgt tcctaagatg      240
gcactctgatt ttctgcatgg aaacaagtct atctccttca ctgggtgtgg gattcagagt      300
ttcttcttct tggcattagg aggtgcagaa gcactacttt tggcatctat ggcctatgat      360
cgttacattg ctatttgcct tcctctccac tatctcatcc gcatgagcaa aagagtgtgt      420
gtgctgatga taacaggggc ttggatcata ggctcgatca atgcttgtgc tcacactgta      480
tatgtactcc atattcctta ttgccgatcc agggccatca atcatttctt ctgtgatgtc      540
ccagcaatgg tgactctggc ctgcatggac acctgggtct atgagggcac agtggttttg      600
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agcaccaccc tcaactgtagt aactttctac tatgcacctt ttgtctacac ttatctacgt      780
ccaagatccc tgcgatctcc aacagaggac aagggtcttg ctgtcttcta caccatcttc      840
accccaatgc tcaaccccat catctatagc ctgaggaaca aggaggtgat gggggccctg      900
acacgagtga gtcagagaat ctgctctgtg aaaatg

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<210> 600

<211> 936

<212> DNA

<213> Unknown (H38g449 nucleotide)

<220>

<223> Synthetic construct

<400> 600

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atgcccaatt caaccaccgt gatggaattt ctctcatga ggttttctga tgtgtggaca      60

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ctacagattt	tacattctgc	atccttcttt	atgttgatt	tggttaactct	aatgggaaac	120
atcctcattg	tgaccgtcac	cacctgtgac	agcagccttc	acatgcccac	gtacttcttc	180
ctcagggaatc	tgtctatctt	ggatgcctgc	tacatttctg	ttacagtccc	tacctcatgt	240
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gctctggggg	taggtggcgg	ctgtttcatc	tttatcatca	ggtcttacat	tcacatcttt	660
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cctgcgatac	ctgcagccac	ccaggatctg	atcctttctg	gtttttattc	cataatgcct	840
ccccctctta	accctattat	ttacagtctt	agaaataagc	aaataaagg	ggccatcaag	900
aaaatcatga	agagaatttt	ttattcagaa	aatgtg			936

<210> 601

<211> 931

<212> DNA

<213> Unknown (H38g450 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(931)

<223> n = A,T,C or G

<400> 601

aggaatgccc	cactggaaaa	atacaatcaa	acatcaactg	atttcatctt	attggggatc	60
ttcccaccat	ccagaattgg	ctttctcttc	ttcattctcc	ttgttctcat	tttgctattg	120
gctttaattg	gcaatcagtc	cgtgatccct	ctcatcttct	tggacactca	tctccacacg	180
cccatttatt	tcttacttag	tcggctctac	ctcattgacc	taaattacat	ctccactatt	240
gtccccagat	gttttctgat	tttctgtttg	gaaacaagtc	tatttctctc	attgggtgtg	300
gaattcagag	tttcttcttt	gtgactttag	cagggtgcaga	aatgctgcca	ctgacatcaa	360
tggcctgtga	tcattatgta	gctgtttgct	ttcctctcca	ctatcccatc	catatgagca	420
agatagtatg	tgctgatgat	aataggatct	tggataatgg	gctctatcga	cacttgtgct	480
cacatttcat	atatgcccc	tatccctggt	gctcagccag	ggctgtgatg	tcccagccat	540
ggtgactctg	gccttcgtgg	acacctgggt	ctatgagtgc	acagtgtttt	tgagcacaac	600
cctctttctc	atgtttacct	ttattgggat	tgcattgttc	tatggtgagg	ttctccttac	660
tgtctaccac	attaaatctg	cagaagggag	gaagaaggcc	tattcgacct	gtagcaccca	720
cctcactgta	gtaattntct	actatgcaat	gtttgcttat	acctatctat	atccaagata	780
cctgcaatct	ccaacagagg	acaagggtct	ggctgtgttc	tacaccatcc	tcacctcaat	840
gctcaacccc	atcatctaca	gcctgagaaa	cagggagggtg	atggggggccc	tgacacgagt	900
gagtcagaga	atcttccctg	tgaagatgaa	g			931

<210> 602

<211> 577

<212> DNA

<213> Unknown (H38g451 nucleotide)

<220>

<223> Synthetic construct

<400> 602

agacacacag	agccacggaa	tctcacaggt	gtctgagaat	tcctcctcct	gggactctca	60
gaggatccag	aactgcagcc	tgtcctcget	ttgctgtccc	tgtccctgtc	cctgtccttg	120
tatctgggtca	tggttctgag	gaacctgtc	agcatcctgg	ctgtcagctc	tgactccccc	180
ctccataccc	ccatgtactt	cttccctctc	aacctgtgct	gggctgacat	cgggttcaat	240
tcggccacgg	ttcccaagg	gactgtggac	atgcagtcgc	atagcagagt	catctctcat	300
gcgggctgcc	tgacacagat	gtctttcttg	gtcctttttt	gcatgtatag	aatgcatgct	360

cctgactgtg atggcctatg acggctttgt agccatctgt ctcctctgc actaccaggt	420
catcatgaat cctcacctct gtgtcttctt cgttttggtg tcctttttcc ttagcctgtt	480
ggattcccag ctgcacggtt ggattgtgtg acaattcacc atcatgaaga atgtggaaat	540
ctctcatttt gtaagtgacc cctctcaact tctcaac	577

<210> 603

<211> 952

<212> DNA

<213> Unknown (H38g452 nucleotide)

<220>

<223> Synthetic construct

<400> 603

atggacagaa gaaaccagac ctgcatctat gaatttcttc tcatgggctt ctctgaacac	60
caggagcagc aggcctcttt gtttgggctt ttctgggtca tgtacttggg cactgtgttg	120
gagaacctgc taatcatcct ggccattggc tctgacctgc acctccacac ccccatgta	180
cctcttcctg tccaacctgt cctttttgga tattggcttt atctctacaa taattcccaa	240
gatgctagat catattagct caggaattaa gctgatttct tatggggagt gtctgacaca	300
actctatttc tctggcctat ttgcagatct ggacaacaac tttctcctgg ctgtgatggc	360
ccttgaccgc tatgtggcca tcagccatcc tctccattat gccctaacca tgaactcca	420
acgtctgtgc ctgttggtgg ctgtgtcatg ggtgatcact attttacatg ccctagtga	480
taccctccta gtgaccaggc tttcctcttg tgggtccaaat attatccctc acttctcttg	540
tgatctgggc ccactcctga agctggcctg ctccagtact tgtgtcaatg atctgggtct	600
catccttctg gcaggaacac tgctgattgc gccctttgtc tgcatcctta tgctcactt	660
ttacattgca ttggccatcc tgagaattga ttccccaagg ggtaagcaaa gggcctctc	720
cagctgcact tcccacctct ctgtagtctc tctgttctat agcacagcta tcggtgtcta	780
tttatgtcct ccatcatccc actcagatgg aaaggacaga gtcttctcag tcatgtacac	840
gggtgtgact cccatgttga accccttcat ctacagcctg aggaacaggg atatgaaggg	900
ggcactggga aaactgcttg gaataaaaac atcctaacac ccttactcaa ga	952

<210> 604

<211> 754

<212> DNA

<213> Unknown (H38g453 nucleotide)

<220>

<223> Synthetic construct

<400> 604

cattttagt ggtgcgtgtt cagatactcg ggtattgtgg tggagataca catagtcttt	60
tgaacattcc gtttaggtc gctggtagct ggatatgtcc tttaaacttt tgtggcaatt	120
catttgagaa gaaacgcagc tttttctatt gaggttctat gctataagta aaggatgcaa	180
gacattaatt agacaaaata aggtaaaatt ttgtattcgc ttagagagtt taagaggcta	240
ttagccacta gtctctatag tgcctaagta aatcgattct gcttaataaa ctgctacctg	300
gcttagtaag taaacaaatt gaaacttatt ttaggaaaga aatatatatt cttatatcta	360
catcagattc tcttatgtag aaacactaga gggtagaatga ggagttaatg taagcagcat	420
catatttttg ctcatctcct tctctatgat ttctgcttct tctgtccaaa ttctgtgagg	480
tgctctctag atgaaattat cacaggcatg gaaaagggtc ttttccactt ggtccatcct	540
catgattgca gttgtaacat actgggactc attcattttc acatatgtat atgagactta	600
aatcatccac atttcaggcc aggttaagtt tctagaaata ttctatgctt tccttgact	660
tacactcaat cctgtcgtct acagcgttgg cactgacagt gttctggtgg caatgaaaaa	720
tatgtcttag agcaacattc tacataaaaa aaag	754

<210> 605

<211> 939

<212> DNA

<213> Unknown (H38g454 nucleotide)

<220>

<223> Synthetic construct

<400> 605
 atggaccaga tcaaccacac taatgtgaag gagtttttct tcctggaact tacacgttcc 60
 cgagagctgg agtttttctt gtttgtggtc ttcttttgctg tgtatgtage aacagtcctg 120
 ggaaatgcac tcattgtggg cactattacc tgtgagtcce gcctacacac tcctatgtac 180
 tttctctgc ggaacaaatc agtcctggac atcgtttttt catctatcac cgtccccaag 240
 ttcttgggtg atctttttatc agacaggaaa accatctcct acaatgactg catggcacag 300
 atctttttct tccactttgc tgggtggggca gatatttttt tcctctctgt gatggcctat 360
 gacagatacc ttgcaatcgc caagcccctg cactatgtga ccatgatgag gaaagagggtg 420
 tgggtggcct tgggtgggtg ttcttgggtg agtgggtggt tgcatccaat catccaggta 480
 attctgatgc ttccattccc cttctgtggc cccaacacac tggatgcctt ctactgttat 540
 gtgctccagg tggtaaaact ggcctgcact gacacctttg ctttggagct tttcatgac 600
 tctaacaacg gactgggtgac cctgctctgg ttctctctgc tcctgggctc ctacactgtc 660
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 cccttcatga cgctgcccac ggacacaacc atatccatta ataacacggt cattaccccc 840
 atgctgaacc ccatcatcta ttccctgaga aatcaagaga tgaagtcagc catgcagagg 900
 ctgcagagga gacttgggccc ttccgagagc agaaaatgg 939

<210> 606

<211> 927

<212> DNA

<213> Unknown (H38g455 nucleotide)

<220>

<223> Synthetic construct

<400> 606
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 cggcctgagg accaaaagac actctttgtt ctcttcctca tcgtgtacct ggtcaccata 120
 acaggggaacc tgctcatcat cctggccatt cgcttcaacc cccatcttca gacccctatg 180
 tattttctct tgagttttct gtctctcact gatatttgct ttacaacaag cgttgtcccc 240
 aagatgctga tgaacttcct gtcagaaaag aagaccatct cctatgctgg gtgtctgaca 300
 cagatgtatt ttctctatgc cttgggcaac agtgacagct gccttctggc agtcatggcc 360
 tttgaccgct atgtggccgt ctgtgacct ttccactatg tcaccaccat gagccaccac 420
 cactgtgtcc tgctgggtgc cttctcctgc tcatttctc acctccactc actcctgcac 480
 acacttctgc tgaatcgtct cacttctgt gactccaatg ttatccacca ctttctctgt 540
 gacctcagcc ctgtgctgaa attgtcctgc tcttccatat ttgtcaatga aattgtgcag 600
 atgacagaag cacctattgt tttgggtgact cgttttctct gcattgcttt ctcttatata 660
 cgaatcctca ctacagttct caagattccc tctactctg ggaaacgcaa agccttctcc 720
 acctgtggtt tttacctcac cgtgggtgac ctcttttatg gaagcatctt ctgtgtctat 780
 ttacagcccc cateccaccta cgctgtcaag gaccacgtgg caacaattgt ttacacagtt 840
 ttgtcatcca tgctcaatcc ttttatctac agcctgagaa acaaagacct gaaacagggc 900
 ctgaggaagc ttatgagcaa gagatcc 927

<210> 607

<211> 939

<212> DNA

<213> Unknown (H38g456 nucleotide)

<220>

<223> Synthetic construct

<400> 607
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 ctgcggtatt tatatgggtg gctcttccca ctgatttacc tggcagccct aatgagtaac 120
 cttctcatca ttactctcat taccctggac gtaaagctcc aaacacccat gtacttcttc 180
 ctgaagaact tacccttttt ggatgtcttc ctgggtgctg ttccaatccc aaaattcatt 240
 gtcaacaacc taaccacaa caattccatt tccattctag gatgtgcctt ccagctactt 300
 ttaatgactt ccttctcagc aggagagata tttatcctca ctgccatgtc ctatgaccgc 360
 tatgtagcca tctgctgtcc cctgaactac gaggtaatca tgaatactgg agtctgtgtg 420

ttaatggcaa	gtgtttcctg	ggccattgga	gggctctttg	gtactgcgta	cacagctggc	480
acattttcca	tgcttttctg	tggtccagtg	gtgattccac	agtttttctg	tgatgttcct	540
tcattactaa	ggattttcctg	ttctgaaaca	ctaattggtaa	tttatgcagg	tattggaggt	600
ggtgcatggt	taagcatttc	ttgtttcatc	tgtattgtga	tctcttacat	ttatatcttc	660
tccactgtac	tgaagatccc	taccactaaa	ggtcagtcga	aagctttttc	cacatgcttc	720
ccccatctca	ctgtttttcac	tggtttttatc	ataactgctt	attttgttta	tcttaagcca	780
ccttcaaatt	caccatctgt	tattgacagg	ctgctttctg	tgatctacac	tgtgatgcct	840
ccagtattta	accctgtaac	ctacagcctg	cggacaatg	acatgaaatg	tgctctgata	900
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<210> 608

<211> 972

<212> DNA

<213> Unknown (H38g457 nucleotide)

<220>

<223> Synthetic construct

<400> 608

atggctgtag	gaaggaacaa	cacaattgtg	acaaaattca	ttctcctggg	actttcagac	60
catcctcaaa	tgaagatttt	ccttttcatg	ttattttctg	ggctctacct	cctgacgttg	120
gcctggaact	taagcctcat	tgccctcatt	aagatggact	ctcacctgca	catgcccctg	180
tacttcttcc	tcagtaacct	gtccttcctg	gacatctgct	atgtgtcctc	caccgcccct	240
aagatgctgt	ctgacatcat	cacagagcag	aaaaccattt	cctttgttgg	ctgtgccact	300
cagtactttg	tcttctgtgg	gatggggctg	actgaatgct	ttctcctggc	agctatggcc	360
tatgaccggg	atgttgcaat	ctgcaacccc	ttgctttaca	cagtcctcat	atcccataca	420
ctttgtttaa	agatgggtgg	tggcgccctat	gtgggtggat	tccttagttc	tttcattgaa	480
acatactctg	tctatcagca	tgatttctgt	gggccctata	tgatcaacca	ctttttctgt	540
gacctccctc	cagtcctggc	tctgtcctgc	tctgatacct	tcaccagcga	gggtggtgacc	600
ttcatagtca	gtgttgctgt	tggaatagtg	tctgtgctag	tggtcctcat	ctcttatggt	660
tacattgttg	ctgctgttgt	gaagatcagc	tcagctacag	gtaggacaaa	ggccttcagc	720
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atgcgaccca	gttccagcta	ctccctaaac	agggacaagg	tggtgtccat	attctatgcc	840
ttggtgatcc	ccgtgggtgaa	tcccatcatc	tacagtttta	ggaataagga	gattaaaaat	900
gccatgagga	aagccatgga	aagggacccc	gggatttctc	acgggtggacc	attcattttt	960
atgaccttgg	gc					972

<210> 609

<211> 942

<212> DNA

<213> Unknown (H38g458 nucleotide)

<220>

<223> Synthetic construct

<400> 609

atgaccaatc	agacacagat	gatggaattc	ttgcttgtga	gatttactga	gaattgggtg	60
ctctgagggc	tgcatgcttt	gctcttctca	ctgatctacc	tcacggctgt	gctgatgaat	120
ttagtcatca	ttctcctcat	gattctggac	catcgtctcc	acatggcaat	gtactttttc	180
ctccgacatt	tgctcttctt	agacctgtgt	ctcatttctg	ccacagtccc	caaatccatc	240
ctcaactctg	tcgctccac	tgactccatc	tccttcctgg	gggtgtgtgt	gcagctcttc	300
ttggtgggtac	tgctggctgg	atcagagatt	ggcctcctta	ctgccatgtc	ctatgaccgc	360
tatgctgcca	ctctgtgccc	cctacactgt	gaggctgtca	tgagcagagg	gctctgtgtc	420
cagttgatgg	ctctgtcctg	gctcaacaga	ggggccttgg	gactcttgta	cacagctgga	480
acattctctc	tgaattttta	tggtctgtgat	gagctacatc	agttcttctg	cgatgtccct	540
gccctactaa	agctcacttg	ttctaaagaa	catgccatca	ttagtgtcag	tgtggccatt	600
gggtctgtgt	atgcattttc	atgttttagt	tgcatgttag	tttcctatgt	gtacattttc	660
tctgtgtgtg	taaggatatc	acagagacag	agacaatcca	aagccttttc	caactgtgtg	720
cctcacctca	ttgttgtcac	tgtgtttctt	gtaacagggtg	ctgttgctta	tttaaagcca	780
gggtctgtag	caccttctat	tctagacttg	ctggtgtctg	tggtctatct	tgctgcacct	840
ccaaccttga	accctgttat	ctactgtctg	aagaacaagg	acattaaatc	cgctctgagt	900

aaagtcctgt ggaatgtag aagcagtggg gtaatgaaaa ga

942

<210> 610

<211> 921

<212> DNA

<213> Unknown (H38g459 nucleotide)

<220>

<223> Synthetic construct

<400> 610

atgaatcaca	gcgttgtaac	tgagttcatt	attctgggcc	tcaccaaaaa	gcctgaactc	60
cagggaatta	tcttcctctt	ttttctcatt	gtctatcttg	tggcttttct	cggaacatg	120
ctcatcatca	ttgccaaaat	ctataacaac	accttgcata	cgcccatgta	tgttttcctt	180
ctgacactgg	ctgttggtga	catcatctgc	acaacaagca	tcataccgaa	gatgctgggg	240
accatgctaa	catcagaaaa	taccatttca	tatgcaggct	gcatgtccca	gctcttcttg	300
ttcacatggt	ctctggggagc	tgagatgggt	ctcttcacca	ccatggccta	tgaccgctat	360
gtggccattt	gtttccctct	tcattacagt	actgttatga	accaccatat	gtgtgtagcc	420
ttgctcagca	tggtcatggc	tattgcagtc	accaattcct	gggtgcacac	agctcttatc	480
atgaggttga	ctttctgttg	gccaaacacc	attgaccact	tcttctgtga	gataacccca	540
ttgctggctt	tgctctgtag	ccctgtaaga	atcaatgagg	tgatgggtga	tgttgctgat	600
attaccctgg	ccatagggga	ctttattctt	acctgcatct	cctatgggtt	tatcattggt	660
gctattctcc	gtatccgcac	agtagaaggc	aagaggaagg	ccttctcaac	atgctcatct	720
catctcacag	tggtgaccct	ttactattct	cctgtaatct	acacctatat	ccgccctgct	780
tccagctata	catttgaaag	agacaaggtg	gtagctgcac	tctatactct	tgtgactccc	840
acattaaacc	cgatgggtga	cagcttccag	aatagggaga	tgcaggcagg	aattaggaag	900
gtgtttgcat	ttctgaaaca	c				921

<210> 611

<211> 810

<212> DNA

<213> Unknown (H38g460 nucleotide)

<220>

<223> Synthetic construct

<400> 611

atggaagtga	gtgggaacca	cacctctgtg	gccatgtttg	ttctcctagg	actctcagat	60
gaaaaagagc	tgagctcat	cctctttcca	gtcttcttg	tgatctacct	tgtgaccctg	120
atttggaaca	tggtcttat	catcctcatc	agaatagact	ctcatctgaa	cacacccatg	180
tacttttttc	tcagtttctt	ctcatttaca	gacatctgct	attcttctac	catcagccca	240
aggatgcttt	cagacttctt	aaaagataag	aagacaattt	ccttccttgc	ctgtgccact	300
cagtattttc	ttggggcctg	gatgagtctg	gctgagtgtc	gcctcttggt	catcatggcc	360
tgtgacagat	atgtggccat	tgagagcccc	ctgcagtact	cagcaatcat	ggtccctagt	420
atctgttggg	agatggtagc	tgaggtctgt	gggggtggat	tccttagtag	cttagttcat	480
acagtccctt	gctttaatct	ctactactgt	gggccaaata	tcattcaaca	tttcttctgt	540
aacacacttc	agattatttc	cttgtcttgc	tccaaccctt	ttatcagcca	aatgattctt	600
tttctggaag	ctatttttgt	tggttggtgg	tctttgcttg	ttatcctttt	gtcttatggg	660
ttcattgtag	cttcatact	gaaaatatca	tcaaccaa	gttggtgcaa	ggccttcaat	720
acctgtgcct	cccacctggc	agctgtggct	ctcttctatg	gcacagccct	ttctgtgtac	780
atgcatacta	gctctagcca	ctccatgaag				810

<210> 612

<211> 988

<212> DNA

<213> Unknown (H38g461 nucleotide)

<220>

<223> Synthetic construct

<400> 612

tactccaaag	aaattataga	ataatgtact	tccaatgata	ttataaaatg	tggttagcat	60
aataagatta	ctttttttac	tgtttatcct	tttagagttc	acagaagatt	tggtgttaca	120
gcaagtgtc	tttttcatct	ttctcatcat	ttatgtcatc	agcctctcag	gcaacatcat	180
tctgaattct	ctcatctgtg	ctgattcttg	gccctacaca	cccatgtatt	tcttctactg	240
aaaccgggtc	cttctggatc	tctgggtatc	ctctgtccac	atccccgata	tctgtctgac	300
ttgcatttct	gatgacaaaa	ccatctcctt	tctgtgctgc	cttgctcagt	tcttctctgc	360
tgtgttgccc	taaaatgagt	gctatatgat	ggcttccatg	gcttatgacc	gctacatggc	420
aatctccaa	cccctgcttt	attccccggc	cacattccca	gagttatgtg	ccagtcttgt	480
tgaggcttca	caccttggcg	gctttgtaaa	ctcaaccatc	atcaccagt	agacacctac	540
cttgagcttc	tgtggcagca	atatcattga	tgatttcttc	tgtgatctgc	ccccacttgt	600
aaagtgtgtg	tgtgatgtga	aggagcgcta	ccaggctgtg	ctgcatttta	tgcttgccctc	660
caatcatcac	tcccactgca	cttattcttg	cgctcatctc	ttcatcattg	cagccatctc	720
gaagatccgt	tccattaagg	gccgcctcca	ggtcttctcc	acttgtgggt	ctccccgtac	780
ggctctcacc	ttgtactatg	gtgcaatctt	ctttatttac	tcccaaccaa	gaactgcta	840
tgcttataaa	atggataaat	tggggtcagt	gttctatact	gtgggtgattc	caatgctaaa	900
ccccttgatc	tatagcttaa	gaaataagga	tgtcaaagat	gccttgaaga	aaatgttaga	960
tagacttcag	tttcttaaag	aaaaatat				988

<210> 613

<211> 1049

<212> DNA

<213> Unknown (H38g462 nucleotide)

<220>

<223> Synthetic construct

<400> 613

atggagcaga	gcaattatc	cgtgtatgcc	gactttatcc	ttctgggttt	gttcagcaac	60
gcccgtttcc	cctggcttct	ttgccctcat	tctcctggtc	tttgtgacct	ccatagccag	120
caacgtggtc	aagatcattc	tcattccacat	agactcccg	ctccacaccc	ccatgtactt	180
cctgtctcag	cagctctccc	tcaggagcat	cttgtatatt	tccaccattg	tgcccaaaat	240
gctggctgac	cagggtgatga	gccagagagc	catttccctt	gcaggatgca	ctgcccaca	300
cttctcttac	ttgaccttag	caggggctga	gttcttcttc	ctaggactca	tgctctgtga	360
tcgctacgta	gccatctgca	accctctgca	ctatctctgac	ctcatgagcc	gcaagatctg	420
ctgggttgatt	gtggcgccag	cctggctggg	agggtctatc	aatgggttct	tgctcacccc	480
cgctaccacg	cagttccctt	tctgtgcctc	tcgggagatc	aaccacttct	tctgcgaggt	540
gcctgccctt	ctgaagctct	cctgcacgga	cacatcagcc	tatgagacag	ccatgtatgt	600
ctgctgtatt	atgatgctcc	tcattccctt	ctctgtgac	tcgggctctt	acacaagaat	660
tctcattact	gtttatagga	tgagcgaggc	agaggggagg	cgaaggctg	tggtccacctg	720
ctctctcac	atgggtggtg	tcagcctctt	ctatggggct	gccatgtaca	catacgtgct	780
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acagaagggt	gttgggaggt	gtgtgtcttc	aggaaaggta	accactttct	aaacaaattg	960
catatgctgc	tagagacttg	aaatgaagga	tacaagactt	tatcattgcc	cttgagttta	1020
aatattctct	gcctggaaac	aagtgacct				1049

<210> 614

<211> 957

<212> DNA

<213> Unknown (H38g463 nucleotide)

<220>

<223> Synthetic construct

<400> 614

atgggtgttc	acaatttgtt	cacggtgact	cagtttatcc	ttatagggtc	ctcttacttc	60
tccaatgagc	actaccttct	ttttgtggcc	cttgccatta	tctgtcaggt	gttcttgggtg	120
cgaagtggag	acattctctt	ggccattggg	actgtgatta	agttgcacac	tactcatgta	180
ttattttttg	gcaaatgtgt	ccatcttaga	catattgtgt	tcattcagcta	ctatacctaa	240
gatgcctaag	attctctaga	ctgaggatca	cagcatttct	tttggttaggt	gagctttgca	300
gccctatttc	ctagtggcct	gggctgggaa	gaaagcttct	tcactgttac	ggcttatgac	360

tggtgtgtgg	tcacatgttt	ctccctttgt	tacatcctga	tcataaaca	attggctctg	420
tccagctggt	ttatgggacc	tgagcagctg	ggtttctaaa	tttctcctc	ctccacgtag	480
tgtctaccct	ctgctgtctt	ttctgcaagc	ctgatcgagt	taaccagtat	tactgtgata	540
tctcaccgat	gggggccctg	ttgtgccagt	ccatgcacct	ggcaaactg	cttgttttag	600
tggaatcagt	tatcttgggg	atcagtgttt	ttctggctgc	ctttaacttt	tacatatata	660
tcattctccac	tatcctaaag	atccagtgtg	tagagtggag	tgcaaagtgc	ttctctacat	720
gcacttccca	cctccttacg	gtctgtttgt	tctatggcat	attgacattt	acctacattt	780
actccttctc	cagtcaaac	tcacatgtct	aaggcaagcc	cagatctagc	cacagacagg	840
ctcatctcta	tgctatacag	agttattacc	ctgatgttta	acttcatcac	tgacaacctg	900
agaaacacag	aggtaaaagg	agcctcagaa	aggttttatg	tcattgaaca	tgtttat	957

<210> 615

<211> 840

<212> DNA

<213> Unknown (H38g464 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(840)

<223> n = A,T,C or G

<400> 615

atgtacctga	ccacgggtgct	ggggaacctg	ctcatcatgc	tgctcatcca	gctggactct	60
caccttcaca	cccccatgta	cttcttcctc	agccacttgg	ctctcactta	tttttccttt	120
tcattctgtca	ctgtccctaa	gatgctgatg	gacatgcgga	ctaagtacaa	atcgatcctc	180
tatgaggaat	gcatttctca	gatgtatttt	tttatatttt	ttactgacct	ggacagcttc	240
cttattacat	caatggcata	tgaccgatat	gttgccatat	gtcaccctct	ccactacact	300
gtcatcatga	gggaagagct	ctgtgtcttc	ttagtggctg	tatcttggat	tctgtcttgt	360
gccagctccc	tctctcacac	ccttctcctg	accgggctgt	ctttctgtgc	tgccaacacc	420
atcccccatg	tcttctgtga	ccttctgtgc	ctgtcgaagc	tgctcctgtc	agatatcttc	480
ctcaatgagc	tggtcatgtt	cacagtaggg	gtgggtggca	ttaccctgcc	attcatgtgt	540
atcctgggtat	catatggcta	cattggggcc	accatcctga	gggtcccttc	aaccaaaggg	600
atccacaaag	catgtgtccac	atgtggctcc	catctctctg	tggtgtctct	ctattatggg	660
tcaatatttg	gccagtacct	tttcccgact	gtaagcagtt	ctattgacaa	ggatgtcatt	720
gtggctctca	tgtacacggg	ggtcacaccc	atgttgaacc	cctttatcta	cngcattngg	780
aacagggaca	tgaaagaggc	ccttgggaaa	ctcttcagta	gagcaacatt	tttctcttgg	840

<210> 616

<211> 909

<212> DNA

<213> Unknown (H38g465 nucleotide)

<220>

<223> Synthetic construct

<400> 616

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cagggctttg	ttctgatggg	catatcagac	catccccagc	tggagatgat	cttttttata	120
gccatcctct	tctctatttt	gtgacccta	cttgggaact	caaccatcat	cttgettcc	180
cgcttgagg	ccgggtcca	tacaccatg	tacttcttcc	tcagcaacct	ctcctccttg	240
gaccttgctt	tcgctactag	ttcagtcccc	caaatgctga	tcaatttatg	gggaccaggc	300
aagaccatca	gctatgggtg	ctgcataacc	cagctctatg	tcttctcttg	gctgggggcc	360
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ctccgctaca	ccgccatcat	gaacccccag	ctctgctggc	tgctggctgt	gattgcctgc	480
ctgggtggct	tgggcaactc	tgtgatccag	tcaacattca	ctctgcagct	cccattgtgt	540
gggcaccgga	gggtggaggg	attcctctgc	gaggtgcctg	ccatgatcaa	actggcctgt	600
ggcgacacaa	gtctcaacca	ggctgtgctc	aatgggtgct	gcaccttctt	cactgcagtc	660
ccactaagca	tcactgtgat	ctcctactgc	ctcattgtgc	aggcagtgct	gaaaatccgc	720
tctgcagagg	ggaggcgaaa	ggcgttcaat	acgtgcctct	cccattctgt	ggtgggtgtc	780

ctcttctatg	gctcagccag	ctatgggtat	ctgcttccgg	ccaagaacag	caaacaggac	840
cagggcaagt	tcatttccct	gttctactcg	ttgggtcacac	ccatgggtgaa	tcccctcatc	900
tacacgctg						909

<210> 617

<211> 926

<212> DNA

<213> Unknown (H38g466 nucleotide)

<220>

<223> Synthetic construct

<400> 617

atgcagagga	gcaatcacac	agtgactgag	ttcatcctgc	tgggcttcac	cacagatcca	60
gggatgcaac	tgggcctctt	tgtgggtgtc	ctgggtgtgt	actgtctgac	tgtggtagga	120
agtagcacc	tcacgtgtt	gatctgtaat	gactcccacc	tacacacacc	catgtatttt	180
gtcattggaa	atctgtcatt	tctggatctc	tgggtattctt	ctgtctacac	cccaaagatc	240
ctagtgcct	gcatctctga	agacaaaagc	atctcctttg	ctggctgcct	gtgtcagttc	300
ttctctgcca	ggctggccta	tagtgagtgc	tacctactgg	ctgccatggc	ttatgaccac	360
tacgtggcca	tctccaagcc	cctgctttat	gctcagacca	tgccaaggag	attgtgcatc	420
tgtttgggtt	tatattccta	tactgggggt	tttgtcaatg	caataatatt	aaccagcaac	480
acattcacat	tggatttttg	tggtgacaat	gtcattgatg	actttttctg	tgatgtccca	540
cccctcgtga	agctggcatg	cagtgtgaga	gctaccaggc	tgtgctgcac	ttccttctgg	600
cctccaatgt	catctcccct	actgtgtctc	tccttgccctc	ttacctctcc	atcatcacca	660
ccatcctgag	gatccactct	acccagggcc	gcatcaaagt	cttctccaca	tgctcctccc	720
acctgatctc	cgttacctta	tactatggct	ccattctcta	caactactcc	cggccaagtt	780
cagctactc	cctcaagagg	gacaaaatgg	tttctacctt	ttatactatg	ctgttcccca	840
tgttgaatcc	catgatctac	agtctgagga	ataaagacat	gaaagacgct	ctgaaaaaat	900
tcttcaagtc	agcataatcc	aaagtc				926

<210> 618

<211> 936

<212> DNA

<213> Unknown (H38g467 nucleotide)

<220>

<223> Synthetic construct

<400> 618

atggacgggg	tgaatgatag	ctccttgcag	ggctttgttc	tgatgagcat	atcggaccat	60
ccccagctgg	agatgatctt	ttttatagcc	atcctcttct	cctatttgct	gaccctactt	120
gggaactcaa	ccatcatctt	gctttcccgc	ctggaggccc	ggctccatac	acccatgtac	180
ttcttctca	gcaacctctc	ctccttggac	cttgctttcg	ctactagttc	agtcqcccaa	240
atgetgatca	atztatgggg	accaggcaag	accatcagct	atgggtggctg	cataaccagg	300
ctctatgtct	tcctttggct	ggggggccacc	gagtgcaccc	tgctgggtgg	gatggcattt	360
gaccgctacg	tggcagtgtg	ccggcccctc	cgctacaccg	ccatcatgaa	ccccagctc	420
tgctggctgc	tggctgtgat	tgcttggctg	gggtggcttg	gcaactctgt	gatccagtca	480
acattcactc	tgacgtctcc	attgtgtggg	caccggaggg	tggagggtatt	cctctgcgag	540
gtgcctgcca	tgatcaaact	ggcctgtggc	gacacgagtc	tcaaccaggc	tgtgtcfaat	600
gggtgtctgca	ccttcttcac	tgacgtccca	ctaagcatca	tcgtgatctc	ctactgcctc	660
attgctcagg	cagtgtctgaa	aatccactct	gcagagggga	ggcgaaaggc	gttcaatacg	720
tgctctctccc	atctgctggg	gggtgttctc	ttctatggct	cagccagcta	tgggtatctg	780
cttcgggcca	agaacagcaa	acaggaccag	ggcaagttca	tttccctgtt	ctactcgttg	840
gtcacacca	tgggtgaatcc	cctcatctac	acgtgcgga	acatggaagt	gaagggcgca	900
ctgaggaggt	tgctgggggaa	aggaagagaa	gttggc			936

<210> 619

<211> 247

<212> DNA

<213> Unknown (H38g468 nucleotide)

<220>

<223> Synthetic construct

<400> 619

ggtgagaggc	ttaagacact	caacacatgt	gtgtcacata	tctatgcagt	gctgatcttc	60
tatgtgccta	tggttagtgt	gtccatggtt	catcgatttg	ggaggcatgc	tcctgaatat	120
gtgcacaagt	tcatgtctct	ttgtacctcc	aatgctctac	ccaattatct	attccatcaa	180
gactaaggag	attcgcagga	gactacacaa	gatgttattg	ggagctaagt	tctgatcaag	240
gaaaact						247

<210> 620

<211> 936

<212> DNA

<213> Unknown (H38g469 nucleotide)

<220>

<223> Synthetic construct

<400> 620

atggaagtgg	gaaattgcac	catcctgact	gaattcatct	tgttgggttt	ctcagcagat	60
tcccagtggc	agccgattct	atttggagtg	tttctgatgc	tctatttgat	aaccttgtca	120
ggaaacatga	ccttggttat	cttaatccga	actgattccc	acttgcatac	acctatgtac	180
tttttcattg	gcaatctgtc	ttttttggat	ttctggtata	cctctgtgta	tacccccaaa	240
atcctggcca	gttgtgtctc	agaagataag	cgcatttccct	tggctggatg	tggggctcag	300
ctgttttttt	cctgtgttgt	agcctacact	gaatgctatc	tcctggcagc	catggcatat	360
gaccgccatg	cagcaatttg	taaccatttg	ctttattcag	gtaccatgtc	caccgccctc	420
tgtactgggc	ttgttgctgg	ctcctacata	ggaggatttt	tgaatgccat	agcccatact	480
gccaatatcat	tccgcctgca	tttttgtggt	aaaaatatca	ttgaccactt	tttctgtgat	540
gcaccaccat	tggtaaaaaat	gtcctgtaca	aacaccaggg	tctacgaaaa	agtctgtctt	600
ggtgtggtgg	gcttcacagt	actctccagc	attcttgcta	tcctgatttc	ctatgtcaac	660
atcctcctgg	ctatcctgag	aatccactca	gcttcaggaa	gacacaaggc	attctccacc	720
tgtgcttccc	acctcatctc	agtcattgtc	ttctatggat	cattgttggt	tatgtattca	780
aggcctagtt	ccacctactc	cctagagagg	gacaaaagtag	ctgctctggt	ctacaccgtg	840
atcaaccac	tgtctaaccc	tctcatctat	agcctgagaa	acaaagatat	caaagaggcc	900
ttcaggaaag	caacacagac	tatacaacca	caaaca			936

<210> 621

<211> 954

<212> DNA

<213> Unknown (H38g470 nucleotide)

<220>

<223> Synthetic construct

<400> 621

atgcctactg	taaaccacag	tggcactagc	cacacagtct	tccacttgct	gggcatccct	60
ggcctacagg	accagcacat	gtggatttct	atcccattct	tcatttecta	tgtcaccgcc	120
cttcttggga	acagcctgct	catcttcatt	atcctcacia	agcgagcct	ccatgaacct	180
atgtacctct	tcctctgcat	gctggtgga	gcagacattg	tcctctccac	gtgcaccatt	240
cctcaggcct	tagctatctt	ctggttccgt	gctggggaca	tctccctgga	tcgttgcatc	300
actcagctct	tcttcatcca	ttccaccttc	atctctgagt	cagggatctt	gctgggtgatg	360
gcctttgacc	actatattgc	catatgctac	ccactgaggt	acaccaccat	tcttacaagt	420
gctctgatca	agaaaatttg	tgtgactgtc	tctctgagaa	gttatggtag	aattttccct	480
atcatatttc	ttttaaaaag	attgactttc	tgccagaata	atattatccc	acacaccttt	540
tgtgaacaca	ttggcctagc	caaatatgca	tgtaattgaca	ttcgaataaa	catttggtat	600
gggttttcca	ttctaattgc	gacggtgggt	ttagatgttg	tactaatttt	tatttccctat	660
atgctgattc	tccatgctgt	cttccacatg	ccttctccag	atgcttgcca	caaagctctc	720
aacacatttg	gctcccatgt	ctgcatcatc	atcctctttt	atgggtctgg	catcttcaca	780
atccttacct	agagggttgg	acgccacatt	ccaccttgta	tccacatccc	gttgggcta	840
gtctgcattc	tggctccacc	tatgctgaat	cccattattt	atgggatcaa	aaccaagcaa	900
atccaggaa	aggtgggtca	gtttttgttt	ataaaacaga	aaataacttt	ggtt	954

<210> 622
 <211> 942
 <212> DNA
 <213> Unknown (H38g471 nucleotide)

<220>
 <223> Synthetic construct

<400> 622
 atggaggctg ccaatgagtc ttcagagggg atctcattcg ttttattggg actgacaaca 60
 agtcctggac agcagcggcc tctctttgtg ctgttcttgc tcttgatgt ggccagcctc 120
 ctgggtaaat gactcattgt ggctgccatc caggccagtc cagcccttca tgcacccatg 180
 tacttcctgc tggcccacct gtcccttctgt gacctctgtt tcgcctccgt cactgtgccc 240
 aagatgttgg ccaacttgtt ggcccatgac cactccatct cgctggctgg ctgcctgacc 300
 caaatgtact tcttctttgc cctgggggta actgatagct gtcttctggc ggccatggcc 360
 tatgactgtc acgtggccat ccggcacccc ctcccctatg ccacgaggat gtcccgggcc 420
 atgtgcgcag ccctgggtggg aatggcatgg ctgggtgtccc acgtccactc cctcctgtat 480
 atcctgtctc tggctcgctt gtcccttctgt gcttcccacc aagtgcceca cttcttctgt 540
 gaccaccagc ctctcttaag gctctcgtgc tctgacaccc accacatcca gctgctcatc 600
 ttcaccgagg gcgcgcagct ggtggtcact cccttccctgc tcatcctcgc ctccatggg 660
 gccatcgcat ctgccgtgct ccagctgccc tcagcctctg ggaggctccg ggctgtgtcc 720
 acctgtggct cccacctggc tgtggtgagc ctcttctatg ggacagtcac tgcagtctac 780
 ttccaggcca catcccagc cgaggcagag tggggccgtg tggccactgt catgtacact 840
 gtagtcaccc ccatgctgaa ccccatcatc tacagcctct ggaatcgca tgtacagggg 900
 gcaactccag cccttctcat tgggcgaagg atctcagcta gt 942

<210> 623
 <211> 946
 <212> DNA
 <213> Unknown (H38g472 nucleotide)

<220>
 <223> Synthetic construct

<400> 623
 atctctatgt tctcctgcaa caccagcact tctgggtcagt ctaccttcct cctcactggg 60
 ttccaggcc tggaaagcctc tcatcattgg gtttccatcc ccatcaacct cttctgtgtg 120
 gtttccatcc tgggtaataa tatcactctc ttctgatcc acacagatcc agccttacat 180
 gaacccatgt atatcttcct gtccatgttg gcagcctctg atctgggcct ctgtgcctct 240
 accttcccca ctatggtgcy tctcttctgy ctgggagctc gtgagctgcc ctttgatctc 300
 tgtgcagcac agatgttctt catccatacc ttcacctatg tggagtccgg tgtactgctg 360
 gccatggcct tcgatcgctt tattgccatc cgggaccctc tgcattatgc cataatcatt 420
 acctgctcag tcacagccga ggtgggaact gccattctgg tgagggtgt tctgctcaac 480
 ctcccgggac ctatcctcct gcagcagctg ctctttccca agatcagcgc tctctgtcac 540
 tgctactgcc tgcactgtga ccttgtgggg ttggcctgct cagacacca gatcaatagc 600
 ctgggtggcc tggtttccat cctcttctca ctgtgccttg actccttcct catcatgctt 660
 tcatatgccc tgatcctatg aactgtgctg ggcattgcat cacctgggga gcggctcaag 720
 gcaactcaaca cgtgtgtctc acacctctgc attgttctca tcttttattt gcccacacgg 780
 gctgtctgtc ttgcaccgag taaagaagca tgactaccct gctctggcag tgctcatggc 840
 caacctacac ttcttggctc caccctcat gaacccatt gtgtattgca tcaagtctag 900
 gcagatccgt cagagcctcc taaagcatt ccagcagaag aggatt 946

<210> 624
 <211> 960
 <212> DNA
 <213> Unknown (H38g473 nucleotide)

<220>
 <223> Synthetic construct

<400> 624

cacacagagc	catggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagcccg	cctcgctggg	ttgtcccgg	ccatgtatct	ggatcatggtg	120
ctgaggaacc	tgtcatcat	cctggctgtc	agctctgact	cccacctcca	cacccccatg	180
tactttcttc	tctccaacct	gtgctgggct	gacatcggtt	tcacctcggc	catggttccc	240
aagatgattg	tggacatgca	gtctcatagc	agagtcattc	cttatgctgg	ctgcctgaca	300
cggatgtctt	tcttggctct	ttttgcatgt	atagaagaca	tgctcctgac	tgcgatggcc	360
tatgactgct	ttgtagccat	ctgtcgccct	ctgcactacc	cagtcatect	gaatcctcac	420
ctctctgtct	tcttagtttt	ggtgtccttt	ttccttagcc	tggtggattc	ccagctgcac	480
agttagattg	tgttacaatt	caccttcttc	aagaatgtgg	aaatctctaa	ttttgtctgt	540
gagccatctc	agcttctcaa	ccttgccctg	tctgacagcg	tcatacaatg	catattctta	600
tatttcgata	gtactatggt	tggttttctt	cccatttcaa	ggatcctttt	gtcttactat	660
aaaattgtcc	cctctattct	aaggatttca	tcgtcagatg	ggaagtataa	agccttctcc	720
acctgtggct	ctcacctggc	agttgtttgc	ttattttatg	gaacaggcat	tggcgtgtac	780
ctgacttcag	ctgtgtcacc	acccccagg	agtgggtgtg	tggcgtcagt	gatgtacgct	840
gtggtcaccc	ccatgctgaa	ccctttcatc	tatagcctga	gaaacagaga	cattcaaagc	900
gccctctgga	ggctgctgag	cagaacagtc	gaatctcatg	atctgttcca	tcctttttct	960

<210> 625

<211> 985

<212> DNA

<213> Unknown (H38g474 nucleotide)

<220>

<223> Synthetic construct

<400> 625

atgaaactca	taaaccatac	catcagaacc	caacctcctt	tctgctcatg	ggaattccag	60
gcccggaggc	atcccacttt	tggattgctt	ttcccttctg	ctccatgtat	gccctggcag	120
tgtctggaaa	catggtggtg	ctgctagtgg	tacattcaga	gcctgtattg	caccagccca	180
tgtacctgtt	cctctgcatg	ctatccacca	ttgacctggg	cctctgcacc	tcactgtgc	240
ccaagctcct	tgcacttttt	tgggcaaagg	atgctgagat	caactttggg	gcctgtgctg	300
cccagatggt	ctttatccat	ggcttctcag	ctgtagaatc	tgggtatactg	ctagcaatgg	360
cctttgaccg	ctacttagcc	atttgctggc	ctctgacta	tgggtcattg	ctctccccag	420
agtctgtagg	caagctgggg	gctgcagcgt	gcttcgtgg	tggggactca	tgacccact	480
cacctgctta	ctggcaagac	tgagctactg	cagtcgagtg	gtggccact	cctactgtga	540
acacatggct	gtggtaaagc	tggcttgtgg	aggaacacag	ccaaacaaca	tctatggcat	600
cactgctgcc	acactggtgg	tgggcactga	ctccatctgt	attgctgtct	cctatgcact	660
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ttgtggctcc	cacctgggtg	tcatacttct	cttctacaca	ccaggactct	tctccttcta	780
cacacagcgg	tttggccagc	acgtgccccg	gcacatccac	atccttctag	ctgacctcta	840
cctggtttgc	ccacccatgc	tcaaccccat	catctatggc	atgaagacca	qacagatctg	900
ggatggggcc	ctccggcttc	tgaagtgggg	ccctgctcag	tcataaagtc	ttcaacccca	960
ccctgaaacc	tttatcttct	ttgcc				985

<210> 626

<211> 989

<212> DNA

<213> Unknown (H38g475 nucleotide)

<220>

<223> Synthetic construct

<400> 626

cacacagagc	cacggcatct	cacaggtgtg	tgagaattcc	tcctcgtggg	actctcagag	60
gatccagaac	tgcagcctgt	cctcggtggg	gtgtccctgt	ccatgtatgg	ggtcacagtg	120
ataaggaacg	tgtcatcat	cctgggtgtg	agctctgact	cccacctcca	cacccccatg	180
tttttttctc	ctccaacgtg	tgggtgggctg	acatcagttt	cacgtcggcc	ggggttccca	240
agatgacggg	ggacatgcag	tcgcatagca	gagtcattcta	ttatgctggc	tgcatgactc	300
ggatgtcttt	tttcgtcctt	ttagcatgta	tagaagacat	gctcgtgtgt	gtgatggcat	360
aggagtgcct	tgtagccatg	tgtcgccctg	tgcaatacac	agttattgta	aatcctcacc	420

tgtgtgtttt	cagagtggg	gtgtcctttc	tccagagcgt	gttgatttcc	caggtgcaca	480
gatagagtgt	gtcacaaattc	acttttttca	agaatgtgga	aatctctcat	tttgtgtgtg	540
agccatctca	atttctccac	tttgctgtgt	gtgacagttt	catcaagagc	atattcatgt	600
atttcgatag	taatatgttt	ggttttcttc	ccatcacagg	gatctttttg	tcttaataata	660
aaagtgtccc	ctccattata	aggatttcat	cgtcagatgg	aaagtataaa	gctttctcca	720
cgtgtggctc	tcacgtggca	gttgttttgc	tattatatgg	aacaggcatt	ggggtgtaca	780
tgacttcagg	tgtggcacca	ccccccagca	atgggtgtgt	ggcatcagtg	aagtacgcgg	840
tggtcacccc	catgctgacc	cctttcatct	acagcgtgag	aaacagggac	attcaaagcc	900
ccctgtggag	tgtgtgcagc	agcacagtta	aatcttttga	tgtgtcccat	cttttttgtg	960
tgtgggtaag	aaagggcacc	cacattaaa				989

<210> 627

<211> 512

<212> DNA

<213> Unknown (H38g476 nucleotide)

<220>

<223> Synthetic construct

<400> 627

cacacacagc	cacggggctc	cacacgtgtg	tgagaattcc	tcctcctggg	actctcacag	60
gattccacaac	tgacgtgtg	ctctctgggc	tgccctgtg	catgtgtctg	ggcacacagc	120
tggggaacct	gctgcatcat	cctgggtgtg	agctctgact	cccacctcca	cacccccatg	180
tactcttttc	tctccaacct	gtgctggggc	tgacatcagt	ttcacctcca	ccacggggcc	240
caagttgatt	gtggacatcc	actcttacac	cagagacatc	tcctatgcac	gctgtctgac	300
tcacacacct	ctctttgcca	tttttgagg	cgtgggaaag	agacatgctc	ctgagagtga	360
tgggctatga	ccgcgttgta	gacatctgtg	accctctata	tcattcacac	gccatgaacc	420
cctgtgtctg	tggtctctca	gatttgtggt	ctcttttttt	tctcacactt	ttatacaccc	480
acctgcacaa	ctcgattgcc	ttacacatga	cc			512

<210> 628

<211> 967

<212> DNA

<213> Unknown (H38g477 nucleotide)

<220>

<223> Synthetic construct

<400> 628

atgaatgaga	caaatcattc	ttgggtgaca	gaatttgtgt	tgtctgggact	gtctagtcca	60
agggagctcc	aacctttctt	gtttcttata	ttttcactac	tttatctagc	aattctgttg	120
ggcaactttc	tcatcatcct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	ccaacctgtc	atttatagac	gtatgtgttg	cctcttctgc	taccctaaa	240
atgattgcag	actttctggt	tgagcacaag	actatttctt	ttgatgccc	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatgggtc	tcctagtttc	catggcctat	360
gaccgttatg	ttgctatatg	caaacctccc	cactacatga	caatcatgag	ctgctgtgta	420
tgtgttgtgc	tcttccctcat	ttcctgggtt	gtgggcttca	tccataccac	cagccagttg	480
gcattcactg	ttaatctgcc	attttgtggt	cctaataagg	tagatagttt	ttttctgtga	540
ccttccctcta	tgaccaagt	tagcctgcat	agacacttat	gttgtcagcc	tactaatagt	600
tgagatagtg	ggctttcttt	ctctgagttc	ctttctcttc	ttggttgtct	cctacactgt	660
aatacttggt	acagtttagga	atagctcttc	tgtaagcatg	gtgaaggcct	gctccacatt	720
gactgtctcac	atcactgtgg	tcactttatt	ctttggaccg	tgtattttca	tctatgtgtg	780
gcccttcagc	agttactcag	ttgacaaaagt	ccttgctgta	ttctacacca	tcttcacgtc	840
tatttttaaac	cctgtaatct	acatgctaag	aaacaaagaa	gtgaaggcag	ctatgtcaaa	900
actgaagagt	cggtatcaga	agcttggtca	ggtttctgta	gtcataagaa	acgttctttt	960
cctagaa						967

<210> 629

<211> 942

<212> DNA

<213> Unknown (H38g478 nucleotide)

<220>

<223> Synthetic construct

<400> 629

atggaggggt	ttaactattc	cagagtatct	gaattcatgt	tacttggact	tactgattct	60
cctgaactcc	agatattcct	ttttgtggtg	ttttctgtct	tctatttaat	gaccatgttg	120
ggcaactgcc	tgattttact	cactgtccta	tccacctcac	accttcactc	tcgcacgtac	180
ttcctgtctc	gcaacctgtc	tcattgacat	gtgcctgtcc	tcctttgcc	caccaaagat	240
gattatggac	ttttttgtct	tgcgtaagac	catctctttt	gaaggctgca	tttctcagat	300
ctttttttta	cacctcttca	atgggactga	gattgtgctg	ctgatctcca	tgtcttttga	360
caggatattt	gccatatgta	aacctctccg	ctattcaaca	attatgagcc	aaagagtgtg	420
tgttgagctt	gtggcagttt	cttgttggac	agtgggcttt	ctacatacaa	tgagccaatt	480
agtttttccc	tctatttgcc	cttctgtgtt	cccaatgttg	tagacagttt	tttctgtgat	540
cttcccttgg	tcattccagt	agcttgtata	gatatttatg	ttcttgggac	ctccatgatt	600
tcaaccagtg	gtgtgactgc	tcttacaagt	tttctgcttt	tgctcacctc	ctacatcatt	660
gttcttaata	ctatcagggg	ctactcctcc	acaggatcct	ccaaggctct	ttctacctgt	720
acagcacatt	ttattgttgt	gttaatgttc	tttgggccct	gtattttcat	ttatgtgtgg	780
ccttccacaa	acttccctgt	agacaaaatt	ctctctgttt	tctataccat	cttcactccc	840
ttcttgaatc	cacttatcta	tactttgaga	aaccagggaag	tgaagacagc	aatgaagaag	900
aaactgaata	ttcagtattt	cagtcttggg	aaaactgtct	cg		942

<210> 630

<211> 595

<212> DNA

<213> Unknown (H38g479 nucleotide)

<220>

<223> Synthetic construct

<400> 630

atgaaccctg	gtttgtgtgg	ctttagagtt	gtgggtgtctt	ttttttttca	cagtctttta	60
ggcgacacag	tgacaaactt	gagcgctcta	caaatacagt	gtttcgagta	tgtggaaatt	120
cataatttct	tgtgtgccct	ttctcaactc	ccccatcgtg	catgggtgtga	cactttcccc	180
aataacataa	tcgtgtatct	tctgtctgcc	atatttggtt	ttcttcccat	cgcggggacc	240
ccttttctct	taatatgaaa	gtgtttcctc	cattgagagg	gtttcatcat	aagggtggaga	300
gtataaggct	ttccccacgt	gtgggtctca	cctctcagtc	gtttgctgat	tatatggcac	360
aggcggttga	gggcacctca	gttcagatgt	gtcatcttcc	ccgagaaagt	ctgcggtggc	420
ctcagtgatg	tacactgtgg	tcacccccat	gctgaaccct	ttcatctaca	gcatgagaaa	480
cagggatact	aaaagtgtcc	tgcgggcgcc	gcacggcagc	acgggtgta	tttgatatct	540
tcttatctgt	ccatttcctt	ttgtagtgtg	ggttaaaaaa	ggcagaaagg	tcaaa	595

<210> 631

<211> 942

<212> DNA

<213> Unknown (H38g480 nucleotide)

<220>

<223> Synthetic construct

<400> 631

atgctgggtc	tcaatggcac	ccccttccag	ccagcaacac	tccagctgac	aggcattcct	60
gggatacaaa	caggcctcac	ctgggttgcc	ctgattttct	gcatcctcta	catgatctcc	120
attgtaggta	acctcagcat	tctcactctg	gtgttttggg	agcctgctct	gcatcagccc	180
atgtactact	tctctctat	gtctgctctc	aatgatctgg	gagtgtcctt	ttctacactt	240
cccactgtga	tttctacttt	ctgcttcaac	tacaaccatg	ttgcgtttaa	tgcttgcttg	300
gtccagatgt	tcttcatcca	cactttctcc	ttcatggagt	caggcatact	gctggccatg	360
agcttggatc	gctttgtggc	tatttgttat	ccattacgct	atgtcactgt	gctcactcac	420
aaecgtatat	tggtatggg	tctgggcac	cttaccaga	gtttcaccac	tctcttccct	480
ttcccttttg	tggtgaaacg	actgcccttc	tgcaaaggca	atgttttgca	tcactcctac	540
tgtctccatc	cagatctcat	gaaagtagca	tgtggagaca	tccatgttaa	caacatttat	600

gggctcttgg	tgatcatttt	tacctatggt	atggactcaa	ctttcatcct	gctttcctac	660
gcattgatcc	tgagagccat	gctggtcac	atatcccagg	aacagcggct	caaggcactc	720
aacacctgca	tgacacacat	ctgtgcagt	ctggcctttt	atgtgccc	aattgctgtc	780
tccatgattc	accgcttctg	gaaaagtgt	ccacctgttg	ttcatgtcat	gatgtccaat	840
gtctacctgt	ttgtaccacc	catgtctaac	cctatcatct	acagtgtgaa	aaccaaggag	900
atccgcaaa	ggattctcaa	gttcttccat	aaatcccagg	cc		942

<210> 632

<211> 936

<212> DNA

<213> Unknown (H38g481 nucleotide)

<220>

<223> Synthetic construct

<400> 632

atggggttgt	tcaatgtcac	tcaccctgca	ttcttctctc	tgactggtat	ccctgggtctg	60
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ggaaatacag	tgatcctgca	ggctgtgcga	gtggagccca	gcctccatga	gcccattgtac	180
tacttctgt	ccatgttgtc	cttcagtgt	gtggccatat	ccatggccac	actgcccact	240
gtactccgaa	cttctgcct	caatgccgc	aacatcactt	ttgatgcctg	tctaattcag	300
atgtttctta	ttcacttctt	ctccatgatg	gaatcaggta	ttctgctggc	catgagtttt	360
gaccgctatg	tggccatttg	tgacccttg	cgctatgcaa	ctgtgctcac	cactgaagtc	420
attgctgcaa	tgggtttagg	tgcagctgt	cgaagcttca	tcaccctttt	ccctcttccc	480
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caccagaca	tgatgaggct	tgccctgtgt	gatatcagta	tcaacagcat	ctatggactc	600
tttgtctctg	tatccacctt	tggcatggac	ctgtttttta	tcttctctc	ctatgtgctc	660
attctgcgtt	ctgtcatggc	cactgcttcc	cgtgaggaa	gcctcaaagc	tctcaacaca	720
tgtgtgtcac	atatactggc	tgtacttgca	ttttatgtgc	caatgattgg	ggtctccaca	780
gtgcaccgct	ttgggaagca	tgtcccatgc	tacatacatg	tcctcatgtc	aaatgtgtac	840
ctatttgtgc	ctcctgtgt	caaccctctc	atttatagcg	ccaagacaaa	ggaaatccgc	900
cgagccattt	tccgcatggt	tcaccacatc	aaaata			936

<210> 633

<211> 467

<212> DNA

<213> Unknown (H38g482 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(467)

<223> n = A,T,C or G

<400> 633

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aatgggatta	tcctggggct	catctacttg	gactctagac	tgacacacc	catgtatgtc	180
ttcctgtcac	acctggccat	tgtggacatg	tcctatgcct	cgagtactgt	ccctaagatg	240
ctagcaaatc	ttgtgatgca	caaaaaagtc	atctcctttg	ctccttgcat	acttcagact	300
tttttgtatt	tggcgtttgc	tattacagag	tgtctgattt	tgggtgatgat	gtgctatgat	360
cggatgtgtg	caatctgtca	cccccttgca	atacaccnt	cattatgaac	tggagagtgt	420
gcactgtcct	ggcctcaact	tgtctggatat	ttagctttct	cttggt		467

<210> 634

<211> 988

<212> DNA

<213> Unknown (H38g483 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(988)

<223> n = A,T,C or G

<400> 634

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gaatgggggc atctttggga ttatctgcct ggactctaag cttcacacac ccatgtactt	180
cttcctctca caccctggcca tcattgacat gtcctatgct tccaacaatg ttcccaagat	240
gttggcaaac ctaatgaacc agaaaagaac catctccttt gttccatgca taatgcagac	300
ttttttgtat ttggcttttg ctgttacaga gtgcctgatt ttggtggtga tgcctatga	360
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cacgacctg gttctcacgt cctggctcatg tgggtttgcc ctgtccctgg tacatgaaat	480
tctccttcta aggttgccct tctgtgggcc cgggatgtg aaccacctct tctgtgaaat	540
tctatctgtc ctcaagctgg cctgtgctga cacctgggtt aaccaagtgg tcatatttgc	600
tacctgtgtg tttgtcttag tcgggcctct ttccttgatt ctggtctcct acatgcacat	660
cctcggggcc atcctgaaga tccagacaaa ggagggccgc ataaaggcct tctccacctg	720
ctcctccac ctgtgtgtgg ttggactatt ctttggcata gccatggtgg ttacatggt	780
cccagactct aatcaacgag aggagcagga gaaaatgctg tccctgtttc acagtgtctt	840
gaacccaatg ctgaaccccc tgatctacag cctgaggaat gctcagttga agggcgccct	900
ccacagagca ctccagagga agaggtccat gagaacggtg tatgggcttt gcctttaaaa	960
catgtggttt gctgaagcaa gaattttg	988

<210> 635

<211> 941

<212> DNA

<213> Unknown (H38g484 nucleotide)

<220>

<223> Synthetic construct

<400> 635

atgggagtca accaatcatg gtcaccagaa ttcatcctgg tggaaatcca gctcagtgcc	60
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aatggcatga tcttgggact catctgtctg gaccacattc tgcctacccc catgtacttc	180
ttcctctcac acctggccat cattgacatg tcctatgctt ccaacaatgt tcccaagatg	240
ttggcaaatc tgatgaacaa gaaaagaacc atctcctttc ttccatgcat aatgcagacc	300
tatttgtatt tctcttttgc tgctacagag tgtctgattt tgggtggtgat gtcctatgat	360
aggatgtgg ccatttgcca cctctccag tacactgtca tcatgagctg gagagtgtgc	420
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cttcttctaa ggttgccgtt ctgcccggcc cgggatgtga accacctctt ctgtgaaatt	540
ctgtctgtcc tcaagctggc ctgttctgac acctgggggtt aaccacagtg gtcataattg	600
ctacctgtgt gtttgtctta gttggacctc tttgtttgat gcttgtctcc tacatgcaca	660
tcctctggcc atcctaaaga tccagacaaa ggaagccgca taaaggcctt ctgcacctgc	720
tcctccacc tgtgtgtggt tggactcttc ttgtggcata gccactggtg gtttacatag	780
tcccagactc taatcaacga gaggagcagg agaaaatgct gtccctgttt cacagtgtct	840
tgaacccaat tctgaacccc ctgatctaca gtctgaggaa tgctcaggtg aaggcgcccc	900
tccacagagc actgcagagg acgctgtcta tgtaaggagt g	941

<210> 636

<211> 1002

<212> DNA

<213> Unknown (H38g485 nucleotide)

<220>

<223> Synthetic construct

<400> 636

atgtgttatc tttctcagct atgcctcagc cttgggggaac acactttaca tatgggggatg	60
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gtgagacata ccaatgagag caacctagca ggtttcatcc ttttaggggtt ttctgattat 120
cctcagttac agaaggttct atttgtgctc atattgattc tgtattttact aactattttg 180
gggaataacca ccatcattct ggtttctcgt ctggaaccca agcttcatat gccgatgtat 240
ttcttctctt ctcatctctc ctctctgtac cgctgcttca ccagcagtggt tattccccag 300
ctcctggtaa acctgtggga acccatgaaa actatcgctt atgggtggctg ttgggttcac 360
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gaccgctatg tggctgtctg ccgtctctc cattacactg tcttaatgca tatccatctc 480
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gtaacccgca tgcttaaccc tcttatttat accttgagga tcaaggaggt gaaaggggca 960
ttaaagaaag ttctagcaaa ggctctggga gtaaatattt ta 1002

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<210> 637

<211> 510

<212> DNA

<213> Unknown (H38g486 nucleotide)

<220>

<223> Synthetic construct

<400> 637

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aatgggggtca tctttgggat tatctgctg gactgtaagc ttcacacacc catgtacttc 180
ttcctctcac acctggccat tgttgacata tctatgctt ccaactatgt cccaagatg 240
ctgacgaatc ttatgaacca ggaaagcacc atctcctttt ttccatgcat aatgcagaca 300
ttcttgtatt tggcttttgc tcacgtagag tgtctgattt tgggtgggtgat gtcctatgat 360
cgctatgcgg acatctgcca ccccttacgt tacaatatcc tcatgagctg gagagtgtgc 420
actgtcctgg ctgtggcttc ctgggtgttc agcttctcc tggctctggt cccgtttagt 480
tctcagtcgc tgagggtgcat gaacgtactg 510

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<210> 638

<211> 924

<212> DNA

<213> Unknown (H38g487 nucleotide)

<220>

<223> Synthetic construct

<400> 638

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ggtaaatgtg ctatcttgat gttggtgagc acctcccatc agttgcatac ccccatgtac 180
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gcaactggcca tctactggg gagaagtcag accatatcat ttacaagctg tcttttgag 300
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gaccgctgtc ttgccatctg ctatccttta cactacggag ccatcatgag tagcctgtc 420
tcagcgcagc tggccctggg ctctgggtg tgtggtttcg tggccattgc agtgccaca 480
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attgcaccct ggattgccct ggcctgcacc aacacacagg cagtagagct tgtggccttt 600
gtgattgctg ttgtggttat cctgagttca tgcctcatca cctttgtctc ctatgtgtac 660
atcatcagca ccactctcag gatccctct gccagtggcc ggagcaaagc cttctccacg 720
tgctcctcgc atctcaccgt ggtgctcatt tggatgggt ccacagtttt ccttcacgtc 780
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ctgctgaaga aatggaaggg aaaa 924

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<210> 639
 <211> 669
 <212> DNA
 <213> Unknown (H38g488 nucleotide)

<220>
 <223> Synthetic construct

<400> 639
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 tgacatggcc tatgcttcca acaatgttcc caagatgctg gtggatcttg caaactagaa 240
 aagcaccatg tgcttttttc catgcataat gcagacattc ttgtatttgg cttttgtcga 300
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 ggtgttcagc ttctctctgg ctctgggtcca tttagtctc attctgaggc tgcccttcag 480
 tgggctcatg aaatcaacca ctactgtgaa atcctgtctg tcctcaagtt ggcctgtgct 540
 gacacctggc tcaaccaggt ggtcatcttt gcaagctgca tgttcacct ggtagggtga 600
 ctctgcctgg tgctgggtctc ttacttgggc atctggcggc atctgagatc agttgcgaag 660
 ccaaaaagg 669

<210> 640
 <211> 927
 <212> DNA
 <213> Unknown (H38g489 nucleotide)

<220>
 <223> Synthetic construct

<400> 640
 atgggattgg gcaatgagag ttccctaattg gatttcatcc ttctaggctt ctgagaccac 60
 cctcgtctgg aggtgttct ctttgtattt gtctttttct tctacctcct gacccttggtg 120
 ggaaacttca ccataatcat catctcatat ctggatcccc ctcttcatac cccaatgtac 180
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 gatcggtaga ttgtgtctg caaacccctc cactatgtag tcatcatgaa cccacggctt 420
 tgccaacagc tggcatctat ctctggctc agtggtttgg ctagtccct aatccatgca 480
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 gttgttagtg ttctgtttgt tgcattcca ccagcactca tctccatctc ctatggcttc 660
 ataactcaag ctgtgctgag gatcaaatca gtagaggcaa ggcacaaagc cttcagcacc 720
 tgctcctccc accttacagt ggtgattata ttctatggca ccataatcta cgtgtacctg 780
 caaccttagt acagctatgc ccaggaccaa ggggaagttta tctccctctt ctacaccatg 840
 gtgaccccca ctttaaattc tatcatctat actttaagga acaaggatat gaaagaggct 900
 ctgaggaaac ttctctcggg aaaattg 927

<210> 641
 <211> 1012
 <212> DNA
 <213> Unknown (H38g490 nucleotide)

<220>
 <223> Synthetic construct

<400> 641
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 tggggaacct gctcatcatc ctggccatca gccctgactc ccacctccac atccccatgt 180

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acttcttctt ctccaacctg tcttgctg acatcggttt cacctccacc acggtcccca 240
agatgattgt ggacatccag tctcacagca gagtcattct ctatgcaggc tgcctgactc 300
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gataatcatg tatttccctg ctgccatatt tggttttctt cccatctcag ggaccctttt 660
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atgatgttac acggtggtca ccccatgcc gaacccttc atctacagcc tgagaaacag 900
ggatattaaa agtgtcctgc ggcggccgca cggcagcaca gtctaattct aatatcttct 960
tatctgttcc attccttttg tagtgtgggt taaaaaaggc agaaagggtca aa 1012

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<210> 642

<211> 879

<212> DNA

<213> Unknown (H38g491 nucleotide)

<220>

<223> Synthetic construct

<400> 642

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ctccaaaccc caatgtatatt ctttttgaga aacttgtctt tcttagattt ttgttacatc 180
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tgtggattca tgcagtgtgat agcaacatc tcatcaccat tctgtgggag caatagaata 480
cgtcaatttt tctgtaatat tccacagctc ctaagcctct tagaccccaa agtaattacc 540
attgagattg gagtcattgt ttttggtaca agtcttctga taatctcctt tgttgtaatt 600
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tcaaaaacat tttctacctg cattccacat cttgtggttg taacactctt tatgatattc 720
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tctgcttctt acacagtcgt gccccgacc ctgaaccccg tcatctatag tctgaggaat 840
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<210> 643

<211> 1020

<212> DNA

<213> Unknown (H38g492 nucleotide)

<220>

<223> Synthetic construct

<400> 643

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tcttcccca caagtgtggt cttcttctta gacaatttgt cattttcatt atgagtgtaa 120
cagaaaatac gctcatgac ctcctcattc gcagtactc ccgactccac actccaatgt 180
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ccagcgctct catggctgga ggctcctggc tcattgggggt tttcaactcc acagtccaca 480
cagcttatgc actgcagttt cccttctgtg gctctagggc aattgatcac ttcttctgtg 540
aagtcctgc catgttgaag ttgtcctgtg cagacacaac acgctatgaa cgagggtttt 600
gtgtaagtgc tgtgatcttc ctgtgatcc ctttctcctt gatctctgct tcttatggcc 660
aaattattct tactgtcttc cagatgaaat catcagaggc aaggaaaaag tcattttcca 720

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cttggttcctt	ccacatgatt	gtgggtcacga	tgtactatgg	gccatttatt	tttacaatata	780
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tcctcacacc	cacactcaac	cctttcatct	acagcttttag	gaataaagat	gttctggcgg	900
tgatgaaaaa	tatgctcaaa	agtaactttc	tgacaaaaaa	aatgaatagg	aaaattcctg	960
aatgtgtgtt	ctgtctattt	ctatgttaaa	tgctgaagg	atactcatga	gagggttcct	1020

<210> 644

<211> 932

<212> DNA

<213> Unknown (H38g493 nucleotide)

<220>

<223> Synthetic construct

<400> 644

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gggaacgccc	tcctcatagg	gctgaacgtg	ctgcaccctc	gcctgcacaa	ccccatgtac	180
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acctgacctt	ggcgctggga	tcaacggagt	gcctgtgtgt	ggctgtgtgt	gcataatgac	360
gttatgtggc	tatctgccag	ccgcttaggt	acccagagct	catgagtggg	cagacctgca	420
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ccgtctgac	actggcccc	ctcttgtctc	tctgcctgtc	ttaccttttc	atcctgtctg	660
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ccaaggatcc	caacgtggat	aagactgtcg	cattgttcta	cggggttgtg	acgccctcgc	840
tgaaccccat	catttacagc	ctgaggaatg	cagaggtgaa	agctgccgtc	ctaactctgc	900
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<210> 645

<211> 957

<212> DNA

<213> Unknown (H38g494 nucleotide)

<220>

<223> Synthetic construct

<400> 645

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tacttctttc	ttgccaacct	ccccttctcg	gacatgagct	tcaccacgag	cattgtccca	240
cagctccttg	ctaacctctg	gggaccacag	aaaaccataa	gctatggagg	gtgtgtgtgc	300
cagttctata	tctcccattg	gctgggggca	accgagtgtg	tcctgctggc	caccatgtcc	360
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tccacgtcca	ccatgctcct	accgctgtgt	gggaacaatt	gcatacacca	cttcttttgc	540
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acctgttctt	cccacgtggc	tgtggtgtct	ctgttttacg	ggagcatcat	cttcatgtat	780
ctccagccag	ccaagagcac	ctcccatgag	cagggcaagt	tcatagtctt	gttctacacc	840
gtagtcactc	ctgcgctgaa	cccacttatt	tacaccctga	ggaacacgga	ggtgaagagc	900
gccctccggc	acatggtatt	agagaactgc	tgtggctctg	caggcaagct	ggcgcaa	957

<210> 646

<211> 792

<212> DNA

<213> Unknown (H38g495 nucleotide)

<220>

<223> Synthetic construct

<400> 646

atgatgggtc	tgagtatcgt	tttgacctcc	ctgtttggca	attccctcat	gatttctctg	60
attcactggg	accaccggtt	ccacacgccc	atgtacttcc	tcctgagcca	acttttccctc	120
atggacgtga	tgtctggttc	caccactgtg	cccaaaatgg	cggtctgacta	cttgaccgga	180
agtaaggcca	tctcccgcgc	tggtctgtgt	gcgcagatct	tcttctctcc	cacactgggt	240
ggtggagagt	gcttcctctt	agcagccatg	gcctatgacc	gctatgcggc	tgtctgccac	300
ccactccgat	atcccactct	catgagctgg	cagctgtgcc	tgaggatgaa	cctgtcgtgt	360
tggtctctgg	gtgcagctga	cgggctcctg	caggctgttg	ctaccctgag	cttcccatat	420
tgcggtgcac	acgagatcga	tcacttcttc	tgcgagaccc	ccgtgtctgt	gcgtttggct	480
tgtgtctgaca	cttcagtctt	cgaaaacgcc	atgtacatct	gctgtgtgtt	aatgtctctg	540
gtccccctttt	ccctcatcct	gtcctcctat	ggtctcatcc	tcgtctgtgt	tctgcacatg	600
cgctctacag	aagcccgcga	gaaggccttt	gccacctgct	cttcacatgt	ggctgtgggt	660
ggactctttt	atggagctgc	catttttacc	tatatgagac	ccaaatccca	caggtccact	720
aaccacgaca	aggttgtgtc	agccttctat	actatgttca	cccctttact	aaacccccctc	780
atctacagtg	tg					792

<210> 647

<211> 662

<212> DNA

<213> Unknown (H38g496 nucleotide)

<220>

<223> Synthetic construct

<400> 647

aatctgtctt	tcttagatct	ctgctttaca	gcaagcattg	cccctcagct	gctgtggaac	60
ctgggggggtc	cagagaagac	catcacctac	cacggctgtg	tggcccaact	ctacatctac	120
atgatgctgg	gtcccaccga	gtgcgtcttc	ctggttgtca	tgtcccatga	ccgctatgtg	180
gccgtctgcc	ggtccctgca	ctacatggca	gtcatgcgcc	cacatctctg	cctgcagctg	240
gtgactgtgg	cctggtgctg	tggtctccta	aactccttca	tcatgtgtcc	tcagacgatg	300
cagctctccc	ggtgtggacg	tcgcagggtg	gaccacttcc	tgtgtgagat	gcctgtctct	360
attgccatgt	cttgtgagga	aaccatgctg	gtagaagcga	ttcacctttg	ccctgggggt	420
ggctctcttc	ctggtgccgc	tctccctcat	cctcatctcc	tacggcgtga	ttgcagccgc	480
ggtgctgagg	atgaagtcag	cagcagggcg	aaagaaagcc	ttccacacct	gctcttctca	540
cctcacagtg	gtctctctct	tctacggaac	catcatctac	ggtgtacctg	aagccggcca	600
acagctactc	ccaagatcag	gggaagtcc	tgactctctt	ctacaccatc	gtcattccca	660
gc						662

<210> 648

<211> 936

<212> DNA

<213> Unknown (H38g497 nucleotide)

<220>

<223> Synthetic construct

<400> 648

atggagccgc	tcaacagaac	agagggtgtcc	gagttctttc	tgaaaggatt	ttctggctac	60
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gggaacacag	ccatcatggc	ggtgagcgtg	ctagatatcc	acctgcacac	gcccggttac	180
ttcttctctg	gcaacctctc	taccctggac	atctgtctaca	cgccacacct	tgtgcctctg	240
atgctgggtc	acctcctgtc	atcccgggaag	accatctcct	ttgtgtctctg	tgccatccag	300
atgtgtctga	gctgtccac	gggtctccacg	gagtgacctg	tactggccat	cacggcctat	360
gaccgtacc	tgcccatctg	ccagccactc	aggtaaccag	tgctcatgag	ccaccggctc	420
tgctgtctgc	tgatgggagc	tgcttgggtc	ctctgcctcc	tcaagtcggt	gactgagatg	480
gtcatctcca	tgaggctgcc	cttctgtggc	caccacgtgg	tcagtcactt	cacctgcaag	540

atcctggcag	tgctgaagct	ggcatgcggc	aacacgtcgg	tcagcgaaga	cttcctgctg	600
gcggtctcca	tctgtctgct	gcctgtaccc	ctggcattca	tctgcctgtc	ctacttgctc	660
atcctggcca	ccatcctgag	ggtgccctcg	gcccgcaggt	gctgcaaagc	cttctccacc	720
tgcttggcac	acctggctgt	agtgtctgctt	ttctacggca	ccatcatctt	catgtacttg	780
aagcccaaga	gtaagggaagc	ccacatctct	gatgaggtct	tcacagtcct	ctatgccatg	840
gtcacgacca	tgctgaaccc	caccatctac	agcctgagga	acaaggaggt	gaaggaggcc	900
gccaggaagg	tgtggggcag	gagtcgggcc	tccagg			936

<210> 649

<211> 940

<212> DNA

<213> Unknown (H38g498 nucleotide)

<220>

<223> Synthetic construct

<400> 649

atggaaaggg	gaaattggac	attggtgact	gagtttattc	ttgtggggat	accaaccacc	60
agagcccttg	ggggcctcct	ctttgtgatt	ttttatcagc	ctatttgggtg	acagtccttg	120
gaaacaccct	tattattatc	ctgattcttg	tggattacag	gctccactca	cccatgtatt	180
tcttcctcag	caatctctct	ttcagtgaag	cattaacccat	aacctgtgct	gttcctaaga	240
tgctggaggg	cttcccgtcg	gaaaggaaga	gcatcacaag	tggcgaatgc	tctgcacagt	300
cctatttcta	ttttctttcc	ggatgcactg	agtttattcc	ttttgctgtc	atgtcctatg	360
accgctatgt	ggcattttgc	agtcctcttc	agtaccctgc	aattatgacc	agctcactct	420
gtgcccacct	cgtcaccttc	tctggggtgg	gtgggtttct	cctcatgctc	ccatccacca	480
tcctcaaggc	aggactgcca	cactgtggtc	ccaacgtgat	tgagcacttt	ttctgtgaca	540
gcgcccctct	cctccacctg	gcctgtgctg	acattcgtgc	tattgagctg	ttggactttc	600
tcagctcact	ggtcctgac	ctcagctccc	tctcactcac	agtgggtctcc	tatgtttaca	660
tcactctccac	cattctgaag	ataccctcag	gccaagggtca	acgcaaagcc	tttgccacct	720
gtgcctctca	cttcacggtg	gtctccgtgg	gctatgggat	ctccatcttt	gtctatgttc	780
acccttcaca	gaagagcagc	ctgcacctca	acaagatcct	ctttatcctc	tccagcatca	840
tcacaccctt	cctgaatccc	ttcgtcttca	gtctgtggaa	tgaaccctatg	aaagatgcac	900
tgaaggacgc	ctcgcccgga	ggacagagct	tgctcaaagg			940

<210> 650

<211> 927

<212> DNA

<213> Unknown (H38g499 nucleotide)

<220>

<223> Synthetic construct

<400> 650

atggcaaadc	tcacaatcgt	gactgaattt	atccttatgg	ggttttctac	caataaaaat	60
atgtgcattt	tgcattcgat	tctcttcttg	ttgatttatt	tgtgtgccct	gatggggaat	120
gtcctcatta	tcatgatcac	aactttggac	catcatctcc	acaccccctg	gtatttcttc	180
ttgaagaatc	tatctttctt	ggatctctgc	cttatttcag	tcacggctcc	caaactctatc	240
gccaattctt	tgatacacia	caactccatt	tcattccttg	gctgtgtttc	ccagggtcttt	300
ttgttgcttt	cttcagcatc	tgagagctg	ctcctctca	cgggtgatgtc	ctttgaccgc	360
tatactgcta	tatgtcaccc	tctgcactat	gatgtcatca	tggacaggag	cacctgtgtc	420
caaagagcca	ctgtgtcttg	gctgtatggg	ggctctgattg	ctgtgatgca	cacagctggc	480
accttctcct	tatcctactg	tgggtccaac	atgggtccatc	agttcttctg	tgacattccc	540
cagttattag	ctatttcttg	ctcagaaaaat	ttaataagag	aaattgcact	catccttatt	600
aatgtagttt	tggatttctg	ctgttttatt	gtcatcatca	ttacctatgt	ccacgtcttc	660
tctacagtca	agaagatccc	ttccacagaa	ggccagtcac	aagcctactc	tatttgccct	720
ccacacttgc	tggttgtgtt	atttctttcc	actggattca	ttgcttatct	gaagccagct	780
tcagagtctc	cttctatttt	ggatgctgta	atttctgtgt	tctacactat	gctgccccca	840
acctttaatc	ccattatata	cagtttgaga	aacaaggcca	taaagggtggc	tctgggggatg	900
ttgataaagg	gaaagctcac	caaaaaag				927

<210> 651

<211> 942
 <212> DNA
 <213> Unknown (H38g500 nucleotide)

<220>

<223> Synthetic construct

<400> 651

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tcaggatcac gccagctcct cttctccctg gtggctgtca tgtttgcac aggccttctg	120
ggcaaacacc ttcttctctt cttgatccgt gtggactccc ggctccacac acccatgtac	180
ttcctgctca gccagctctc cctgtttgac attggctgtc ccatggtcac catccccaag	240
atggcatcag actttctgcg gggagaaggt gccacctcct atggagggtg tgcagctcaa	300
atattcttcc tcacactgat ggggtgtggc gagggcgctc tgttggctcct catgtcttat	360
gaccgttatg ttgctgtgtg ccagcccctg cagtatcctg tacttatgag acgccaggta	420
tgtctgctga tgatgggctc ctccctgggtg gtaggtgtgc tcaacgcctc catccagacc	480
tccatcacc ttgattttcc ctactgtgcc tcccgtattg tggatcactt cttctgtgag	540
gtgccagccc tactgaagct ctccgtgtga gatacctgtg cctacgagat ggcgtgtgcc	600
acctcagggg tgctgaccc taaatgtccct ctttccctca tcgccacctc ctacggccac	660
gtgttgacag ctgttctaag catgcgctca gaggaggcca gacacaaggc tgtcaccacc	720
tgctcctcgc acatcacggt agtggggctc ttttatgggt ccgccgtgtt catgtacatg	780
gtgccttgcg cctaccacag tccacagcag gataacgtgg tttccctctt ctatagcctt	840
gtcaccctca cactcaaccc ccttatctac agtctgagga atccggagggt gtggatggct	900
ttggtcaaag tgcttagcag agctggactc aggcaaatgt gc	942

<210> 652

<211> 936

<212> DNA

<213> Unknown (H38g501 nucleotide)

<220>

<223> Synthetic construct

<400> 652

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tggaacttc aaattttctt ctttgtgaca ttttccctga tctacgggtg tactgtgatg	120
ggaaacattc tcattatggc cacagtgcac tgtaggtcaa cccttcattc tccctgttac	180
ttctccttg gaaatctctc ttttttggac atgtgtctct ccaactgccac aacacccaag	240
atgatcatag atttgctcac tgaccacaag accatctctg tgtggggctg cgtgaccag	300
atgttcttca tgcacttctt tgggggtgct gagatgactc ttctgataat catggccttt	360
gacaggatag tagccatatg taaacccctg cactatagga caatcatgag ccacaagctg	420
ctaaaggggt ttgcgatact ttcatggata attggttttt tacactccat aagccagata	480
gttttaacaa tgaacttgcc tttctgtggc cacaatgtca taaacaacat attttgtgat	540
cttccccttg tgatcaagct tgcttgcat gaaacatata ccctggaatt atttgtcatt	600
gctgacagcg ggctgctctc tttcacctgt ttcactctct tgcctgttct ttacattgtc	660
atcctgggtc gtgtaccaaa aaaatcatca catgggctct ccaaggcgct gtccacattg	720
tctgccaca tcattgtggc cactctgttc tttggacctt gtatttttat ctatgtttgg	780
ccattcagta gtttggcaag caataaaact cttgccgtat tttatacagt tatcacacc	840
ttactgaatc cgagtattta taccctgaga aataagaaaa tgcaagaggc cataagaaaa	900
ttacggttcc aatatgttag ttctgcacag aatttc	936

<210> 653

<211> 972

<212> DNA

<213> Unknown (H38g502 nucleotide)

<220>

<223> Synthetic construct

<400> 653

atgccaacag acaaacaaat ggaaaaacaa aatcagtcca tgggtgcctga atttattttg	60
--	----

ttgggattca	aaaatctcat	gagctacaga	ttttctttat	cttatttttc	cattctctac	120
atatccataa	ttaagtaacc	taatcattat	ctttgtagtg	aaactggatc	ctcaattgca	180
tttccccatg	tacttcctac	tggccaacct	gtcatctact	gatatgcccc	tggcctcctt	240
tgctactcct	aagaaaatcg	ataatgtaat	tagtgaatat	aggaccatct	cctatgaagg	300
ctgcatgaca	tagagatttt	tccttcactt	tttaagtgga	agtgagatgg	ttttactcct	360
agccatggca	atcgatagat	aatttgccat	atgcaaacc	ctccattaca	agtccattgc	420
atcggacttg	ctcctcgctc	ctggactatg	gatttcatgc	acaccatgag	ccaaattggt	480
ctcacagtga	ctttgccatt	ctgtggtctc	agtgtgtgtg	atatttttgt	gtgtgtgtga	540
tctgccttgt	gataaaactt	gcctgtacag	acacttacat	cttggagcta	tgagtcattg	600
cagacagtgg	actactttct	ttgctgtgtt	tcattgtttc	gttaatctcc	tatagcaccg	660
tcctgattat	tatttgacat	cattctcca	gggggtcttc	caaaactctg	tccacgcttt	720
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ccaatcatct	acacattcag	gaataacgac	atgaagaaag	cattaagaaa	aatgaagatt	900
aactttgtga	gttctagatc	aacttgataa	ctaaaatatt	ataatcacta	aaagcatcat	960
cattattggt	gt					972

<210> 654

<211> 936

<212> DNA

<213> Unknown (H38g503 nucleotide)

<220>

<223> Synthetic construct

<400> 654

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cggaagatcc	agctcctcct	cttcctcttt	ttctcagtg	tctatgtgtc	aagcctgatg	120
ggaaatctcc	tcattgtgct	aactgtgacc	tctgaccctc	gtttacagtc	ccccatgtac	180
ttcctgctgg	ccaacctttc	catcatcaat	ttggtatttt	gttcctccac	agctcccaag	240
atgatttatg	accttttcag	gaagcacaag	accatctctt	ttgggggctg	tgtagttcag	300
atcttcttta	tccatgcagt	tgggggaact	gagatggtgc	tgctcatagc	catggctttt	360
gaccgatatg	tggccatag	taagcctctc	cactacctga	ccatcatgaa	cccacaaagg	420
tgcattttgt	ttttagtcac	ttcctggatt	ataggtatta	ttcactcagt	gattcagttg	480
gcttttgttg	tagacctgct	gttctgtggc	cctaataaat	tagatagttt	cttttgtgat	540
cttcctcgat	ttatcaaact	ggcttgcata	gagacctaca	cattgggatt	catggttact	600
gccaatagtg	gatttatttc	tctggcttct	tttttaattc	tcataatctc	ttacatcttt	660
attttgggtga	ctgttcagaa	aaaatcttca	ggtggtatat	tcaaggcttt	ctctatgctg	720
tcagctcatg	tcattgtggt	ggttttgggtc	tttgggccat	taatcttttt	ctatattttt	780
ccatttccca	catcacatct	tgataaattc	cttgccatct	ttgatgcagt	tatcactccc	840
gttttgaatc	cagtcatcta	tacttttaga	aataaagaga	tgatggtggc	aatgagaaga	900
cgatgctctc	agtttgtgaa	ttacagtaaa	atcttt			936

<210> 655

<211> 967

<212> DNA

<213> Unknown (H38g504 nucleotide)

<220>

<223> Synthetic construct

<400> 655

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tgggagactc	aagatttttc	ttttttgctt	ttcttgtctt	ttctatgtgt	ccggtgtgat	120
ggcaaaccctc	attgtagtgg	tcattgtaac	ctctgaccct	tacttgcaat	cctccttgta	180
tattttgctg	gccaacctct	ctgtcattga	tctcacattt	tgctccattg	cagcacgcaa	240
gatgatttgt	gatattttca	ggaaacagaa	agtcatttcc	ttttggggct	gtgtagctca	300
gatcttcttt	agccatgctg	ttggggggcac	tgagatgggtg	ctgctcatag	ccatggcctt	360
tgacagatat	gttgccgtat	gtaagccctt	tcactacctg	accatcatgc	atccaagaat	420
gtgcattttg	attctagtgg	cttcctgggc	cattggtctc	attcactcat	tggtccaatt	480
gtcttttgta	gtaaaactgc	ccttctgtgg	ccctaattgt	ttggacagct	tttactgtga	540

catacctcag	ctcatcaaac	ttgcttgac	aaatacctat	aaactgcagt	tcatgggttac	600
tgctaatagt	gggttcattt	ccttgagtgc	tttcttcttg	ctcatcctct	cttacatctt	660
cattctggcc	actcttcaga	aacactcctc	aggaggctca	tccaaggctg	tctctactct	720
gtcagctcat	attactgttg	tggttttatt	ccttggtcca	ctgatttttt	tctatgtatg	780
gccctctcct	ccaacacatc	tgaataaatt	tctagccata	tttgatgcca	tttctactcc	840
ttttctgaat	ccagtcactc	acacattcag	gaacagggaa	atgaagattg	caataaggag	900
agtgttcggt	caatttatgg	gttttagaaa	aactacttaa	gtggctttat	taaaacacag	960
aatttcc						967

<210> 656

<211> 873

<212> DNA

<213> Unknown (H38g505 nucleotide)

<220>

<223> Synthetic construct

<400> 656

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tgaggagatcc	gacttctcct	ccttggtgtc	tcttccatgt	tttacatggc	cagtatgatg	120
ggaaactctc	tcattttgct	cactgtgact	tctgaccctc	acttgcactc	ccccatgtat	180
tttctgttag	ccaacctctc	cttcattgac	ctgggtgttt	cctctgtcac	ttctcccaaa	240
atgatttatg	acctgttcag	aaagcacgaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcat	tggcgggtg	gagatgggtg	tgctcatagc	catggccttt	360
gacagatatg	tgcccatatg	taagcccctc	cagtacctga	ccattatgag	cccaagaatg	420
tgcatgttct	tcttagtggc	tgccgtgggtg	accggcctta	tccactctgt	agttcaattg	480
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tcagctcacg	tcagtgtggt	agttttgttc	tttggtcctt	tgatttttgt	ctatacgtgg	780
ccactctccct	ccacacacct	ggataagttt	ctggccatct	ttgatgcagt	tctcactcct	840
gttttaaatc	ctatcatcta	cacattcagg	aat			873

<210> 657

<211> 936

<212> DNA

<213> Unknown (H38g506 nucleotide)

<220>

<223> Synthetic construct

<400> 657

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cgggagattc	agcttctact	ttttgttttc	tctttgttgt	tctactttgc	gagcatgatg	120
ggaaaccttg	tcattgtatt	cactgtaacc	atggatgtc	atctgcactc	ccccatgtat	180
ttctctctgg	ctaacctctc	aatcattgat	atggcatttt	gctcaattac	agcccctaag	240
atgatttggtg	atattttcaa	gaagcacaa	gccatctcct	ttcggggatg	tattactcag	300
atcttcttta	gccatgctct	tgggggcact	gagatgggtg	tgctcatagc	catggccttt	360
gacagataca	tgcccatatg	taaacctctc	cactacctga	ccatcatgag	cccaagaatg	420
tgtctatact	ttttagccac	ttcctctatc	attggcctta	tccactcatt	ggtccaatta	480
gtttttgtgg	tagatttacc	ttttgtggt	cctaatatct	ttgacagttt	ttactgtgat	540
ctccctcggc	tctcagact	tgccgtgacc	aacacccaag	aactggagtt	catgggtcact	600
gtcaatagtg	gactcatttc	tgtgggctcc	tttgtcttgc	tggttaatttc	ctacatcttc	660
attctgttca	ctgtttggaa	acattcttct	ggtggtctag	ccaaggccct	ctctaccctg	720
tcagctcatg	tcactgtggt	catcttgttc	tttgggccac	tgatgttttt	ctacacatgg	780
ccttctccca	catcacacct	ggataaatat	cttgctattt	ttgatgcatt	tattactcct	840
tttctgaatc	cagttatcta	cacattcagg	aacaaagaca	tgaaagtggc	aatgaggaga	900
ctgtgcagtc	gtcttgcgca	ttttacaaag	attttg			936

<210> 658

<211> 980
 <212> DNA
 <213> Unknown (H38g507 nucleotide)

<220>
 <223> Synthetic construct

<400> 658
 atggagcaaa ggaaaaatgt gactgagttt gtccttgtgg ggctcactca gagccccag 60
 ggacagaaaa tattatttct tgtgttcttg ctcatctacg ttgtgacaat ggtaggcaac 120
 atattcattg ttgtgactgt ggtggtcagc ccaactttgg atgccccatg tacttcttcc 180
 ttggctactt atcatttatg gatgctgttc attctactac agttaccca aatatgatta 240
 tagacttact ctatgagaag aaaaccattt cgttccaagc ttgattacc agatttttat 300
 aggacacctt tttgggggtg ctgagatttt actccttgtt gtcattggcct atgatggcta 360
 cgtgaccatc tgcaaacccc tgcattattt gaccatcatg aaccaacggg tgtgcattct 420
 actgctgtg ttggcctggg ctggagggtt cttgcatgct gtagttcaac ttctttttgt 480
 ttacaacctt cccttctgtg gccccaatgt cattgaccat ttcattctgtg acatgtaccc 540
 tttattaaaa cttgcctgca ctgacacctt tgttactggc ctactgtgg ttgccaatga 600
 tggggcaatc tgtgtgggtc tctttatgct cttactcttc tcctatgggg tcattctgca 660
 ctccctgaag aatcttagtc aggaaggag gcacaaagcc ttatccacct gtggctccca 720
 tatcactgtg gtgatctct tctttgtccc ttgtattttc atgtatgtga gacctcttt 780
 gaccttacct attgataaat ccttgactgt gttttacact gttatcacac ctatgttgaa 840
 ccctctaata tatactttaa gaaatgcaga gatgaaaaat gctatgaaga agctctggac 900
 tagaaaaaga aaatgagggtg gcagacaaat gtatcatcta ttttcagtga agagttgctc 960
 cctccaggaa agccatttgt 980

<210> 659
 <211> 917
 <212> DNA
 <213> Unknown (H38g508 nucleotide)

<220>
 <223> Synthetic construct

<400> 659
 atgaatctta aaaatggatc tctagtgacc gagtttattt tactaggatt ttttggacga 60
 tgggaacttc aaattttctt ctttgtgaca ttttcctga tctacggtgc tactgtggtg 120
 ggaaacattc tcattatggt cacagtgaac tgtagtgcga cccttcattc tcccttgtag 180
 tttctccttg gaaatctctc ttttttgac atgtgtctct ccactgccac aacacccaag 240
 atgatcaca gaccatctct gtgtggggct gcgtgacca gaagttcttc atgcaactct 300
 ttgggagtgc tgagatgact cttctgataa tcatggcctt tgacaggatg gtagccatat 360
 gtaaacccct gactatagg acaatcatga gccacaagct gctaaagggg tttgcgatac 420
 tttcatggat aattggtttt ttacactcca taagccagat agttttaaca atgaacttgc 480
 ctttctgtgg ccacaatgtc ataaacaaca tattttgtga tcttccctt gtgatcaagc 540
 ttgcttgcat tgaaacatac accctggaat tatttgcatt tgctgacagc gggctgctct 600
 ctttcacctg tttcatcctc ttgcttgttt cttacattgt catcctgggc agtgtacca 660
 aaaaatcac acatgggctc tccaaggcgc tgtccacatt gtctgccac atcattgtgg 720
 tcaactctgt ctttggacct tgtattttta tctatgtttg gccattcagt agtttggcaa 780
 gcaataaaac tcttctgtga ttttatacag ttatcacacc gttactgaat ccgagtattt 840
 ataccctgag aaataagaaa atgcaagagg ccataagaaa attacgggtc caatatgtta 900
 gttctgcaca gaatttc 917

<210> 660
 <211> 1008
 <212> DNA
 <213> Unknown (H38g509 nucleotide)

<220>
 <223> Synthetic construct

<400> 660

tctacagacc	cacagaatct	aacagatgtc	tctatatcc	tcctcctaga	acctcagagg	60
atccagaatg	acagccggtc	ctcgctgggc	tggttcctgtc	catgtgcctg	gtcacgggtgc	120
tggggaacct	gctcatcatc	ctggccgtca	gccctgactc	ccacctccac	acccccatgt	180
acatcttctt	ctccaacctg	tccttgccctg	acatcggttt	cacctccacc	acgggtcccca	240
agatgactgt	ggacatccag	tctcacagca	gagtcattctc	ctatgcaggc	tgcttgactc	300
agatgtctct	ctttgccatt	tttggaggca	tggaagagag	acatgttcct	gagtgtgatg	360
gcctatgacc	ggtttgtagc	catctgtcac	cctctatatc	attcagccat	catgaacccg	420
tgtttctgtg	gctttctagt	tttggtgtct	tttttttttt	ctctcagtct	tttagacgtc	480
cagctgcgca	acttgattgc	cttacaaatg	acctgcttca	aggatgtgga	aattcctaata	540
ttcttctgtg	acccttctca	actcccccat	cttgcatgtt	gtgacacctt	caccaataac	600
ataatcctgt	atttccctgc	tgccatattt	ggttttcttc	ccatcttggg	gaccttttc	660
tcttactata	aaatcgtttt	ctccattctg	agggtttcat	catctggtgg	gaagtataag	720
gccttctcca	cctgtgtgtc	tcacctgtca	gtggtttgct	gatttttatgg	aacaggcggt	780
ggagggtacc	tcagttcaga	tgtgtcatct	tccccgagaa	aggctgcagt	ggcctcagtg	840
atgtacacgg	tggtcaccac	catgctgaac	cccttcatct	acagcctgag	aaacagggat	900
attaaaagtg	tcctgcggcg	gccgcacagc	agcacggtct	aatcttgata	tcttcttatc	960
gtttccattc	cttttgtagt	gtgggttaaa	aaaggcagca	aggtcaaa		1008

<210> 661

<211> 957

<212> DNA

<213> Unknown (H38g510 nucleotide)

<220>

<223> Synthetic construct

<400> 661

atgatggaaa	tagccaatgt	gagttctcca	gaagtctttg	tcctcctggg	cttctccaca	60
cgacctcac	tagaaactgt	cctcttcata	gttgtcttga	gtttttacat	ggtatcgatc	120
ttgggcaatg	gcatcatcat	tctggtctcc	catacagatg	tgcaacctca	cacacctatg	180
tacttcttct	ttgccaacct	ccccttctctg	gacatgagct	tcaccacgag	cattgtccca	240
cagctcctgg	ctaacctctg	gggaccacag	aaaaccataa	gctatggagg	gtgtgtgtgc	300
cagtctctata	tctcccatg	gctgggggca	accgagtgtg	tcctgctggc	caccatgtcc	360
tatgaccgct	acgtgccat	ctgcaggcca	ctccattaca	ctgtcattat	gcatccacag	420
ctttgccttg	ggctagcttt	ggcctcctgg	ctgggggggc	tgaccaccag	catggtgggc	480
tccacgctca	ccatgctcct	accgctgtgt	gggaacaatt	gcatcgacca	cttcttttgc	540
gagatgcccc	tcattatgca	actggcttgt	gtggatacca	gcctcaatga	gatggagatg	600
tacctggcca	gctttgtctt	tggtgtcctg	cctctggggc	tcactctggt	ctcttacggc	660
caattgccc	gggcccgtgt	gaagatcagg	tcagcagaag	ggcggagaaa	ggcattcaac	720
acctgttctt	cccacgtggc	tgtggtgtct	ctgttttacg	ggagcatcat	cttcatgtat	780
ctccagccag	ccaagagcac	ctcccatgag	cagggcaagt	tcatagctct	gttctacacc	840
gtagtcactc	ctgcgtgaa	cccacttatt	tacaccctga	ggaacacgga	ggtgaagagc	900
gccctccggc	acatggtatt	agagaactgc	tgtggctctg	caggcaagct	ggcgcaa	957

<210> 662

<211> 912

<212> DNA

<213> Unknown (H38g511 nucleotide)

<220>

<223> Synthetic construct

<400> 662

atggaaagag	caaaccattc	agtggatatc	gaatttattt	tggtgggact	ttccaaatct	60
caaaatcttc	agattttatt	cttcttggga	ttctctgtgg	tcttcgtggg	gattgtgtta	120
ggaaacctgc	tcattcttgg	gactgtgacc	tttgattcgc	tccttcacac	accaatgtat	180
tttctgctta	gcaacctctc	ctgcattgat	atgatcctgg	cttcttttgc	tacccttaag	240
atgattgtag	atttccctcg	agaacgtaag	accatctcat	ggtggggatg	ttattccag	300
atgttcttta	tgcacctcct	gggtgggagt	gagatgatgt	tgcttgtagc	catggcaata	360
gacaggtatg	ttgcatatg	caaaccctc	cattacatga	ccatcatgag	cccacgggtg	420
ctcactgggc	tactgttatc	ctcctatgca	gttggaattg	tgcactcatc	tagtcaaatg	480

gctttcatgt	tgactttgcc	cttctgtggt	cccaatgtta	tagacagctt	tttctgtgac	540
cttccccttg	tgattaaact	tgccgtcaag	gacacctaca	tcctacagct	cctgggcatt	600
gctgacagt	ggctcctgtc	actggctctg	ttcctcctct	tgcttgtctc	ctatggagtc	660
ataatattct	cagttaggta	ccgtgctgct	agtcgatcct	ctaaggcttt	ctccactctc	720
tcagctcaca	tcacagttgt	gactctgttc	tttgctccgt	gtgtctttat	ctacgtctgg	780
cccttcagca	gatactcgg	agataaaatt	ctttctgtgt	tttacacaat	tttcacacct	840
ctcttaaatc	ctattattta	tacattaaga	aatcaagagg	taaaagcagc	cattaaaaaa	900
agactctgca	ta					912

<210> 663

<211> 963

<212> DNA

<213> Unknown (H38g512 nucleotide)

<220>

<223> Synthetic construct

<400> 663

atgggtcaatt	tgacttcaat	gagtggattc	cttcttatgg	ggttttctga	tgagcgtaag	60
cttcagattt	tacatgcatt	ggtatttctg	gtgacatacc	tgetggcctt	gacaggcaac	120
ctcctcatta	tcaccatcat	taccgtggac	cgctgtctcc	attcccccat	gtattacttt	180
ttaaagcacc	tctctcttct	ggacctctgc	ttcatctctg	tcacagtccc	ccagtccatt	240
gcaaattcac	ttatgggcaa	cggttacatt	tctcttgttc	agtgcatctc	tcagggtttc	300
ttcttcatag	ctctggcctc	atcagaagtg	gccattctca	cagtgatgtc	ttatgacagg	360
tacgcagcaa	tctgtcaacc	acttcattat	gagactatta	tggatccccg	tgctgtagg	420
catgcagtga	tagctgtgtg	gattgctggg	ggcctctctg	ggctcatgca	tgctgccatt	480
aacttctcca	tacctctctg	tgggaagaga	gtcattcacc	aattcttctg	tgatgttcc	540
cagatgctga	aactagcctg	ttcttatgaa	ttcattaatg	agattgcact	ggctgcattc	600
acaacgtctg	cagcatttat	ctgtttgatc	tccattgtgc	tctcctacat	tcgcatcttc	660
tctacagtgc	tgagaatccc	atcagctgag	ggccggacca	aggtcttctc	cacctgccta	720
ccacacctat	ttgtagccac	cttctttctt	tcagctgcag	gctttgagtt	tctcagactg	780
ccttctgatt	cctcatcgac	tgtggacctt	gtattctccg	tattctatac	tgtgatacct	840
ccaacactca	atccagtcac	ttatagctta	cggaaatgatt	ccatgaaggc	agcactgagg	900
aagatgctgt	caaaggaaga	gcttctctcag	agaaaaatgt	gcttaaaagc	catgtttaaa	960
ctc						963

<210> 664

<211> 930

<212> DNA

<213> Unknown (H38g513 nucleotide)

<220>

<223> Synthetic construct

<400> 664

atgggacccac	agaactattc	cttgggtgtca	gaatttgtgt	tgcatggact	ctgcacttca	60
cgacatcttc	aaaatttttt	ctttatatatt	ttctttgggg	tctatgtggc	cattatgctg	120
ggtaaccttc	tcatttttgt	cactgtaatt	tctgatccct	gcctgcactc	ctccccatg	180
tacttctctg	tggggaacct	agctttcctg	gacatgtggc	tggcctcatt	tgccactccc	240
aagatgatca	gggatttcct	tagtgatcaa	aaactcatct	cctttggagg	atgtatggct	300
caaactcttct	tcttgcactt	tactgggtgg	gctgagatgg	tgctcctgg	ttccatggcc	360
tatgacagat	atgtggccat	atgcaaacc	ttgcattaca	tgactttgat	gagttggcag	420
acttgcacat	ggctgggtgct	ggcttcatgg	gtcgttggat	ttgtgcactc	catcagtcac	480
gtggctttca	ctgtaaaatt	gccttactgt	ggccccaatg	aggtagacag	cttcttctgt	540
gacctccctc	tgggtgatcaa	acttgcctgc	atggacacct	atgtcttggg	tataattatg	600
atctcagaca	gtgggttgct	ttccttgagc	tgttttctgc	tcctcctgat	ctcctacacc	660
gtgatcctcc	tcgctatcag	acagcgtgct	gccggtagca	catccaaagc	actctccact	720
tgctctgcac	atatcatgg	agtgacgctg	ttctttggcc	cttgcathtt	tgtttatgtg	780
cggcctttca	gtaggttctc	tgtggacaag	ctgctgtctg	tgttttatac	catttttact	840
ccactcctga	accctattat	ctacacattg	agaaatgagg	agatgaaagc	agctatgaag	900
aaactgcaaa	accgacgggt	gacttttcaa				930

<210> 665
 <211> 957
 <212> DNA
 <213> Unknown (H38g514 nucleotide)

<220>
 <223> Synthetic construct

<400> 665
 atggaagaa agaatcaaac agctataact gaattcatca tcttgggatt ctccaaccta 60
 aatgaattgc agtttttact attcaccatc ttctttctga cttatttctg tactttggga 120
 ggaaatatat taattatctt gacgactgtg actgatccac acctgcatac acctatgtat 180
 tattttctag ggaacttggc ctttattgac atctgtctaca ccaccagcaa tgtccccag 240
 atgatgggtgc acctcctctc aaagaaaaaa agcatttctt atgtgggggtg tgtggttcaa 300
 ctttttgcac ttgttttctt tgtaggatca gagtgtctcc tactggcagc aatggcatat 360
 gatcgttaca ttgcaatctg caatccttta aggtattcag ttattctgag caaggttcta 420
 tgcaatcaat tagcagcctc atgctgggct gctggtttcc ttaactcagt ggtgcataca 480
 gtgttgacat tctgcctgcc cttctgtggc aacaatcaga ttaattactt cttctgtgac 540
 atccccctt tgctgatctt gtctgtgga aacacttctg tcaatgagtt ggcactgcta 600
 tccactgggg tcttcattgg ttggactcct ttcttttcta tctactttc ctacatttgc 660
 ataactccca ccattctgag gatccagtc tccaggggaa gacgaaaagc cttttctaca 720
 tgtgcctccc acctggccat tgtctttctc ttttatggca gcgccatctt tacatatgta 780
 cggcccatct caacttactc attaaagaaa gatagggttg tttcagtgtt gtacagtgtt 840
 gttaccoccca tgctaaaccc tataatttac acattgagga ataaggacat caaagaagct 900
 gtcaaaacta tagggagcaa gtggcagcca ccaatttctt ctttggatag taaactc 957

<210> 666
 <211> 910
 <212> DNA
 <213> Unknown (H38g515 nucleotide)

<220>
 <223> Synthetic construct

<400> 666
 atgagagaat ttttcttctc agggttctca cagacacccat ctattgaagc agggctatctt 60
 gtactatttc ttttcttcta tatgtccatt tgggttggca atgtcctcat catggtcaca 120
 gtagcatctg ataaatacct gaattcatca cccatgtatt tccttcttgg caacctctca 180
 tttctggacc tatgttatcc aacagtaacg acccctaagc ttctggctga cttctttaat 240
 catgaaaaac tcatttccta tgaccaatgc attgtgcaac tcttcttccct gcattttgta 300
 ggggcagctg agatgttcct gctcacagtg atggcgtagc atcgctatgt tgcaatctgt 360
 cgcccgctgc actacaccac tgcatgagt cgggggttat gctgtgtgtt ggttgctgcc 420
 tcttgatgg gaggatttgc gcaactccact gtccagacca ttctcactgt ccatctacct 480
 ttttgtgggc caaatcaggt ggaaaacttt ttttgtgat gttccccctg tcatcaaac 540
 tgcttgtgct gacacttttg tcattgaatt gctcatggta tctaacagtg ggttgatctc 600
 caccatctcc tttgtggtgc tgatttctc ctacaccact atcctagtca agattcgctc 660
 caaggaagga aggcgaaagg cactctccac gtgtgcctct cactcatgg ttgtaacact 720
 gtttttttga ccctgtatct tcatctacgc tctcctttc tctacatttt ctgtggacaa 780
 gatggtgtct gtactctaca atgttattac ccaatgcta aacccccctc tctacacact 840
 tcggaacaaa gaggtaaagt cagccatgca gaagctctgg gtcagaaatg ggcttacttg 900
 gaaaaagcag 910

<210> 667
 <211> 945
 <212> DNA
 <213> Unknown (H38g516 nucleotide)

<220>
 <223> Synthetic construct

<400> 667

atggagaatg	tcactacaat	gaatgagttt	cttctacttg	gcctgactgg	tggtcaggag	60
ctgcagcctt	tcttcttttg	gattttctta	atcatttacc	tgataaactt	gattggaaat	120
ggatctatat	tggatgatgg	tgttttggaa	ccacaactcc	actcccttat	gtattttttt	180
ctgggaaacc	tttcttgtct	ggatatttct	tattcttcag	tgacactgcc	caagctgctc	240
gtaaacctcg	tgtgcagtcg	cagggtata	tcttttctag	gctgtatcac	ccagctacac	300
ttcttccact	ttttgggaag	cacagaggcc	attttactgg	ctatcatggc	ctttgaccgt	360
tttgttgcca	tctgcaatcc	tcttcgctac	actgtcatca	tgaaccccca	ggtgtgtatt	420
ctgttggcag	ctgcggcctg	gctcatcagc	ttcttttacg	ctctgatgca	ttctgtcatg	480
actgcacacc	tgagtttttg	tggctctcag	aaactcaatc	acttcttcta	cgatgtcaag	540
ccgctcttag	aattggcctg	tagtgacaca	ttactcaatc	aatggcttct	ttccattgtc	600
acaggcagca	tatccatggg	agctttcttt	ctgactcttc	tctcctgctt	ctatgtaatt	660
ggcttccttc	tgtttaagaa	caggtcctgc	agaatactcc	acaaggctct	gtccacttgt	720
gcctccatt	ttatggtggt	atgtcttttc	tatggacctg	tgggcttcac	atatattcgt	780
cctgcttcag	ccacctccat	gattcaggac	cggataatgg	ccatcatgta	tagcgccgtc	840
acccctgtac	tgaatccact	aatctacacc	cttaggaaca	aagaagtgat	gatggctctg	900
aagaaaatct	ttggtaggaa	gttgtttaaa	gactggcagc	aacac		945

<210> 668

<211> 966

<212> DNA

<213> Unknown (H38g517 nucleotide)

<220>

<223> Synthetic construct

<400> 668

atgaatgaga	caaatcattc	tcgggtgaca	gaatttgtgt	tgctgggact	gtctagttca	60
agggagctcc	aacctttctt	gtttcttaca	ttttcactac	tttatctagc	aattctgttg	120
ggcaactttc	tcatactcct	cactgtgacc	tcagattccc	gccttcacac	ccccatgtac	180
tttctgcttg	caaacctgtc	atttatagac	gtatgtgttg	cctcttttgc	taccctaaa	240
atgattgcag	actttctggt	tgagcgcaag	actatttctt	ttgatgcctg	cctggcccag	300
attttctttg	ttcatctctt	cactggcagt	gaaatgggtg	tcctagtttc	catggcctat	360
gaccgttatg	ttgtatatg	caaacctctc	cactacatga	cagtcatgag	ccgtcgtgta	420
tgtgttgctg	tcgtccctcat	ttcatggttt	gtgggcttca	tccatactac	cagccagttg	480
gcattcactg	ttaatctgcc	attttgtggt	cctaataagg	tagacagttt	tttctgtgac	540
cttctcttag	tgaccaagtt	agcctgcata	gacacttatg	ttgtcagctt	actaatagtt	600
gcagatagtg	gctttctttc	tctgagttcc	tttctcctct	tggttgtctc	ctacactgta	660
atacttggtta	cagttaggaa	tcgtcctctc	gcaagcatgg	cgaaggcccg	ctccacattg	720
actgttcaca	tcactgtggt	cactttatct	tttggaccat	gcattttcat	ctatgtgtgg	780
cccttcagca	gttactcagt	tgacaaagtc	cttgctgtat	tctacaccat	cttcacgctt	840
attttaaac	ctgtaatcta	cacgctaaga	aacaaagaag	tgaaggcagc	tatgtcaaaa	900
ctgaagagtc	ggtatctgaa	gcctagtcag	gtttctgtag	tcataagaaa	tgttcttttc	960
ctagaa						966

<210> 669

<211> 594

<212> DNA

<213> Unknown (H38g518 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(594)

<223> n = A,T,C or G

<400> 669

gnnccgctac	tactacccat	gtactgtttc	ctgnctatac	tgtccgccac	tgacctcggc	60
ctgtccatat	ccactctggt	caccatgctg	agtatattct	ggttcaatgt	gagggaaatc	120
agctttaatg	cctgcttgct	ccacatgttc	tttattaaat	tcttcactgt	catggaatcc	180

tcagtgcgtg	tggccatggc	ttttgatcgt	tttgtggccg	tctctaatacc	ccttaggtat	240
gccatgattt	taactgactc	cagaatagct	caaattggag	tggcaagtgt	catcaggggg	300
ctcctaagtc	tgaccaaat	ggtagcactt	cttataagac	tttctactg	ccacagcccg	360
agtactccac	cactcctact	gctaccaccc	tgatgtgatg	aagttctcat	gcacagacgc	420
cagaatcaac	agtgcagttg	ggctgactgc	catgtttctt	actggttggt	gtagacttac	480
ttctcatcct	cctttcttat	gttttgatca	ttaggactgt	ccttancgtt	gcttccccag	540
aagagaggaa	ggaaaccctt	cagtacatgt	gtctcccaca	ttgggggctt	ttgc	594

<210> 670

<211> 939

<212> DNA

<213> Unknown (H38g519 nucleotide)

<220>

<223> Synthetic construct

<400> 670

atgagccctg	agaaccagag	cagcgtgtcc	gagttcctcc	ttctgggcct	ccccatccgg	60
ccagagcagc	aggctgtgtt	cttcacccctg	ttcctgggca	tgtacctgac	cacgggtgctg	120
gggaacctgc	tcatcatgct	gtcatccag	ctggactctc	accttcacac	ccccatgtac	180
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atgctgatgg	acatgcggac	taagtacaaa	tcgatcctct	atgaggaaatg	cattttctcag	300
atgtattttt	ttatattttt	tactgacctg	gacagcttcc	ttattacatc	aatggcatat	360
gaccgatatg	ttgccatag	tcaccctctc	cactacactg	tcatcatgag	ggaagagctc	420
tgtgtcttct	tagtggctgt	atcttggatt	ctgtcttgtg	ccagctccct	ctctcacacc	480
cttctctctga	ccggctgtc	tttctgtgct	gcgaacacca	tcccccatgt	cttctgtgac	540
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acagtatggg	tggtggtcat	taccctgcca	ttcatgtgta	tcctggatc	atatgggtac	660
attggggcca	ccatcctgag	ggctcccttca	accaaaggga	tccacaaagc	attgtccaca	720
tgtggctccc	atctctctgt	gggtgtctctc	tattatgggt	caatatttgg	ccagtacctt	780
ttcccgactg	taagcagttc	tattgacaag	gatgtcattg	tggctctcat	gtacacggtg	840
gtcacacca	tggtgaaccc	ctttatctac	agccttagga	acagggacat	gaaagaggcc	900
cttgggaaac	tcttcagtag	agcaacattt	ttctcttgg			939

<210> 671

<211> 586

<212> DNA

<213> Unknown (H38g520 nucleotide)

<220>

<223> Synthetic construct

<400> 671

ckactactac	tacctatgta	ttttttctk	kgcaacctgt	cactgttaga	tctctgcctt	60
ccttcaatcc	ctgtgccccaa	gatgctgcag	aatttattaa	ctcaaaggta	aaccatctct	120
atgtggtaact	gcattgtcca	gagtttcttt	ctcatattct	ctgggagcac	agaagcctgc	180
ctactccttg	ccatggcctg	tgatcactct	acttccaact	gccaccctcg	gctcaacgat	240
gtggttatga	atcagcctgt	ctgtgtcagg	atgggtattg	cagcatgggc	agtgggatcc	300
ctaaactcct	tgacaaagaa	tcttttcatt	tacaacttac	acttctgtgg	ccccagtgtc	360
atccctcact	tctgctgtga	gctgccttca	ctctccctc	tctcttgat	tgatccagct	420
gccagtgagg	tccttctctgc	tgggtcatgt	acattgctag	gatttgtgac	ttgccgctgg	480
tcctcttttc	ttactctaac	accatctctg	cctcctagcc	atttgktttt	ctgagggtca	540
aggcaaagcc	ttctccacct	gtccttccca	cctcaccgtg	gtgctt		586

<210> 672

<211> 918

<212> DNA

<213> Unknown (H38g521 nucleotide)

<220>

<223> Synthetic construct

<400> 672

atgagccctg	agaaccagag	cagcgtgtcc	gagttccctc	tectgggcct	ccccatccgg	60
ccagagcagc	aggccgtgtt	cttcgcccctg	ttcctgggca	tgtacctgac	cacggtgctg	120
gggaacctgc	tcatcatgct	gtcatccag	ctagactctc	accttcacac	ccccatgtac	180
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atgctgatga	acatgcagac	tcagcaccta	gccgtctttt	acaagggatg	catttcacag	300
acatattttt	tcatattttt	tgtgacttta	gacagtttcc	ttatcacttc	aatggcatat	360
gacaggatg	tggccatctg	tcatcctcta	cattatgcca	ccatcatgac	tcagagccag	420
tgtgtcatgc	tgggtggctgg	gtcctgggtc	atcgcttggtg	cgtgtgctct	tttgcatacc	480
ctcctcctgg	cccagctttc	cttctgtgct	gaccacatca	tccctcacta	cttctgtgac	540
cttgggtgcc	tgctcaagtt	gtcctgctca	gacacctccc	tcaatcagtt	agcaatcttt	600
acagcagcat	tgacagccat	tatgcttcca	ttcctgtgca	tectggtttc	ttatgggtcac	660
attgggggtca	ccatcctcca	gattccctct	accaagggca	tatgcaaagc	cttgtccact	720
tgtggatccc	acctctcagt	gggtgactatc	tattatcgga	caattattgg	tctctatttt	780
cttcccccat	ccagcaacac	caatgacaag	aacataattg	cttcagtgat	atacacagca	840
gtcactccca	tgttgaaccc	attcattttac	agtctgagaa	ataaagacat	taagggagcc	900
ctaagaaaac	tcttgagt					918

<210> 673

<211> 591

<212> DNA

<213> Unknown (H38g522 nucleotide)

<220>

<223> Synthetic construct

<400> 673

ctactactac	cyatgtat	ttttcttggc	aacctstccc	tcatggacat	ctgcggcacc	60
tcttcctttg	tgctctcat	rtagacaat	ttcctggaaa	cccagaggac	catttccttc	120
cctggctgtg	ccctgcagat	gtacctgacc	ctggcgctgg	gatcaacgga	gtgcctgctg	180
ctggctgtga	tggcatatga	ccgttatgtg	gctatctgcc	agccgcttag	gtacycagag	240
ctcatgagtg	ggcagacctg	catgcagatg	gcagcgctga	gctggggggac	aggctttgcc	300
aactcactgc	tacagtccat	ccttgtctgg	cacctcccct	tctgtggcca	cgtcatcaac	360
tactttctatg	agatcttggc	agtgtctaaa	ctggcctgtg	gggacatctc	cctcaatgcg	420
ctggcattaa	tgggtggccac	agccgtcctg	acactggccc	ccctcttgct	catctgcctg	480
tcttaccttt	tcatectgtc	tgccatcctt	agggtaccct	ctgctgcagg	ccggtgcaaa	540
gcctttcca	cctgctcagc	ccaccgcaca	gtggtggtgg	ttttttatgg	g	591

<210> 674

<211> 985

<212> DNA

<213> Unknown (H38g523 nucleotide)

<220>

<223> Synthetic construct

<400> 674

gttaatggat	ggagtaataa	atcagtgggt	actgaattca	atgtgttggg	gctgtctagc	60
tcttgggaac	tccaagtctt	ctttttcttt	atcttctctg	tgttttatgg	agctgcagtg	120
ttgggaaaca	tccttatcat	catcacagta	attatagact	ctcatttgca	ttccccaatg	180
tactttcttc	ttagcaatct	ctcttccatc	gatgtgtgtc	aggctacatt	tgccactccc	240
aagatgattg	cagacttcct	caacgaacac	aagaccacca	ctttccaggg	atgcatgtca	300
caaattcttt	tcttgcattg	ttttgggggt	agtgcagatg	tgcttcttgt	tgccatggcc	360
tatgatagat	acattgctat	atgcaaacct	ctgcaactaca	tgaccatcat	gaaccggagg	420
gtgtgaactg	ttctggtggg	ggtttcctgg	gccattggca	tctcactc	agccaccac	480
ctggcattca	aagtcaatct	gcctttctgt	ggaccaca	gggtagacaa	ttttttctgt	540
gacctcctcc	tagtgatcaa	gcttgccctg	ttagacacct	atggttttga	gatactgggtg	600
ctcactaaca	gtggctgtgct	ctcacttatg	tgtttctctc	ttttgtcat	ttctgacact	660
atcatccttg	ctactgtgca	tcgccaagcc	tctgatggga	tgtccaaggc	cctttccact	720
ctgtctgccc	acattactgt	tgtgcttctc	ttctttggcc	cattaatatt	catctatatt	780

tggccctttg	aaagcttccc	aattgataaa	tttatctctg	tgttttttta	ctgtcttcac	840
tcctctcctt	aaccccatga	tttatactct	gaggaataaa	gatataaagg	aagccatgag	900
gaagctaagg	agatgacatg	tggggttccaa	gcagggtttt	tagacaacta	caaagaagta	960
atacaaattc	ctacttttgg	gctttt				985

<210> 675

<211> 780

<212> DNA

<213> Unknown (H38g524 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(780)

<223> n = A,T,C or G

<400> 675

atgtatttct	tcttgagttt	tttgtctctc	actgatattt	gctttacaac	aagcgttgct	60
cccaagatgc	tgatgaactt	cctgtcagaa	aagaagacca	tctcctatgc	tggtgtgctg	120
acacagtatg	tattttctct	atgccttggg	caacagtgc	agctgccttc	tttcgtaant	180
gcctttgacc	gctatgttgc	cgtctgtgac	cctttccact	atgtcaccac	catgagccac	240
caccactgtg	ttctgctggt	ggccttctcc	tgctcattta	cttaccttca	ctcactcctg	300
cacacacttc	tgctgaatcg	tctcaccttc	tgctgactcca	atgttatcca	ccactttctc	360
tgtgacctca	gccctgtgct	gaaattgtcc	tgctcttcca	tatttgtaa	tgaaattgtg	420
cagatgacag	aagcacctat	tgttttgggt	actcgttttc	tctgcattgc	tttctcttat	480
atacgaatcc	tcactacagt	tctcaagatt	ccctctactt	ctgggaaacg	caaagccttc	540
tccacctgtg	gtttttacct	caccgtgggt	acgctctttt	atggaagcat	cttctgtgtc	600
tatttacagc	ccccatccac	ctacgctgtc	aaggaccacg	tggaacaac	tgtttacaca	660
gtttgtcat	ccatgtctaa	tccttttatc	tacagcctga	gaaacaaaga	cctgaaacag	720
ggcctgagga	agcttatgag	caagagatcc	taggaagcac	cctcttgaaa	aactcgtaag	780

<210> 676

<211> 576

<212> DNA

<213> Unknown (H38g525 nucleotide)

<220>

<223> Synthetic construct

<400> 676

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accacgagca	ttgtcccaca	gtctctggct	aacctctggg	gaccacagaa	aaccataagc	120
tatggagggt	gtgtgggtcca	gttctatata	tccattggc	tgggggcaac	cgagtgtgtc	180
ctgctggcca	ccatgtccta	tgaccgctac	gctgccatct	gcaggccact	ccattacact	240
gtcattatgc	atccacagct	ttgccttggg	ctagctttgg	cctcctggct	gggggggtctg	300
accaccagca	tggtggggtc	cacgctcacc	atgctcctac	cgctgtgtgg	gaacaattgc	360
atcgaccact	tcttttgcga	gatgccctc	attatgcaac	tggttgtgtg	ggataccagc	420
ctcaatgaga	tggtgatgtg	acctggccag	ctttgtcttt	gttgcctctc	ctctggggct	480
catcctgggtc	tcttacggcc	acattgccgg	gccgkgttga	agaacaagtc	agcagaaggg	540
cggagaaagg	cattcaacac	ctgttctttc	cacgtg			576

<210> 677

<211> 929

<212> DNA

<213> Unknown (H38g526 nucleotide)

<220>

<223> Synthetic construct

<400> 677

atggatataa	gaaacagctc	aataataatc	tgagtttgtt	ttgttagaat	tcacagcac	60
ttgggaactt	gaaattttgt	ttcttaaata	tttttgttgg	cctatgcagc	aatcatggca	120
ggaaacctca	ctgcaatcgc	tgtaacctcc	aatcctcccc	tttgctcaac	acctatgtac	180
ttcctccttg	gaaatctctc	ctttctcagt	atgtttatct	ccacagtcac	aatctctaag	240
atgggtccaga	cgttctcagg	gagaataaaa	ccacttcctc	atggggctgt	atggctcaga	300
tctccacttc	ttaggaggca	gtgagatgac	tcttctcata	tttatggctg	ttgatcagca	360
cattgcaata	tgacagacctc	ttcactgcag	aaccatcacg	aactgcaggg	tactcatggc	420
cactcatggg	ctctgtgctg	ctatcacggg	ctgttggttt	tgtgcatact	ataagccaga	480
ttgtttttat	tatcaccttg	cccttctgtg	gccccagtg	ggtggacaat	ttattttgag	540
accttcctct	agttctgaag	cttgctgca	ctgagactta	tgatctggag	ttgctggtaa	600
ttgctaaaag	tggacagtgt	tctttcatct	gcttcatagt	cttgctcatt	ttctacacta	660
ttattctggt	aactgtgcag	catcgatcct	ctgatgcact	ctccaaggct	ctgtccacac	720
tgtctgctca	tatcactgca	gtcactctat	ttttatgagc	catgtgtcta	catttacact	780
tggccattta	ggagcttttc	agtggataca	tttctttctg	tgttttattc	agttacaccc	840
ttactgaacc	ccattactta	cagtctgaga	tgaagcatc	tatacatcaa	ctgaggaccc	900
aacacatcat	ctccagacaa	accttctct				929

<210> 678

<211> 595

<212> DNA

<213> Unknown (H38g527 nucleotide)

<220>

<223> Synthetic construct

<400> 678

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tcagctgtca	ctcccaagg	gatggtgggg	tttctcacag	gagacaaatt	catattatat	120
aatgcttgtg	ccacacaatt	cttcttcttt	gtagccttta	tactgcaga	aagtttcctc	180
ctggcatcaa	tgccctatga	ccgctatgca	gcattgtgta	aaccctgca	ttacaccacc	240
accatgacaa	caaagtgtatg	tgctcgctg	gccataggct	cctacatctg	tggtttcctg	300
aatgcatcca	ttcatactgg	gaacactttc	aggctctcct	tctgtagatc	caatgtagtt	360
gaacactttt	tctgtgatgc	tcctcctctc	ttgactctct	catgttcaga	caactacatc	420
agtgagatgg	ttattttttt	ttgtggggg	attcaatgac	ctcttttcta	tcctggtaat	480
cttgatctcc	tacttattta	tatttatcac	catcatgaag	atgcgctcac	ctgaaggacg	540
ccagaaggcc	ttttctactt	gtgcttccca	ccttactgca	gtttccatct	tttat	595

<210> 679

<211> 945

<212> DNA

<213> Unknown (H38g528 nucleotide)

<220>

<223> Synthetic construct

<400> 679

atggaggcca	tgaaactatt	aaatcaatct	caagtgtcag	aattcatttt	gctgggactg	60
accagctccc	aggatgtaga	gtttcttctc	tttgccctct	tctcggttat	ctatgtgggc	120
acagttttgg	gtaaccttct	tattatagtc	acagtgttta	acacccctaa	cctgaatact	180
cccatgtatt	ttctccttgg	taatctctct	ttttagata	tgacccctgc	ttcttttgcc	240
acccctaagg	tgattctgaa	cttggttaaaa	aagcagaagg	taatttcttt	tgctgggtgc	300
ttcactcaga	tatttctcct	tcacttactg	ggtgggggtg	aaatgggtact	gttgggtctcc	360
atggcttttg	acagatatgt	ggccatttgt	aagccctac	actacatgac	catcatgaac	420
aagaaggat	gtgttttgct	tgtagtgacc	tcattgctct	tggtgtcct	tcactcaggg	480
tttcagatac	catttgctgt	gaacttgccc	ttttgtgggc	ccaatgtggg	agacagcatt	540
ttttgtgacc	tccttttgg	tactaagctt	gcctgtatag	acatatattt	tgtacaggta	600
gtcattgttg	ccaacagtgg	cataatctcc	ctgagctgtt	tcattatttt	gcttatctcc	660
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tccactttga	ctgctcacat	cacagtgggt	attctcttct	ttggcccatg	catctttatc	780
tacatttggc	ccttcggcaa	ccactctgta	gataagttcc	ttgctgtgtt	ttataaccatc	840
atcactccta	tcttgaatcc	aattatctat	actctgagaa	acaaagaaat	gaagatatcc	900

atgaaaaaac tctggagagc ttttgtgaat tctagagaag atact

945

<210> 680

<211> 951

<212> DNA

<213> Unknown (H38g529 nucleotide)

<220>

<223> Synthetic construct

<400> 680

atggagcccc	aaaatacctc	cactgtgact	aactttcagc	tgtaggatt	ccagaacctt	60
cttgaatggc	aggccctgct	ctttgtcatt	ttcctgctca	tctactgcct	gaccattata	120
gggaatgttg	tcatcatcac	cgtggtgagc	cagggcctgc	gactgcactc	ccctatgtac	180
atgttcctcc	agcatctctc	ctttctggag	gtctggtaca	cgtccaccac	tgtgcccctt	240
ctcctagcca	acctgctgtc	ctggggccaa	gccatctcct	tctctgcctg	catggcacag	300
ctctacttct	tcgtattcct	cggcgccacc	gagtgccttc	tcttggcctt	catggcctat	360
gaccgttacc	tggccatctg	cagccactc	cgctaccctt	ttctcatgca	tcgtgggcta	420
tgtgccagggt	tggtgggtgt	ctcatggtgc	acaggggtca	gcacaggctt	tctgcattcc	480
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tgtggctccc	acctggctgt	tgctactctc	tactacggga	ccatgatctc	catgtatgtg	780
tgtccagtc	cccactgtt	gcctgaaatc	aacaagatca	tttctgtctt	ctacactgtg	840
gtcacaccac	tgctgaacc	agttatctac	agcttgagga	acaaagactt	caaagaagct	900
gttagaaagg	tcattgagaag	gaaatgtggt	attctatgga	gtacaagtaa	a	951

<210> 681

<211> 1005

<212> DNA

<213> Unknown (H38g530 nucleotide)

<220>

<223> Synthetic construct

<400> 681

tctacagacc	cacagaatct	aacagatgtc	tctatatctc	tcctcctaga	agctcagagg	60
atccagaatg	gcagccggtc	ctcactgggc	tgtgctgtgc	catgtgcctg	gtcacgggtgc	120
tggggaacct	gtcatcatc	ctggccgtca	gccctgactc	ccacctccac	atccccatgt	180
acttcttctt	ctccaacctg	tccttgcttg	acatcggttt	cacctccacc	acgggtcccca	240
agatgattgt	ggacatccag	tctcacagca	gagtcacttc	ctacgcaggc	tgctgacttc	300
agatgtctct	ctttgccatt	tttggaggca	tggaagagag	acatgtcctt	gagtgtgata	360
gcctatgagc	ggttttagc	catctgtcac	cctctatatc	attcagccat	catgaaccca	420
tgtttctgtg	gctttctagt	tttgttgtct	tttttttttt	ctcagtcttt	tagacgcccc	480
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atcatgtatt	tccttgccgc	catatttggt	tttcttccca	tctcggggac	gcttttctct	660
tacgataaaa	ttgttttctc	cattctaagg	gtttcatcat	caggtgggaa	gtataaggcc	720
ttctccacct	gtgggtctca	cctgtcagtt	gtttgtgat	tttatggaac	aggcattgga	780
ggctacctga	gttcagatgt	gtcatcttcc	ccgagaaagg	ctgcagtggc	ctcagtgatg	840
tacacgggtg	tcattcccat	gccgaacccc	ttcatctaca	gcctgagaaa	cagggatatg	900
aaaagtgtcc	tgcatcgggc	acatggcagc	acgatctcat	ctcaatatct	tcttatttgt	960
tccattcctt	ttgtagtgtg	ggttaaaaaa	ggcagcaagg	tcaaa		1005

<210> 682

<211> 990

<212> DNA

<213> Unknown (H38g531 nucleotide)

<220>

<223> Synthetic construct

<400> 682

cacacagagc	cacagaatct	cacaggtatc	tgagaattcc	tcctcctggg	actctcagag	60
gattccagaac	tgagccgggt	cctcgctggg	ctgtccctgt	ccatgtatct	ggtcacgggtg	120
ctgaggaacc	tgctcagcac	cctggctgtc	agctctgact	ccccctcca	cacccccatg	180
tactttcttc	tctccaacct	gtgctgggct	gacatcggtt	tcaccttggc	catagtctcc	240
aagatgactg	tgacatgca	gtctcatagc	agagtcactc	ctcatgcggg	ctgcctgaca	300
cagatgtctt	tcttggtcct	ttttgcatgt	atagaagaca	tgttcctgac	tgtgatggcc	360
tatgacagat	ttgtagccat	ctgtcgccct	ctttactacc	cagtcacatc	aaatcctcac	420
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agttggattg	tgtgacaatt	caccttcttc	aagaatgtgg	aaatctctaa	ttttgtctgt	540
gagccatctc	aacttctcta	ccttgctgtg	tctgacagca	tcataaatag	catattcata	600
tattttgata	gtactatgtt	tggttttctt	ccattttcaa	ggatcctttt	gtcttactat	660
aaaattgtcc	cctccattct	aaggatttca	tcgtcagatg	ggaagtataa	agccttcacc	720
acctgtggct	ctcacctagc	agttgtttgc	ttatttgatg	gaacaggcat	tgcatgttac	780
ctgacttcag	ctgtggcacc	acccccagg	aatgggtgtg	tggtgcagct	gatgtacgct	840
gtggtcacc	ccatgctgaa	ccctttcatc	tacagcctga	gaaacaggga	cattcaaaac	900
accctgtgga	ggctgcgcag	cagaagagtg	gaatctcatg	atctgttcca	tccttttttt	960
gtgtgggtga	gaaagggcaa	ccacattaaa				990

<210> 683

<211> 1005

<212> DNA

<213> Unknown (H38g532 nucleotide)

<220>

<223> Synthetic construct

<400> 683

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atccagaacg	gcagctgggc	cttgctgggc	tgttcctgtc	catgtgcctg	gtcacgggtg	120
tggggaacct	gtcatcatc	ctggccgtca	gccctgactc	ccacctccac	acccccatgt	180
actttcttct	ctccaacctg	tccttgctgt	acatcggttt	cacctccacc	acgggtcccca	240
agttgattgt	ggacatccaa	tcttacagca	gagtcacttc	ctatgcagge	tgcttgactc	300
agacgtctct	ctttgccatt	tttgagggca	tggaagagag	acatgctcct	gagtggtgatg	360
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tacactgtgg	tcacccccat	gctgaacccc	ttcatctaca	gcctgagaaa	cagggatact	900
aaaagtgtcc	tgcggcggcc	gcacggcagc	acgggtgtaat	cttgatatct	tcttatctgt	960
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<210> 684

<211> 960

<212> DNA

<213> Unknown (H38g533 nucleotide)

<220>

<223> Synthetic construct

<400> 684

cacacagagc	cacggcatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgagcctgt	cctcgctggg	ctgtccctgt	ccatgtatct	ggtcacagtg	120
ctaagggaacc	tgtcatcat	cctggctgtg	agctctgact	ccacctcca	cacccccatg	180
tactttcttc	tctccaacct	gtgctgggct	gacatcagtt	tcacctcggc	cacggttccc	240

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aagatgacgg tggacatgca gtcgcatagc agagtcacatc cttatgcggg ctgcctgaca      300
cggatgtcct tcttcgtcct ttttgcatgt atagaagaca tgctcctgac tgtgatggcc      360
taggactgct ttgtagccat ctgtcgccct ctgcactacg cagtcacgt gaatcctcac      420
ctctgtgtct tcttagtttt ggtgtccttt ttccttagcc tgttggtatc ccagctgcac      480
agttagattg tgttacaatt cacttcttc aagaatgtgg aaatctctca tttgtctgt      540
gagccatctc aacttctcaa ccttgccgtg tctgacagct tcatcaatag catattcatg      600
tatttcgata gtactatgtt tggttttctt cccatttcag ggatcctttt gtcttactat      660
aaaattgtcc cctccattct aaggatttca tctgcagatg ggaagtataa agccttctcc      720
acctgtggct ctcacctggc agttgtttgc ttattttatg gaacaggcat tggcgtgtac      780
ctgacttcag ctgtggcacc accccccagc aatgggtgtg tggcatcagt gaagtacacc      840
gtggtcaccc ccatgtgaa ccctttcatc tacagcctga gaaacaggga cattcaaagc      900
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```

<210> 685

<211> 982

<212> DNA

<213> Unknown (H38g534 nucleotide)

<220>

<223> Synthetic construct

<400> 685

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atttccttcc ttttctgggt ccttctcttg gtcatttcta gagttttggt agccatggca      60
tgaggaaaca gcactgaagt gactgaattc tgtcttctgg gatttgggtc ctagcaagag      120
ttttggtgta tctcttcat tatattcctt ctcatctatg tgacctccat aatgggtaat      180
agtgaataaa tcttactcat caacacagat tccagatttc aaacacccat gtactttttt      240
ctacaacatt tggcttttgt tgatatctgt tacacttctg ctatcactcc caagatgctc      300
caaagcttca cggaagaaaa gaatttgata tcattttggg gctgcatgat acaattattg      360
gtttatgcaa catttgcaac cagtgactgt tatctcctgg ctatgatagc agtggaccat      420
tatgttgcaa tctgtaagcc ccttactat accgtaatca cgtcccaaac agtctgcatc      480
catttggtag ctggttcata catcatgggc tcaataaatg cctctgtaca tacaggtttt      540
gcattttcac tgtcttctg caagtcacat aacatcaacc actttttctg tgatggctcc      600
ccaattcttg ccctttcatg ctccaatatt gacatcaaca tcatgctact tgttgtcttt      660
gtgggattta acttgatgtt cactgggttg gtagtcatct tttcctacat ctacatcatg      720
gccaccatcc tgaaaatgtc ttctagtga ggaaggaaaa aatccttctc aacatgtgcc      780
tcccacctga ccacagttgc cattttctat gggacactct cttacatgca cttaccagtc      840
tcattctaata aattcccagg agaatatgaa agtggcctct atattttatg gcactgttat      900
tcccatgttg aatcctttaa tctatagctt gagaaataag gaagtaaaag aagctttaaa      960
attgataggg aaaaagttct tt

```

<210> 686

<211> 927

<212> DNA

<213> Unknown (H38g535 nucleotide)

<220>

<223> Synthetic construct

<400> 686

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atgacactag gaaacagcac tgaagtcact gaattctatc ttctgggatt tggtgcccag      60
catgagtttt ggtgtatcct cttcattgta ttccttctca tctatgtgac ctccataatg      120
ggtaaatagtg gaataatctt actcatcaac acagattcca gatttcaaac actcacgtac      180
ttttttctac aacatttggc ttttgttgat atctgtttaca cttctgctat cactcccaag      240
atgtccaaaa gcttcacaga agaaaagaat ttgatgttat ttcagggtcg tgtgatacaa      300
ttcttagttt atgcaacatt tgcaaccagt gactgttatc tcttggctat gatggcagtg      360
gatccttatg ttgccatctg taagccctt cactatactg taatcatgtc ccgaacagtc      420
tgcatccggt tggtagctgg ttcatacatc atgggctcaa taaatgcctc tgtacaaaaca      480
ggttttacat gttcactgtc cttctgcaag tccaatagca tcaatcactt tttctgtgat      540
gttcccccta ttcttgcctt ttcattgtcc aatgttgaca tcaacatcat gctacttgtt      600
gtctttgtgg gatctaactt gatattcact gggttggctg tcatcttttc ctacatctac      660
atcatggcca ccatcctgaa aatgtcttct agtgcaggaa ggaaaaaatc cttctcaaca      720

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tgtgcttccc	acctgaccgc	agtcaccatt	ttctatggga	cactctctta	catgtatttg	780
cagtctcatt	ctaataattc	ccaggaaaat	atgaaagtgg	cctttatatt	ttatggcaca	840
gttattccca	tgtaaatacc	tttaattctat	agcttgagaa	ataaggaagt	aaaagaagct	900
ttaaaagtga	tagggaaaaa	gttattt				927

<210> 687

<211> 894

<212> DNA

<213> Unknown (H38g536 nucleotide)

<220>

<223> Synthetic construct

<400> 687

atgggtcgag	gaaacagcac	tgaagtgact	gaattccatc	ttctgggatt	tggtgtccaa	60
cacgaatttc	agcatgtcct	tttcattgta	cttcttctta	tctatgtgac	ctccctgata	120
ggaaatattg	gaatgatctt	actcatcaag	accgattcca	gacttcaaac	acccatgtac	180
ttttttccac	aacatttggc	ttttgttgat	atctgttata	cttctgctat	cactcccaag	240
atgctccaaa	gcttcacaga	agaaaataat	ttgataacat	ttcggggctg	tgtgatacaa	300
ttcttagttt	atgcaacatt	tgcaaccagt	gactgttacc	tcctagctat	tatggcaatg	360
gattgttatg	ttgccatctg	taagccccct	cgctatccca	tgatcatgtc	ccaaacagtc	420
tacatccaac	tcgtagctgg	ctcatatatt	ataggctcaa	taaatgcctc	tgtacataca	480
ggttttacat	tttcaatgtc	cttctgcaag	tctaataaaa	tcaatcactt	tttctgtgat	540
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gtctttgtgg	gatttgactt	gatgttcaat	gagttgggtc	tcactctttc	ctacatctac	660
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tgtgcctccc	acctgacagc	agtaaccatt	ttctatggga	cactctctta	catgtactta	780
cagcctcagt	ctaataattc	tcaggagaat	atgaaagtag	cctctatatt	ttatggcact	840
gttattccca	tggtgaatcc	tttaattctat	agcttgagaa	ataaggaagg	aaaa	894

<210> 688

<211> 444

<212> DNA

<213> Unknown (H38g537 nucleotide)

<220>

<223> Synthetic construct

<400> 688

acgtacgacg	gcgcgagggg	ggctctctgta	ttgtttctta	caatacatgc	aaatctacaa	60
tgatgtcaat	aaaaattcaa	ttaaaaatac	atgtagtaaa	aatagttgct	aatctatgct	120
ggagtttact	tgaatgtcac	tatgctgac	gtcaccttca	agtacacaca	tatcttccat	180
catcctgagc	ttgccctctg	ctatgtgtct	ttttccgcag	ttgtcttcca	cctgacagct	240
gtcaccattt	tctttggagc	tctctcttac	atggacttac	aacctgaatc	tactgtgttt	300
caagagcaag	aaaagccagc	atccatattt	tgtygcatta	tgactctcgt	gttaaaacttc	360
cttatctact	gcctgtgaaa	ttaggaagta	aaagaagctc	tacagttaac	aaggaaaaag	420
tattaataca	tgtagactga	gggt				444

<210> 689

<211> 888

<212> DNA

<213> Unknown (H38g538 nucleotide)

<220>

<223> Synthetic construct

<400> 689

atgctagtgt	cacaacagga	gcagcctctt	ctgtttggca	tcttccttgg	catgtacctg	60
gtcaccatgg	tggggaacct	gctcattatc	ctggccatca	gctctgaccc	acacctccat	120
actcccatgt	acttctttct	ggccaacctg	tcattaactg	atgcctgttt	cacttctgcc	180
tccatcccca	aaatgctggc	caacattcat	acccagagtc	agatcatctc	gtattctggg	240

tgtcttgcac	agctatatatt	cctccttatg	tttgggtggcc	ttgacaactg	cctgctggct	300
gtgatggcat	atgaccgcta	tgtggccatc	tgccaaccac	tccattacag	cacatctatg	360
agtcccccagc	tctgtgcact	aatgctgggt	gtgtgctggg	tgctaaccac	ctgtcctgcc	420
ctgatgcaca	cactgttgct	gacccgcgtg	gctttctgtg	cccagaaaagc	catccctcat	480
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tcctatgtcc	gcattttctg	ggctgtgttt	gtcatctcat	ctcctggagg	gagatggaag	660
gccttctcta	cctgtgggtc	tcatctcacg	gtggttctgc	tcttctatgg	gtctcttatg	720
gggtgtgtatt	tacttcctcc	atcaacttac	tctacagaga	gggaaagtag	ggctgctgtt	780
ctctatatgg	tgattattcc	cacgctaaac	ccattcattt	atagcttgag	gaacagagac	840
atgaaggagg	ctttgggtaa	actttttgtc	agtggaaaaa	cattcttt		888

<210> 690

<211> 939

<212> DNA

<213> Unknown (H38g539 nucleotide)

<220>

<223> Synthetic construct

<400> 690

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ccagagcagc	aggtgtgtt	cttcaccctg	ttcttgggca	tgtacctgat	cacgggtgctg	120
gggaacctgc	tcatcatcct	gtcctccgg	ctggactctc	accttcacac	ccccatgttc	180
ttcttccctca	gccacttggc	tctcactgac	atctcccttt	catctgtcac	tgtcccaaag	240
atgttattaa	gcattgcaaac	tcaggatcaa	tccattcttt	atgcagggtg	tgtaactcag	300
atgtattttt	tcatattttt	cactgatcta	gacaatttcc	ttctcacttc	aatggcatac	360
gatcgggatg	tggccatctg	tcacccctc	cgctacacca	ctatcatgaa	agagggactg	420
tgtaacttac	tagtcactgt	gtcctggatc	ctctcctgta	ccaatgccct	gtctcacact	480
ctcctcctgg	cccagctgtc	cttttgtgct	gacaacacca	tccccattt	cttctgtgat	540
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acagtgggac	aggcagtcac	tactctacca	ctaatatgca	tcttgatctc	ttatggccac	660
attgggggtca	ccatcctcaa	ggctccatct	actaagggca	tcttcaaagc	tttgtccacc	720
tgtggctctc	acctctctgt	gggtgtctctg	tattatggca	caattattgg	actgtatttt	780
ctccctcat	ccagtgcctc	cagtgcacag	gacgtaattg	cctctgtgat	gtacacgggtg	840
atcaccccat	tgttgaatcc	cttcattttat	agcctaagga	acagggacat	aaagggagcc	900
ctggagagac	tcttcaacag	ggcaacagtc	ttatctcaa			939

<210> 691

<211> 933

<212> DNA

<213> Unknown (H38g540 nucleotide)

<220>

<223> Synthetic construct

<400> 691

atggaaaacc	aatccagcat	ttctgaattt	ttcctccgag	gaatatcagc	gcctccagag	60
caacagcagt	ccctcttcgg	aattttctctg	tgtatgtatc	ttgtcacctt	gactgggaac	120
ctgctcatca	tcttgcccat	tggctctgac	ctgcacctcc	acaccccat	gtactttttc	180
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gtgaatatac	agactcgga	tcacaccatc	tcctatacgg	gttgccctcac	gcaaattgat	300
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atggctcggg	tgtccttctg	tgtgactggg	gaaattgctc	actttttctg	tgacatcact	540
cctgtcctga	agctgtcatg	ttctgacacc	cacatcaacg	agatgatggg	ttttgtcttg	600
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tcccacctct	gcgttggttg	tgtgttctat	gggacctctc	tcagtgccta	cctgtgtcct	780
ccctccattg	cctctgaaga	gaaggacatt	gcagcagctg	caatgtacac	catagtgtgact	840

cccatgttga acccctttat ctatagccta aggaacaagg acatgaaggg ggccctaaag 900
 aggctcttca gtcacaggag tattgtttcc tct 933

<210> 692

<211> 945

<212> DNA

<213> Unknown (H38g541 nucleotide)

<220>

<223> Synthetic construct

<400> 692

atgggaggca agcagccctg ggtcacagaa ttcactcttg tgggattcca ggttggtcca	60
gcactggcga ttctcctctg tggactcttc tctgtcttct atacactcac cctgctgggg	120
aatgggggtca tctttgggat tatctgcctg gactctaagc ttcacacacc catgtacttc	180
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ttggcaaacc taatgaacca gaaaagcacc atctcctttg ttccatgcat aatgcagact	300
tttttgtatt tggtcttttg tgttacagag tgcctgattt tgggtggtgat gtcctatgat	360
aggatatgtg ccactctgcca ccctttccag tacactgtca tcatgagctg gagagtgtgc	420
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catattctga ggccgccttt ttgtggccca caaagatca accactttat ctgtcaaact	540
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ttcaaccgga tgctgaaccc cttgatctac agcctgagga acgcagaggt caagggtgcc	900
ctgaaaagag tggttgaggaa acagagatca aagtgaggga tgcca	945

<210> 693

<211> 575

<212> DNA

<213> Unknown (H38g542 nucleotide)

<220>

<223> Synthetic construct

<400> 693

ttgaagggtt attaaaaggc aatatgagtg cagaagcaag gtaagttttt tgtaataatt	60
ttttgttaat aatgtgaaat gtaaggaaaa aatatacaac tttaagtttc tgactgtcct	120
gctagaaaact agttttgccc tgcagcgacc cctctgtggg aatctcattg atgacaagtg	180
aaattcttga agtgctaaag ttagtttgct caagttcact gtcctatgat atgatcatga	240
tgggtgggtca acattcttct cttgccaatt ccaatgtact tatttataac tatgtgtctt	300
gtaatcttat ttttaaagag atcttatggt aatcttccaa gggagttag tttctgcatt	360
tcctggatat atgggttttc gtatattgcc tggctataat ttttagagct ctttacaac	420
tcacaaagat atggggctca acaatgaatg aaattgtacg gtggatgtat tagtattaaa	480
cgtattagta ttaaattgtg tgacataaac tggctcttaa atataatcac aaattagtag	540
ctacaatgct tcaagcattg ttgtcctttt tgaaa	575

<210> 694

<211> 942

<212> DNA

<213> Unknown (H38g543 nucleotide)

<220>

<223> Synthetic construct

<400> 694

atggctgaag aaaatcatat catgaaaaat gagtttatcc tcacaggatt tacagatcac	60
cctgagctga agactctgct gtttgtggtg ttctttgcca tctatctgat caccgtggtg	120
gggaatatta gtttgggtggc actgatattt acacaccgtc ggcttcacac accaatgtac	180

atctttcttg	gaaatctggc	tcttgtggat	tcttgtctgt	cctgtgctat	tacccccaaa	240
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ttttattttc	tttgactgtg	ggaaactgca	gactgctttc	ttctggcagc	aatggcctat	360
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attcttctta	ctattttcaa	aatgaaatcc	aaagagggaa	gggccaaaagc	tttttctacc	720
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agaccaaatt	tgcttgaaga	aggggataaa	gatataccag	ctgcaatttt	atttacaata	840
gtagttccct	tactaaatcc	tttcatttat	agcctgagaa	atagggaagt	aataagtgtc	900
ttaagaaaaa	ttctgatgaa	agaaataatc	tcaagaagat	gg		942

<210> 695

<211> 948

<212> DNA

<213> Unknown (H38g544 nucleotide)

<220>

<223> Synthetic construct

<400> 695

atgcaaggag	aaaacttcac	catttggagc	atttttttct	tggagggatt	ttcccagtac	60
ccagggttag	aagtgttct	cttcgtcttc	agccttgtaa	tgtatctgac	aacgctcttg	120
ggcaacagca	ctcttatttt	gatcactatc	ctagattcac	gccttaaaac	ccccatgtac	180
ttattccttg	gaaatctctc	tttcatggat	atltgttaca	catctgcctc	tgttcctact	240
ttgctggtga	acttgctgtc	atcccagaaa	accattatct	tttctgggtg	tgctgtacag	300
atgtatctgt	cccttgccat	gggctccaca	gagtgtgtgc	tcctggccgt	gatggcatat	360
gaccgttatg	tgcccatttg	taaccgcgtg	agatactcca	tcacatgaa	caggtgcgtc	420
tgtgcacgga	tgccacgggt	ctcctgggtg	acgggttgcc	tgaccgctct	gctggaaacc	480
agttttgccc	tgcatatacc	cctctgtggg	aatctcatcg	atcacttcac	gtgtgaaatt	540
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gtcagcattc	tcctcttgcc	aattccaatg	ctcttagttt	gcctctctta	catcttcate	660
ctttccacta	ttctgagaat	cacctcagca	gagggaaagaa	acaaggcttt	ttctacctgt	720
gggtgcccatt	tgactgtggt	gattttgtat	tatggggctg	ccctctctat	gtacctaaag	780
ccttcttcat	caaatgcaca	aaaaatagac	aaaatcatct	cgttgcttta	cggagtgtct	840
accctatgt	tgaaccccat	aatttacagt	ttaagaaaca	aggaagtcaa	agatgctatg	900
aagaaattgc	tgggcaaaat	aacattgcat	caaacacacg	aacatctc		948

<210> 696

<211> 936

<212> DNA

<213> Unknown (H38g545 nucleotide)

<220>

<223> Synthetic construct

<400> 696

atgatgggta	gaaggaataa	cacaaatgtg	gctgacttca	tccttatggg	actgacactt	60
tctgaagaga	tccagatggc	tctgtttatg	ctatttctcc	tgatatacct	aattactatg	120
ctgggggaatg	tggggatgat	attgataatc	cgcttgacc	tccagcttca	cactcccatg	180
tattttttcc	ttactcacct	gtcatttatt	gacctcagtt	actcaactgt	cgtcacacct	240
aaaaccttag	cgaacttact	gacttccaac	tatatttccct	ttacgggctg	ctttgcccag	300
atgttctttt	ttgccttctt	gggtactgct	gaatgttacc	ttctctctc	aatggcccat	360
gatcgctatg	cagcgatctg	cagtcctcta	cactacacag	ttattatgtc	caaaaggctc	420
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gtttccatga	gcagattgca	tttctacgac	tcaaacgtaa	ttcatcactt	tttctgtgac	540
actttcccaa	ttttagctct	gtcctgcact	gatacataca	acaccgaaat	cctgatattc	600
attattgttg	gttccaccct	gatgggtgcc	cttttcacaa	tatctgcate	ctatgtgttc	660
attctcttta	ccatcctgaa	aattaattcc	acttcaggaa	agcagaaaagc	tttctctact	720

tgcgtctctc atctcttggg agtcaccatc ttttatagca ctctgatttt tacttattta	780
aaaccaagaa agtccttattc cttgggaaga gatcaagtgg cttctgtttt ttatactatt	840
gtgattcccg tgctgaatcc actcatttat agtccttagaa acaaagaggt gaaaaatgct	900
gtcatcagag tcatgcagag aagacaggac tccagg	936

<210> 697

<211> 634

<212> DNA

<213> Unknown (H38g546 nucleotide)

<220>

<223> Synthetic construct

<400> 697

acaatgttct ataaaaattag tgctttgttc taatgttttg tatcacttta ttttagtaaa	60
aattgagtaa gcaaaaaata tactgggttc tgactatctt tggcttttta gaggcattca	120
ttgccatgaa taaattataa aagttatata gttctctaata atgtttatat ttataatat	180
gaatatttag ttctctaata tgtttatatt ttataatatg aatatttctg tacattattt	240
cctaaaatgt atttttttct tttgtatctg ttgtcttttag ctattaattt ttgatagttt	300
ttctaccat cctcctcttc ccctacttta agaggcagat atctgtgcaa attcctagcc	360
atgctacact aatactacag cttcctgatg acactttttac attatcctca acttttgcct	420
ctcttattga ccctctgtat catcgatgct ctatggaaga ctgttcctta tgtacttaat	480
gtcagaaaaa ttctcttgac acagacagga tggcctctgt cttctacaca gtagtcattc	540
ccatgttaaa cccattgatc tggagcccca ggaacaagga tgtgacattg ccctgaggaa	600
agtcatgggc aatagaaaaac aggcattatt ttgc	634

<210> 698

<211> 682

<212> DNA

<213> Unknown (H38g547 nucleotide)

<220>

<223> Synthetic construct

<400> 698

tgcattgttct ctttttattt taattttttac cattttttttt cccacatgaa aggtcttgca	60
gtcacttaga aatgctgaga taaattgact ggtataaagt aaggatatctg attaataaaa	120
tttactctaa aactaattgg ctttttcatg gactataaga ctatgcacaa ccacttcgta	180
ctcaaacatg caattctctt tccaatgttg tatgaccag taccagctc ttcaaagcac	240
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agggccatct gaaagtcctt gcagtatttg gttgtcatga agcaatggct gtgtgttggtg	360
ctgctgggtg tgccctgggc tggaggattt ttgcacacag taattcaact tggccttatt	420
catgggctcc catcttatga cccaatgtc attggctggt ttgtctgtga catggacccc	480
ttaataagc ttgtctgtga ctatacactc aacagatttg tctattttgc aggtcatgac	540
ttaaatacta ggttttatat atttcgttta tattcagact ggactgtttc cttttggtga	600
tttgactttg gtatcctttt gtaatttttt ccctagagga catgattcta taaatcttgt	660
tatacatagt tattatccct gt	682

<210> 699

<211> 897

<212> DNA

<213> Unknown (H38g548 nucleotide)

<220>

<223> Synthetic construct

<400> 699

atggagccaa ggaaaaatgt gactgacttt gtctctcttg gcttcacaca gaatccaaag	60
gagcagaaag tactttttgt tatgttcttg ctcttctaca ttttgacctt ggtgggcaac	120
ctgtcattg tagtgaccgt aactgtcagt gagaccctgg gctcaccaat gtccttcttt	180
cttgcctggct taacatttat agatatcatt tattcttcat ccatttcccc cagattgatt	240

tcagacttgt	tctttgggaa	taattccata	tccttccaat	ctttcatggc	ccagctcttt	300
atcgagcacc	tttttgggtg	gtcagaggtc	tttctcctgt	tggtgatggc	ctatgaccgc	360
tatgtggcca	tctgtaagcc	cttgcatatt	ttggttatca	tgagacaatg	ggtgtgtgtt	420
ttgctgctgg	tagtgtcctg	ggttggagga	ttctgtcaat	cagtatttca	acttagcatt	480
atttatgggc	tcccattctg	tggccccaat	gtcattgatc	attttttctg	tgacatgtat	540
cccttattga	aactggcctg	cactgacacc	catgttattg	gcctcttagt	ggtggccaat	600
ggaggactgt	cttgcaactat	tgcgtttctg	ctcttactca	tctcttatgg	tgatcatcctg	660
cactctctaa	agaaacttag	tcagaaaggg	aggcaaaaag	cccactcaac	ctgcagttcc	720
cacatcactg	tggttgtcct	cttctttgtt	ccttgtatatt	ttatgtgtgc	tagacctgct	780
aggaccttct	ccattgacaa	atcagtgagt	gtgttttata	cagtcataac	cccaatgctg	840
aaccccttaa	tctacactct	gagaaattct	gagatgacaa	gtgctatgaa	gaagctt	897

<210> 700

<211> 945

<212> DNA

<213> Unknown (H38g549 nucleotide)

<220>

<223> Synthetic construct

<400> 700

atgagtcctg	atgggaacca	cagtagtgat	ccaacagagt	tcgtcctggc	agggctccca	60
aatctcaaca	gcgcaagagt	ggaattatct	tctgtgtttc	ttcttgtcta	tctcctgaat	120
ctgacaggca	atgtgttgat	tgtgggggtg	gtaagggctg	atactcgact	acagaccctt	180
atgtacttct	ttctgggtaa	cctgtcctgc	ctagagatac	tgctcacttc	tgatcatcatt	240
caaagatgc	tgagcaatct	cctctcaagg	caacacacta	tttcccttgc	tgcatgtatc	300
acccaattct	atttctactt	ctttctcggg	gcctccgagt	tcttactgtt	ggctgtcatg	360
tctgctggatc	gctacctggc	catctgtcat	cctctgcgct	accccttgct	catgagtggg	420
gctgtgtgct	ttcgtgtggc	cttggcctgc	tgggtggggg	gactcgtccc	tggtgcttgg	480
cccacagtgg	ctgtggcctt	gcttcccttc	tgtaagcagg	gtgctgtggg	acagcacttc	540
ttctgcgaca	gtggcccact	gctccgcctg	gcttgaccca	acaccaagaa	gctggaggag	600
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tacggcctca	ttgtgctggc	agtcctgagc	atcccctctg	cttcaggccg	tcagaaggcc	720
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ctctatgtgc	ggccatcgca	gagtggttct	gtggacacta	actgggcagt	gacagtaata	840
acgacatttg	tgacaccact	gttgaatcca	ttcatctatg	ccttacgtaa	tgagcaagtc	900
aaggaagctt	tgaaggacat	gttttaggaag	gtagtggcag	gcgtt		945

<210> 701

<211> 772

<212> DNA

<213> Unknown (H38g550 nucleotide)

<220>

<223> Synthetic construct

<400> 701

gtactctgtg	tcataattttg	taaataaagt	catcatataa	gtttattgag	tttttttgag	60
tacctaataa	cttaataaaa	aaaatatggg	agcatatgta	gtacctgctt	tgatcaataa	120
cggataaagt	atctggaagt	ctttgctgag	aatctttttg	tgctgctgag	attattccac	180
tgatgtggat	gggccatggc	tggttatgtg	cgtctgtac	tacatgacca	tcgtgaatca	240
atataggtgt	agccatctca	ctggaatggc	atgtactgaa	agctttatcc	aggcacagtt	300
tagatcctct	ccccagtctg	acttcccttc	tatgacccca	atgtcatagc	tcattcatgt	360
gtgacttaaa	cacttttttg	aaactcctct	gcatgggtac	tactaataca	attgggttct	420
ttgttgctgc	caatgggtgg	ttcaactacc	tgtaaacaat	cattttcttg	atgggttctt	480
aagtggccat	cctatgtact	ttgaaaactc	acagcttggg	ggaaagatgc	ttaaagttctc	540
tacctgcac	tctcacacca	ccatggtcat	cttatctttg	agttctgtat	atctgtgtat	600
ctgtgccccag	tgacccttcc	ccaatcaata	aagcaatggc	tggtgttcat	accgtgataa	660
atcctatgtt	aaaaccttta	gtctaaccct	cagaaatgca	gaggtgaaaa	gtgctttgag	720
aaaggtctgg	gtcaaaagat	gacctgaaga	gagaaataat	ctaaacataa	ga	772

<210> 702
 <211> 954
 <212> DNA
 <213> Unknown (H38g551 nucleotide)

<220>
 <223> Synthetic construct

<400> 702
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 ccaagacttg agttactctt ttttgtgctc atcttcataa tgtagtggtg catccttctg 120
 gggaatggta ctctcatttt aatcagcatc ttggaccctc accttcacac ccctatgtac 180
 ttctttctgg ggaacctctc cttcttggac atctgctaca ccaccacctc tattccctcc 240
 acgctagtga gcttcctttc agaaagaaag accattttccc tttctggctg tgcagtgcag 300
 atgttcctca gcttggccat ggggacaaca gagtgtgtgc ttctgggcgt gatggccttt 360
 gaccgctatg tggctatctg caacctctg agatatccca tcatcatgag taaggatgcc 420
 tatgtaccca tggcagctgg gtcctggatc ataggagctg tcaattctgc agtacaaca 480
 gtgtttgtgg tacaattgcc tttctgcagg aataacatca tcaatcattt cacctgtgaa 540
 attctagctg tcatgaaact ggcctgtgct gacatctcag gcaatgagtt catcctgctt 600
 gtgaccacaa cattgttctt attgacacct ttgtatttaa ttattgtctc ttacacgtta 660
 atcattttga gcatcttcaa aattagctct tcggagggga gaagcaaacc ttctcttacc 720
 tgctcagctc gtctgactgt ggtgataaca ttctgtggga ccattcttct catgtacatg 780
 aagcccaagt ctcaagagac acttaattca gatgacttgg atgccactga caaacttata 840
 ttcatattct acagggtgat gactcccatg atgaatcctt taatctacag tcttagaaac 900
 aaggatgtga aggaggcagt aaaacaccta ctgagaagaa aaaattttta caag 954

<210> 703
 <211> 999
 <212> DNA
 <213> Unknown (H38g552 nucleotide)

<220>
 <223> Synthetic construct

<400> 703
 atggaagga ccaattggac agagatagag ttcattctgc aaggactttc aggttaccca 60
 agagctgaaa aattcctttt cgtgatgtgc ttagtgatgt acctgggtgat tctcctaggt 120
 aatggcacct tgatcattct gacactcctg gatgctcgtc tccacacacc catgtacttc 180
 ttcttggga atctttcctt cctagacatt tggtagacat cctcctccat cccctcaatg 240
 ctgatacact tcctatcaga gaagaaaacc atctccttca ctagatgtgt gattcaaatg 300
 tctgtctctt acactatggg atccaccgag tgtgtgcttc tagcagtgat ggcatatgac 360
 cgttatgtag ccattctgcaa cctctgaga tatcccatca tcatgggcaa ggcactttgt 420
 attcagatgg tggctgtctc ttggggacta ggctttctca actcattgac agaaactgtt 480
 cttgcaatac ggttaccctt ctgtggaaaa aaatgtcatt aatcattttg tttgtgaaat 540
 attggccttt gtcaagctgg cttgcacaga tacttccttg aatgagatta ttataatgtt 600
 gggcaatgta atatttttgt tttctccatt actgctgatt tgtatctcct acatctttat 660
 cctttctact gtactaagaa tcaattcagc tgaaggaagg aaaaaggcct tttccacctg 720
 ctgagccac atgacagtgg tgattgtgtt ttatgggaca atcctcttca tgtacatgaa 780
 ggcaagtc aaagactctg cttttgacaa actgattgcc ctgttctatg gcatagtcac 840
 ccccatgctc aatcctatca tctatagcct gaggaatata gaggtgcatg gagctatgag 900
 gaaattaatg agtagaccct ggttctggag gaaatgatga cacactgaca cctttgagtt 960
 tatgcacaaa atacgctcac aagtttgaga caacacttt 999

<210> 704
 <211> 966
 <212> DNA
 <213> Unknown (H38g553 nucleotide)

<220>
 <223> Synthetic construct

<400> 704

cacacagagc	catggaatct	cacagatgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggt	cctcgctttg	ctctccctgt	ccctgtccat	gtgtctggtc	120
atggtgctga	ggaacctgct	cagcatcctg	gctgtcagct	ctgtctctcc	cctccacacc	180
cccgtgtact	tcttctcttc	taaaactgtc	tgggctgaca	tcggtttcac	cttgggccacg	240
gttcccaaga	tgattgtgga	catgcagtcg	catagcagag	tcattctctca	tgcgggctgt	300
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cctcacctct	gtgtctcctt	cctttttggt	tcctttttcc	ttagcatggt	ggattcccag	480
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tactgtaaaa	tcgtcccctc	cattctaaag	atttcatcat	cagatgggaa	gtataaagcc	720
ttctccacat	gtggctctca	cctagcagtt	gtttgctgat	tttatagaac	aggcattggc	780
atgtacctga	cttcagctgt	gtcaccaccc	cccaggaaatg	gtgtggtggc	gtcagcgatg	840
ttctctgtgg	tcacccccat	gctgaacctt	ttcatctaca	gcctgagaaa	cagggacata	900
caaagtgcc	tgcgagggt	gctcagcaga	acagtcgaat	cttatgatct	gttccatcct	960
ttttct						966

<210> 705

<211> 937

<212> DNA

<213> Unknown (H38g554 nucleotide)

<220>

<223> Synthetic construct

<400> 705

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aaggccctgc	agggccccct	gttctgggtg	gtgcttctgg	tctacctggg	caccttgctg	120
ggtaactccc	tgatcatcct	cctcacacag	gtcagccctg	ccctgcactc	ccccatgtac	180
ttcttctctg	gccaaactctc	agtgttgagg	ctcttctaca	ccactgacat	cgtgcccagg	240
accctggcca	atctgggtgc	cccgcacccc	caggccatct	ctttccaggg	ctgtgcagcc	300
cagatgtacg	tcttcattgt	cctggggcatc	tcggagtgtc	gcctgctcac	ggccatggcc	360
tatgaccgat	atgttgccat	ctgccagccc	ctacgtatt	ccacctctt	gagcccacgg	420
gcctgcatgg	ccatggtggg	tacctcctgg	ctcacaggca	tcacacggc	caccacccat	480
gcctccctca	tcttctctct	accttttcgc	agccacccga	tcaccccgca	ctttctctgt	540
gacatcctgc	cagtactgag	gctggcaagt	gctgggaagc	acaggagcga	gatctccgtg	600
atgacagcca	ccatagtctt	cattatgata	cccttctctc	tgattgtcac	ctcttacatc	660
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acctgtcctt	cccatctgct	cggtggtctc	tctcttcttt	ggaacagcca	gcataccta	780
catccggccg	caggcaggct	cctctgttac	cacagaccgc	gtcctcagtc	tcttctacac	840
agtcatacaca	ccatgctca	accccatcat	ctacacctt	cggaacaagg	acgtgaggag	900
ggccctgcga	cacttggtga	agaggcagcg	ccccca			937

<210> 706

<211> 930

<212> DNA

<213> Unknown (H38g555 nucleotide)

<220>

<223> Synthetic construct

<400> 706

atggctggca	acaatttcac	tgaggttacc	gtcttcatcc	tctctggatt	tgcaaatcac	60
cctgaattac	aagtcagttc	tttcttgatg	tttctcttca	tttatctatt	cactgttttg	120
ggaaacctgg	gactgatcac	gttaatcaga	atggattctc	agcttcacac	ccctatgtac	180
tttttctctg	gcaatttagc	atttattgac	atatcttact	cctctactgt	aacacctaaag	240
gcattggtga	atttccaatc	caatcggaga	tccatctcct	ttgttggtctg	ctttgttcaa	300
atgtactttt	ttgttggtg	ggtgtgtgtg	gagtgtttcc	ttctgggata	aatggcctac	360
aatcgctaca	tagcaatctg	caatccctta	ctgtattcag	tagtcatgtc	ccaaaaagtg	420

tccaactggc	tgggagtaat	gccatatgtg	ataggcttca	caagctcgct	gatatctgtc	480
tgggtgataa	gcagtttggc	gttctgtgat	tccagcatca	atcatttttt	ttgtgacacc	540
acagctcttt	tagcactctc	ctgtgtagat	acattcggca	cagaaatggg	gagctttgtc	600
ttagctggat	tcactcttct	tagctctctc	cttatcatca	cagtcactta	tatcatcacc	660
atctcagcca	tcctgaggat	ccagtcagca	gcaggcaggc	agaaggcctt	ctccacctgc	720
gcacccacc	tcattggctgt	aactatcttt	tatgggtctc	tgattttcac	ctatttgcaa	780
cctgataaca	catcatcgct	gacccaggcg	cagggtggcat	ctgtattcta	tacgattgtc	840
attcccatgc	tgaatccact	catctacagt	ctgaggaaca	aagatgtgaa	aaatgctctt	900
ctgagagtca	tacatagaaa	actttttcca				930

<210> 707

<211> 471

<212> DNA

<213> Unknown (H38g556 nucleotide)

<220>

<223> Synthetic construct

<400> 707

atctgtagcc	ccttgcgtga	cagtgctcgc	atatccaata	aggcttgctt	ttctctgatt	60
ttaggggtgt	atataatagg	cctgggttgt	gcacagttc	atacaggctg	tatgtttagg	120
gttcaattct	gcaaatttga	tttgattaac	cattatttct	gtgatcttct	tcccctcta	180
aagctctctt	gctctagtat	ctatgtcaac	aaactactta	ttctatgtgt	tggtgcattt	240
aacatccttg	tcccagctt	gaccatcctt	tgctcttaca	tctttattat	tgccagcatc	300
ctccacattc	gctccactga	gggcagggtc	aaagccttca	gcactttag	ctcccacatg	360
ttggcggttg	taatcttttt	tggtatcgca	gcattcatgt	acttgcagcc	atcttcaatc	420
agctccatgg	accaggggaa	agtatcctct	gtgttttata	ctattattgt	g	471

<210> 708

<211> 529

<212> DNA

<213> Unknown (H38g557 nucleotide)

<220>

<223> Synthetic construct

<400> 708

ctggccccgt	cctccagctc	ggccttgggg	acatggcggt	ggcaatggca	cagcatgact	60
gagcttggtt	tgttggtgct	ctcagggttt	ggttccgtcc	ggggccttct	gttttgggca	120
gtgctctgca	aacatctggg	gaccctgctg	gacaactccc	tgatcgctgt	cctcgccctg	180
gcagcctctg	cctgcgctgg	cccacgcact	tcctcctgca	ccacttctcc	ttaggggagg	240
tcccacgcca	cagcggcgga	gtctcggtat	caggccgatt	cccttcccc	gccgcactag	300
cccaccggta	ggcggtcttc	cgctgctggg	ttcttctgcc	ctccctggca	tcgccgaatg	360
cgcttgcgca	gggcatggc	ctccgcgcgt	gtgacgccat	ctgccggccg	ctgcattcta	420
ctacctgagg	agccctagtc	ttccgagccc	gcttcgcctt	caccttgccc	ttctgcggcg	480
cagcaccacc	cgctacttcc	ggctggattc	tcggcctgtg	ctgagacct		529

<210> 709

<211> 942

<212> DNA

<213> Unknown (H38g558 nucleotide)

<220>

<223> Synthetic construct

<400> 709

atgaccagaa	aaaattatac	ctcaactgact	gagttcgtcc	tattgggatt	agcagacacg	60
ctggagctac	agattatcct	ctttttgttt	tttcttgtga	tttatacact	tacagtactg	120
ggaaatctcg	ggatgatcct	cttaatcagg	atcgattccc	agcttcacac	acccatgtat	180
ttcttctctg	ctaacctgtc	ctttgtggac	gtttgtaact	caactacat	caccccaaag	240
atgctggcag	atattattatc	agagaagaaa	accatctctt	ttgctggctg	cttctctacag	300

atgtacttct	ttatctccct	ggcgacaacc	gaatgcatcc	tctttgggtt	aatggcctat	360
gacaggtag	cggccatag	tcgcccgtg	ctttactcct	tgatcatgtc	caggaccgtc	420
tacctaataa	tggcagccgg	ggcttttgct	gcagggttgc	tgaacttcat	ggtcaacaca	480
agccatgtca	gcagcttgct	attctgtgac	tccaatgtca	tccatcactt	cttctgtgac	540
agccccccac	ttttcaagct	ctcttggtct	gacacaatcc	tgaagaaag	cataagttct	600
attttggtg	gtgtgaatat	tgtggggact	ctgcttgtea	tcctctctc	ctactcctac	660
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tgtgcctctc	acctgacagc	cataattctg	ttctatgcca	cctgcatcta	tacttacctg	780
agacctagtt	ccagctactc	cctgaatcag	gacaaagtgg	cttctgtgtt	ctacacagtg	840
gtgattccca	tgttgaatcc	tctgatctac	agcctcagga	gtaagggaag	aaagaaggct	900
ttagcgaatg	taattagcag	gaaaaggacc	tcttccttct	tg		942

<210> 710

<211> 941

<212> DNA

<213> Unknown (H38g559 nucleotide)

<220>

<223> Synthetic construct

<400> 710

atgaccagaa	aaaattatac	ctcactgact	gagttcatcc	tattgggatt	agcagacacg	60
ctggagctac	agattatcct	ctttctgtta	tttcttggtg	tttacacact	taccgtactg	120
ggaaatatcg	ggatgatcct	cttaatcagg	atcgattccc	ggcttcacac	acccatgtat	180
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acttttctg	gtgtgaataa	ggtcggggct	ctgcttgtea	tcctctctc	ctattcctac	660
gttctcttct	ccattttttc	tatgcattca	ggggagggga	ggcacagagc	tttctccacg	720
tgtgcctctc	acctgacagc	cataatcctc	ttctacacca	cctccatcta	tacctacctg	780
agacctagtt	ccagctactc	cctgatcagg	acaaagtggg	ttctgtgttc	tacacagtgg	840
tgatccccc	attgaatcct	ctgatctaca	gcctcaggaa	taagggaagta	aagaaggctt	900
tagcgaatgt	aattagcagg	aaaaggatcc	cttcatttct	g		941

<210> 711

<211> 939

<212> DNA

<213> Unknown (H38g560 nucleotide)

<220>

<223> Synthetic construct

<400> 711

atgagtgggg	agaatgtcac	caaggtcagc	accttcatcc	tggtgggcct	ccccacggcc	60
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gagaacctgg	ccatcatcct	catcgtctgg	agcagcacct	ccctccacag	gccccatgtac	180
tactttctga	gctccatgtc	tttctggag	atctggtacg	tgtctgacat	cacccccaag	240
atgctggagg	gcttctcct	ccagcagaaa	cgcatctctt	tcgtcgggtg	catgacgcag	300
ctctacttct	tcagctccct	ggtgtgcacc	gagtgtgtgc	ttctgcctcc	atggcctacg	360
accgctacgt	ggccatctgc	cacccgctgc	gctaccacgt	ccttgtgacc	gccgggctgt	420
gtccagctg	gtgggcttct	cctttgtgag	tgcttctcca	tctccatgat	caaggctctgt	480
tttatctcca	gcgtcacgtt	ctgtggctcc	aacgtcttga	acccacttct	tctgtgacat	540
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gcctctcacc	tcaccgtggg	caccgtcttc	tatacagcct	tgcttttcat	gtatgtccgg	780
ccccaaagca	ttgattccca	gagctccaac	aagctcatct	ctgccgtgta	cactgtttgtc	840

acgccataa ttaacccttt gatttactgc ctgaggaaca aggaatttaa ggacgccttg 900
 aaaaaggcct tgggcttggg tcaaacttca cactaagac 939

<210> 712
 <211> 642
 <212> DNA
 <213> Unknown (H38g561 nucleotide)

<220>
 <223> Synthetic construct

<400> 712
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 ggggtgtacc agtgccctcct tcttgagtg atgtcctatg atcgctatgt tgcaatctgc 180
 aatcctctgc gttaccctaa catcatgacc tggaaagtgt gtgtccagct ggcaacagca 240
 ccatggacca gtggtattct ggtgtctgtg gtagacacca ccttcacact gaggctaccc 300
 taccgaggca gtaacagcat tgctcatttc tgggtgtgagg cccctgcact attgatctta 360
 gcatccacag acacccatgc atcagagatg gccatttttc ttacgggggt tgtgattctc 420
 ctcatacctg tttttctgat tctggtatcc tatggccgta tcatagtaac tgtggtcaag 480
 atgaagtcaa ctgtggggag tctcaaggca ttttctacct gtggctccca cctcatggtg 540
 gtcatacttt tttatggatc agcaattatc acttacatga cacccaagtc ttccaaacag 600
 caggaaaaat cgggtgtctgt tttctatcca atagtgtact cc 642

<210> 713
 <211> 948
 <212> DNA
 <213> Unknown (H38g562 nucleotide)

<220>
 <223> Synthetic construct

<400> 713
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 ctacctctca gagtcacact gttcttggta ttcttcttgg tatatacatt aactatggtc 120
 ggaaatatac tcttaataat tctagttaat attaatcaa gccttcaaact tcccatgtat 180
 tattttctta gcaacttatac tttcttagac atcagctggt ctacagcaat cactcctaaa 240
 atgtcggcaa acttcttggc atccaggaaa agcatctctc cttatgggtg tgcactacaa 300
 atgtttttct tcgcttcttt tgctgatgct gagtgcctta tcctggcagc aatggcttat 360
 gaccgctatg cagccatctg caacccactg ctctatacta cactgatgtc taggagagtc 420
 tgtgtctgct tcattgtgtt ggcatatttc agtgggaagta caacatcact ggtccatgtg 480
 tgctcacat tcaggctgtc attttgtggc tccaatatcg tcaatcattt tttctgtgat 540
 atcccacctc tttgtgcttt atcatgtaca gaactcaga tcaaccagct tctgctcttt 600
 gctttgtgca gttcatcca gaccagcact tttgtggtaa tatttatttc ttacttctgc 660
 atcctcatca ctgtgttgag catcaagtcc tcagggtggca gaagcaaac attctccact 720
 tgtgcttccc acctcatagc agtcacctta ttctatggag cgctcctggt tatgtactta 780
 cagcccacca ctagctattc cctagacact gataaggtgg tggcagtggt ttatactggt 840
 gtatttccca tgtttaatcc aataatttat agtttcagaa acaaggatgt gaaaaatgct 900
 ctcaaaaagc tattagaaag aattggatat tcaaatgaat ggtattta 948

<210> 714
 <211> 939
 <212> DNA
 <213> Unknown (H38g563 nucleotide)

<220>
 <223> Synthetic construct

<400> 714
 atgtcaaccc acagaaatgg aaatctctca gtggttcctt tgtgggagag catgctgaag 60
 ggacttgagg gtggcctgga gaaccaggcc ctgctctttg ctgtgttccc aggtctatac 120

atggtgacca	tcccgggaaa	cctcaccatg	accatgggtca	tcatacctgga	cacgcacctg	180
cacttcccag	tgaacttctt	cctcaggagc	ctcccccttc	ctggaccttg	gccatgcctc	240
catcacccca	atgccctggt	taacttctct	tcctcgtcca	aggctcgtcac	ctttgcaggc	300
tgtgctgccc	ggttcttttt	ctccttgctg	tctaccactg	agactttcct	gctggccgtg	360
atggcctatg	actgcttcgt	ggccatctgt	agtctggtgt	ggtgcccagt	gaccacgtgc	420
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gtgacatgcc	ccagctgctc	cggctggcct	gtgcatgcct	ggccctcaat	gagctgacca	600
agttcagcct	ttgtgggctc	atgatgggaa	cgccactctt	gtggtcctcg	tctccttttg	660
ctgtgtcaca	gtgaccatcc	tgaggacacc	ctccgcagcc	agtgcataaa	ggtcttcacc	720
tgtagctccc	acgtgatgac	cgtgtccctg	tttgatggga	ctgtgtttgt	cacatatgcc	780
cagccaggga	ctatggagtc	catggagcag	ggcaagggtg	tgtctgtctt	ctacagcctg	840
gtcatcccga	tgcttggccc	cttcactctac	agcctacgaa	acaaggacat	gaaggaggcc	900
ctgcgagggc	tgggccagag	acaagcactc	atgggaagg			939

<210> 715

<211> 756

<212> DNA

<213> Unknown (H38g564 nucleotide)

<220>

<223> Synthetic construct

<400> 715

atgtacttct	tccttggcaa	cctctccttt	tgtgatatct	gctactctac	tgtctttgct	60
cctaagatgc	tagtcaattt	cctatcaaaa	cataagtcca	gtacattttc	tggtgtgttt	120
ctacagagtt	tcctttttgc	agtatatgta	accacaaagg	acattctcct	gtccatgatg	180
gcttatgacc	attacgtggc	catagctaata	cccttggtgt	atacagtcac	tatggcccaa	240
aaagtttgta	ttcagatggt	ccttgcttct	tacttaggtg	ggctcattaa	ttccctgaca	300
cacacaatag	gtttgctcaa	attagacttc	tgtggtccta	atattgtgaa	tcattatttc	360
tgtgatgttc	ctcctcttct	gaggctttct	tgctctgatg	ctcatatcaa	tgaaatgctg	420
cccttggtct	tctctgggct	cattgcaatg	ttcactttca	ttgtcattat	ggtgtcttat	480
atctgcatca	tcattggccat	ccagagaatc	catgcagctg	agggaaggta	caaagccttc	540
tccacttggt	tctccacact	aaccacggtg	accttattct	atgggtctgt	ttcttttagt	600
tatatccagc	caagttctca	gtattccttg	gaacaggaga	aggctctggc	tgtgttttat	660
acactggtga	tcccctatgct	aaaccactt	atttatagcc	tgagaaataa	ggatgtaaaa	720
gatgcagcca	aaaggttgat	atggtggggg	gaaaaa			756

<210> 716

<211> 954

<212> DNA

<213> Unknown (H38g565 nucleotide)

<220>

<223> Synthetic construct

<400> 716

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ccagggtgct	agtacctgct	cttcctcttc	ttcctgctca	cctacctctt	tgtcctgggtg	120
gagaacctgg	ccatcatcct	caccgtctgg	agcagcacct	ccctccacag	gcccatgtac	180
tactttctga	gtcccatgct	tttcttagag	atctggtacg	tgtctgacat	cacccccaag	240
atgctggagg	gcttctcctc	ccagcagaaa	cgcactctct	tcgtcgggtg	catgacgcag	300
ctctacttct	tcagctccct	ggtgtgcacc	gagtgtgtgc	ttctggcctc	catggcctac	360
gaccgctacg	tggccatctg	ccaccgctg	cgctaccacg	tccttgtgac	cccgggctgt	420
gcctccagct	ggtgggcttc	tcctttgtga	gtggcttcac	catctccatg	atcaaggctc	480
gttttatctc	cagcgtcacg	ttctgtggct	ccaacgtctt	gaaccacttc	ttctgtgaca	540
tttcccccat	cctcaagctg	gcctgcacgg	acttctccac	tgacagagctg	gtggatttca	600
ttctggcctt	catcatcctg	gtgtttccac	tcctggccac	catgctgtca	tatgcgcaca	660
tcaccctggc	tgtcctgcgc	atccctctgc	caccggctgc	tggagagcct	tcttcacctg	720
cgcctctcac	ctcaccgtgg	tcaccgtctt	ctatacagcc	ttgtctttca	tgtatgtccg	780
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acccccatct tgaacccctt gatatactgc ctgaggaata aggaatttaa gaatgccttg 900
 aaaaacagtc ggcttgacga ctgcgccgta gaggggaggc tttctagtct tctg 954

<210> 717
 <211> 960
 <212> DNA
 <213> Unknown (H38g566 nucleotide)

<220>
 <223> Synthetic construct

<400> 717
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 gctgaactga agatggctct cttcgtgttg ttcctgctga tctacacat ttccctggtg 120
 ggaaatatag gaatgctctt tctaattctat gtaactccca aactccacac acccatgtat 180
 tatttctca gctgtctgtc atttgttgat gcctgctatt catcagtttt tgcacccaga 240
 atgctgctga acttctttgt tgagcgggag acaatcttat tctctgcatg tattgtgcag 300
 tattttttat tctgtctctc ccttaccact gagggcttct tgctggccac aatggcttac 360
 gaccgttaca tggccattgt gaacccttta ctttatacag tagctatgac taaaatagtt 420
 tgtattgtgc tcgcatttgg gtcattgtat ggaggtttaa tcaactcatt gacacataca 480
 attggcttgg tgaaactgtc tttctgtggg ccaaagtca tcagtcactt cttctgtgat 540
 cttcccccac tgttgaagct gtcattgtct gagacatcta tgaatgaatt gttgcttttg 600
 atcttctctg gcattattgc cagcctcact tttttgactg tgggtgatctc ctacatcttc 660
 attgttctg ctatcctgag gatccgctaa gcagcaggta gacgtaaagc cttctccacc 720
 tgcacctctc acctgattac cgtgacctta ttctatggat cgataagctt tagttacatt 780
 cagccaaact ccagtatct cctagaacaa gaaaagggtg tgtctgtatt ttataccctg 840
 gtggttcccta tgttaaacc attgatttac agcctaagga acaaggaagt gaaggaagct 900
 gtgaaaaggg ctatagaaat gaaacatttt ccttggttaat ttcattttc catatccaaa 960

<210> 718
 <211> 938
 <212> DNA
 <213> Unknown (H38g567 nucleotide)

<220>
 <223> Synthetic construct

<400> 718
 atgttgggga attactctag cgccactgaa tttttctct taggcttccc tggtcccaa 60
 gaagtacgcc gtatcctttt tgtgaacttc ttcttctgt acgcagtgc agtgatggga 120
 aacacggtca tcatcgtcac tgtctgtgtt gataaacatc tgcagtcccc catgtatttt 180
 ttcttgggccc acctctgtgt cctggagatc ctgatcacat ccaccgctgc cccttttatg 240
 ctgggggggt gctgcttcca agcaccaga tcatgtcttt gacagcctgt gctgcacagc 300
 tatatacctt tctttgggta cctcggagtt ggcattaatg ggagtgatgg ctgtggacca 360
 ttatgtggct gtgtgtaacc ctttgaggta caacatcatt atgaacagca gcacatgtgt 420
 ctggatggtc attgtatcat ggggtgtttg gttccttttt caaatctggc cagtttatgc 480
 cacttttcag cttactttct gcaaatcaaa tgtgttagat catttttact gtgactgagg 540
 acaattgtct aaggtatcct gtgaggacac tcttttcaca gagtttatc tttttctaatt 600
 ggctgttttc attatcattg gttcctttga tccctacgat tgtctcctac acctacatca 660
 tctccaccat cctcaagatc ccgttagcct ctggctggag gaaatccttt tccacttgtg 720
 cctcccaatt cacctgtgtt gtgacggct acagcagctg cttgtttctc tacacgaaac 780
 ccaagcaaac acaggcagcc aagtataacc ggatagcgtc actgctgggt ttagtgggtga 840
 ccccttttct gaacccttct atcttcaccc tgaggaatga caaattcata caggcctttg 900
 gagatggcat gaaacactgc tatcaactcc tcagaatt 938

<210> 719
 <211> 942
 <212> DNA
 <213> Unknown (H38g568 nucleotide)

<220>

<223> Synthetic construct

<400> 719

atataaatgg	ctgacagaaa	tgtcactgtg	ataactgaat	tcacccctcct	ggggttgact	60
gataaccctg	aaatgaatgt	tgtcccttct	gtgctcttct	tattaatcta	tctcattact	120
gtcttgggca	acttttggat	tatcataata	attctggcta	gtgcccaact	ccattcaccc	180
atgtactttt	tccttagcca	gttggcttct	ttagatttct	gctattcttc	agtcttgatt	240
cctaaaatgt	tggatgaatta	catagcagga	cagaaagtca	tctcttatca	cggttgccctc	300
cttcagtatt	cctttgtcag	cttgttcctg	actactgaat	gcttcctcct	ggctgccatg	360
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actttctgaa	tctatttggg	gactgtttct	tacctgctgg	gctctgtaaa	ctccctcacc	480
cacctgagta	gcttactcag	tttgtcttct	tgtgggtcca	atgttatcaa	ccgttatctc	540
tgtgacattc	cattgtctct	ccaactctcc	tgttccaaca	cccaacacag	taagatttta	600
tttactgtcc	tttctggagc	aacatcagtg	actacctttt	tgatagtggg	tagttcctat	660
ctggtaatcc	tactcattgt	cctgaagata	cattccacca	ggggcagaaa	taaagccata	720
tccacatgtg	cctccacact	aatggtagtg	actctcttct	acagaacagt	gatatttact	780
tatctgggag	ccaaccctgg	atactcacag	gatagaccca	aaattctgcc	tgtggagtgc	840
acacttttgt	tgtcaatact	aaatcttcta	atatatagcg	tgagaaacag	agaagtcaaa	900
gaagccataa	aaataattat	taagagaaaa	atacttctct	ag		942

<210> 720

<211> 942

<212> DNA

<213> Unknown (H38g569 nucleotide)

<220>

<223> Synthetic construct

<400> 720

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gaactacatc	atatcctttt	tgctatatcc	ttctttttct	acttggtgac	attaatggga	120
aacacagtc	tcacatgat	tgtctgtgtg	gataaacgtc	tgcatgcccc	catgtatttc	180
ttcctcggcc	acctctctgc	cctggagatc	ctggtcacaa	ccataatcgt	ccccgtgatg	240
ctttggggat	tgctgtctcc	tggtatgcag	acaatatatt	tgtctgcctg	tggtgtccag	300
ctcttcttgt	accttgctgt	ggggacaaca	gagttcgcat	tacttggagc	aatggctgtg	360
gaccgttatg	tggtctgtctg	taaccctctg	aggtacaaca	tcattatgaa	cagacacacc	420
tgcaactttg	tggttcttgt	gtcatgggtg	tttgggtttc	tttttcaaat	ctggccggtc	480
tatgtcatgt	ttcagcttac	ttactgcaaa	tcaaatgtgg	tgaacaattt	tttttgtgac	540
cgaggccaat	tgctcaaaact	atcctgcaat	aatactcttt	tcacggagtt	tatcctcttc	600
ttaatggctg	tttttgttct	ctttgggtct	ttgatcccta	caattgtctc	caacgcctac	660
atcatctcca	ccattctcaa	gatcccgtea	tcctctggcc	ggaggaaatc	cttctccact	720
tgtgcctccc	acttcacctg	tggtgtgatt	ggctacggca	gctgcttgtt	tctctacgtg	780
aaaccacaagc	aaacgcaggc	agctgattac	aattgggtag	tttccctgat	ggtttcagta	840
gtaactcctt	tcctcaatcc	tttcatcttc	accttccgga	atgataaagt	catagaggcc	900
cttcgggatg	gggtgaaacg	ctgctgtcaa	ctattcagga	at		942

<210> 721

<211> 936

<212> DNA

<213> Unknown (H38g570 nucleotide)

<220>

<223> Synthetic construct

<400> 721

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tctgaagagg	tccagatggc	tctgtttatg	ctatttctcc	tcataacct	aattactatg	120
ctggggaatg	tggggatgct	attgataatc	cgctggacc	tccagcttca	cactcccatg	180
tatttttttc	ttactcacct	gtcatttatt	gacctcagtt	actcaactgt	cgtcacacct	240
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atgttctgtt	ttgtcttctt	gggtactgct	gaatgttata	ttctctctct	aatggcctat	360

gatecgtatg	cagcgatctg	cagtcctcta	cactacacag	ttattatgcc	caaaaggctc	420
tgccctcgctc	tcatcactgg	gccttatgtg	attggcttta	tggaactcctt	tgtcaatgtg	480
gtttccatga	gcagattgca	tttctgtgac	tcaaacataa	ttcatcactt	tttctgtgac	540
acttccccaa	tttttagctct	gtcctgcact	gacacagaca	acactgaaat	gctgatattc	600
attatcgctg	gttccaccct	gatgggtgtcc	cttatcacaa	tatctgcatac	ctatgtgtcc	660
attctctcta	ccatcctgaa	aattaattcc	acttcaggaa	agcagaaagc	tttctctact	720
tgcgtctctc	atctcttggg	agtcaccatc	ttctatggaa	ctatgatttt	tacttactta	780
aagccaagaa	agtcttattc	cttgggaaga	gatcaagtgg	ctcctgtgtt	ttatactatt	840
gtgattccca	tgctgaatcc	actcatttat	agtcttagaa	acagagaagt	gaaaaatgct	900
ctcattagag	tcatgcagag	aagacaggac	tccagg			936

<210> 722

<211> 730

<212> DNA

<213> Unknown (H38g571 nucleotide)

<220>

<223> Synthetic construct

<400> 722

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gatgctttta	atttagagac	acgggttttt	ctggaagagg	acttcccatg	tggaattcagc	120
ttgtggattg	tacgtcaatt	gtcttttttc	ttggaaataa	attaatttgc	tcatttaaaa	180
aaatgatgca	ggaagcatat	gagtactttt	tctctgagca	acttggcttt	ttaagtttct	240
gttatgcttc	agtcattaca	tccaaaatgt	ttggaagttt	cttgtacaaa	caaaaaaaat	300
taaccttcaa	tgacatagag	ctgctctctc	accttcatga	ccaccgagtg	cttgctctag	360
ctttcatggc	ctgtgatcaa	tacctgggtca	tttgtaatcc	tcctttgtat	atggtcacca	420
tgtccccccc	gcaaggagtc	tgcatcagc	ttatgcctgc	ctcctatagc	tatagcttcc	480
tgatgacact	ttcacattat	cctcagcctt	tgtctcccct	attgcccctc	tgtatcattg	540
atgttcaatg	gaagcctgtt	ccttatgtac	ttaatgtcca	gaaaattctc	ttgacacaga	600
caggatggcc	tctgtcttct	acacagtagt	cattcccatg	ttgagccctt	tgatctggag	660
cctcaggaac	aaggatgtga	aagatgcctt	gaggaaagtc	attgtcaaca	gaaaccaggc	720
attattttgt						730

<210> 723

<211> 936

<212> DNA

<213> Unknown (H38g572 nucleotide)

<220>

<223> Synthetic construct

<400> 723

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cagccccaaa	ccaaccactc	actggatact	gataagatgg	cttctgtgtt	ttacacattg	840
gtgattccta	tgctgaatcc	cttgatctac	agcctgagga	ataatgatgt	aaatgttgcc	900
ttaaagaaat	tcatggaaaa	tccatgttac	tccttt			936

<210> 724

<211> 481
 <212> DNA
 <213> Unknown (H38g573 nucleotide)

<220>
 <223> Synthetic construct

<400> 724
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 catcatagta tgtgttgaga aatgcctgct gtctctccta tatttattct atgggtgacct 180
 ctctgtcatg gaaatcctta tcacatatac tgcgtgttccc ttgatgctca ggggttggtta 240
 ctttccatga ttcaaacaat acctttaatg acatgtgctg tccaactcta tatgaacttt 300
 tttgggggta cacaaaattt gcattactgg gagtgatgac tgtgaacctat tatgtggctc 360
 tctgtaactc tttgaagtaa aacatcatta tgagcagaca cactgcatct ggctggtaat 420
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 t 481

<210> 725
 <211> 971
 <212> DNA
 <213> Unknown (H38g574 nucleotide)

<220>
 <223> Synthetic construct

<400> 725
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 ctgacacaga tgtttttctt ggctcctttt gcatgtatag aaggcatgat cctgactgtg 360
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 cctcacctct gtgtcttctt cattttgatg tctttttcc ttagcctgtt ggattcccag 480
 ctgcacagtt ggattgtgtt acaattcaca atcatcaaga atgtggaaat ctctaatttt 540
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 ttcacatatt tccatagtag tatgtttgtt tttcttccca tttcagcaat ccttttatct 660
 tactataaaa tgcgcacctc cattctcagg atttcatctt cagatgggaa gtataaagcc 720
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 caaagtgcct tgcggaggct gcgcagcaga acagtcgaat ctcatgatct gttccatcct 960
 ttttcttggtg t 971

<210> 726
 <211> 960
 <212> DNA
 <213> Unknown (H38g575 nucleotide)

<220>
 <223> Synthetic construct

<400> 726
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 gatccagaac tgcagcccat cctggctggg ctgtccctgt ccatgtatct ggtcacgggtg 120
 ctgaggaacc tgctcatcat cctggctgtc agctctgact cccacctcca cactcccatg 180
 tgcttcttcc tctccaacct gtgctgggct gacatcggtt tcacctcggc cacggttcct 240
 aagatgattg tggacatgca gtcgcatagc agagtcattc cttatgaggg ctgcctgaca 300
 aggatgtctt tcttggctct ttttgcatgt acagaagaca tgcttctgac tgtgatggcc 360
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gagccatctc	aacttgtcaa	ccttgccagt	tctgacagcg	tcgtcaatag	catattcata	600
tatttcgata	gtactatgtt	tggttttctt	cccattttag	gggtcctttt	gtctcactat	660
aaaattgtcc	cctccattct	aaggatttca	tcgtcagatg	ggaagtataa	agtcttcgct	720
acctgtggct	ctcacctggc	agttgtttgc	tgattttagt	gaacaggcat	tgacatgtac	780
ctgacttcag	ctgtgtcacc	acccacaggg	aatgggtgtg	tggcatcagt	gatgtatget	840
gttttcaccc	ccatgtctga	ccctttcatc	tacagcctga	gaaacaggga	catacaaagt	900
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<210> 727

<211> 806

<212> DNA

<213> Unknown (H38g576 nucleotide)

<220>

<223> Synthetic construct

<400> 727

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attgattttt	acaattgtat	tgttattttac	accaataaaa	tgtaaatttt	tgttgtggat	180
cagaataaca	tttcttatta	tgcattgtgc	acacatatga	ctttcttatg	ttcattatca	240
ctgaactttt	aatcttggta	agcatggcct	atgattgcta	tgtgggtgaac	tccaaccctt	300
tgtttttacat	tgttatcatg	tgtctgtgac	tgtaacatgt	gctgatgagc	attccatacc	360
tctgtaatac	atttcaatct	ctaattatca	caatgacctt	tttttgacct	tctgtagctt	420
tatcatcagt	catttctatt	gttatgatgt	tctcttcttc	catatgctat	gctcaaattgc	480
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ggatctctac	tttttgatat	ggataaatgg	cctccttggt	ctacacttta	atgacctca	720
ggtttaacct	cttgatctac	agcttttagca	acttaggggt	taaaaatgtc	ttttatagag	780
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<210> 728

<211> 384

<212> DNA

<213> Unknown (H38g577 nucleotide)

<220>

<223> Synthetic construct

<400> 728

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aatggcatga	acatgggact	cacctatctg	gatgacagag	acgacagact	acacaccctc	180
atatacattt	tcctctcaca	cctggccatc	aatgacatgt	actatgcttc	caacaatgtt	240
ccaaagaggg	aggtgaacca	aatgaaccag	aaaaaaaaaa	actttgttct	atggataaag	300
cagatatttt	tgtatttggc	ttttgtctac	acagagtgc	taatttaggc	aatgatgtcc	360
tgtaatagat	atgtggcaat	ctgc				384

<210> 729

<211> 921

<212> DNA

<213> Unknown (H38g578 nucleotide)

<220>

<223> Synthetic construct

<400> 729

atggggccaac	acaatctaac	agtgctaact	gaattcattc	tgatggaact	cacaaggcgg	60
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cctgagctgc agattcccct ttttggagtc ttctctgca tctacctaata cacagtgggtg 120
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cagcccaatt ccactcactt ctttgatact gataaaatgg cttctgtgtt ttacacttta 840
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```

<210> 730

<211> 654

<212> DNA

<213> Unknown (H38g579 nucleotide)

<220>

<223> Synthetic construct

<400> 730

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ctgagggttt catcgtcagg tgggagggtat aaagccctct ccacctgtgg gtctcacgtg 540
tcagttgttt gctgagttta tggacaggc gttggagggt acctcagttc ggatgtgtca 600
ttttcccca gaaagggtgc agtggcctca gtgatgtacg cggttgtcac cccc 654

```

<210> 731

<211> 683

<212> DNA

<213> Unknown (H38g580 nucleotide)

<220>

<223> Synthetic construct

<400> 731

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cccaaagatg attgtggaca tccagtctca cagcagagtc acctcctatg caggctgcct 120
gactcagatg tctctctttg ccatttttgg aggcattgaa gagagacatg ctctgtagtg 180
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acataatcat gtatttccct gcagccatat ttggttttct tcccatctcg gggaccttt 480
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aggccttctc caccaggggg tctcacctgt cagttgtttg ctgattttat ggaacaggca 600
ttggaggcta cctcagttca gatgtgtcat cttccccgag aaaggctgca gtggcctcag 660
tgatgtacac ggtggccatc ccc 683

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<210> 732

<211> 582

<212> DNA

<213> Unknown (H38g581 nucleotide)

<220>

<223> Synthetic construct

<400> 732

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gggatgctgg	tcaacctctg	ggagccaaag	aagaccatca	tcttactggg	ctgctctgtc	120
cagttcttca	tcttctctgt	cctggggacc	actgagtga	tcctcctgac	ggtgatggcc	180
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acaccatcca	ccctccactt	gcctttctgc	cccgatcggc	aggtggatga	ttttgtctgt	360
gaggtcccag	ctctaattcg	actctcctgt	gaagacacct	cctacaatga	aatccagttg	420
gctgttgcca	gtgtcttcat	cttggctgtg	cctctcagcc	tcacccctgt	ctcttatgga	480
gccattgcct	gggcagtgtc	aaggactaac	tctgcaaaag	ggcagaggaa	agcttttggg	540
acctgctcct	cccctctcac	tgtggtcacc	ctcttctaca	gc		582

<210> 733

<211> 959

<212> DNA

<213> Unknown (H38g582 nucleotide)

<220>

<223> Synthetic construct

<400> 733

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catccaaagc	tggagaagac	attcttctgt	ctcatcctgc	tgatgtacct	ggtgatccta	120
ctgggcaatg	gggtcctcat	cctggtgacc	atccttgact	cccgcctgga	cacaccatg	180
tactttctcc	tggggaacct	ctccttctct	gacatctgct	atacaacctc	ctcatccttg	240
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tctcccttgc	catggggagc	acagagtgtg	ttctcctgag	catgatggcg	tttgatcgct	360
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ccaccatcct	gaggatcccc	tcagctgagg	ggaggaaaaa	ggccttctcc	acctgctctg	720
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agtctaagga	ccactggga	gcagacaaac	aggaccttgc	agacaaactc	atttcccttt	840
tctatggggt	ggtgaccccc	atgctcaacc	ccatcatcta	cagcctgagg	aacaagggaag	900
tgaaggctgc	tgtgagggaac	ctggtatttc	agaaacgctt	cctgcagtga	tggtggagg	959

<210> 734

<211> 954

<212> DNA

<213> Unknown (H38g583 nucleotide)

<220>

<223> Synthetic construct

<400> 734

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cacccaaagc	tggagaaaac	gttctttgtg	ctcatcctgc	tgatgtacct	ggtgatccta	120
ctgggcaatg	gggtcctcat	cctgatgact	gtgtccaact	cccacctgca	catgccatg	180
tactttctcc	tggggaacct	ctccttctct	gacatctgct	atacaacata	ctcagtcctc	240
ctcatccttg	acagcttctt	gacccccagg	aaaaccatct	ccttctcagc	ctgtgcagtg	300
cagatgttcc	tctcctttgc	catgggagcc	acagagtgtg	ttctcctgag	catgatggcg	360
tttgatcgct	acgtggccat	ctgcaacccc	cttaggtacc	ctgtggtcat	gagcaaggct	420
gcctacatgc	ccatggctgt	cggctcctgg	gtagctggaa	gcactgcttc	catggtgcag	480

acatcccttg	caatgagget	gcccttctgt	ggagacaaca	tcatcaatca	cttcacctgt	540
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<210> 735

<211> 962

<212> DNA

<213> Unknown (H38g584 nucleotide)

<220>

<223> Synthetic construct

<400> 735

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ctgggcaacg	gggtcctcat	cctggtgacc	atccttgact	cccgcctgca	cacacccatg	180
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caatgtgact	gcccttctgt	ggggacaatg	tcataaatca	cttcacctgt	gagatcctgg	540
cagttctaaa	gttggcctgt	gctgacatct	gcataacgt	gatcagcatg	gttgtgacca	600
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agtctaagga	cccaatggga	gcagacaaac	aggaccttgc	agacaaactc	atctccattt	840
tctatggagt	ggtgaccccc	attctcaacc	ccatcatcta	cagcccagg	aacaaagatt	900
tgaaagctgc	tatgaggaac	ctgggtggctc	aaaaacacct	aacagagtga	ctatcacaga	960
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<210> 736

<211> 375

<212> DNA

<213> Unknown (H38g585 nucleotide)

<220>

<223> Synthetic construct

<400> 736

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gaggtcctgg	ctgtcctgaa	gttggcctgt	gctgacatct	ctatcaacat	gatcaggcaa	120
aaggccttct	ccacctgtc	tgeccacctc	acagttgtgg	tcatcttcta	caggaccatc	180
ctcttcacgc	atgggaagcc	caagtcgaag	gacccactgg	gggcagacaa	gcaggatttt	240
gcagacaaac	tcatctccct	ctcctatgga	gtggtcaccc	ccatgctgaa	caccatcatc	300
tacagcctga	ggaaaaaggg	tgtgaaggct	gctgtgaaga	acctggtatt	tcagaaaccc	360
ctaactgaat	gacag					375

<210> 737

<211> 648

<212> DNA

<213> Unknown (H38g586 nucleotide)

<220>

<223> Synthetic construct

<400> 737

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cggcatcaca	ccatcaccta	tacgggttgc	ctcacgcaaa	tgtatttctt	tctgatgttt	120
ggtgatctag	acagcttctt	cctggctgcc	atggcgtatg	accgctatgt	ggccatctgc	180
cacccctct	gctactccac	ggtcatgagg	ccccaaagtct	gtgccctaata	gcttgcatgt	240
tgctgggtcc	tcaccaatat	cggtgccctg	actcacacgt	tcctcatggc	tcggttgctc	300
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gtttgtgtgt	tctatgggac	cctcttcagt	gcctacctgt	gtcctccctc	cattgcctct	600
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<210> 738

<211> 957

<212> DNA

<213> Unknown (H38g587 nucleotide)

<220>

<223> Synthetic construct

<400> 738

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cacccagagc	tggaaaagac	attcttctgt	ctcatcctgc	tgatgtacct	cgtgatcctg	120
ctgggcaatg	gggtcctcat	cctggtgacc	atccttgact	cccgcctgca	cacgcccattg	180
tacttcttcc	tagggaaacct	ctccttccctg	gacatctgct	tcactacctc	ctcagtccca	240
ctggctcctg	acagcttttt	gactccccag	gaaaccatct	ccttctcagc	ctgtgctgtg	300
cagatggcac	tctcctttgc	catggcagga	acagagtgtc	tgctcctgag	catgatggca	360
tttgatcgct	atgtggccat	ctgcaacccc	cttaggtact	ccgtgatcat	gagcaaggct	420
gcctacatgc	ccatggctgc	cagctcctgg	gctattgggtg	gtgctgcttc	cgtgggtacac	480
acatccttgg	caattcagct	gcccttctgt	ggagacaatg	tcatcaacca	cttcacctgt	540
gagattctgg	ctgttctaata	gttggcctgt	gctgacattt	ccatcaatgt	gatcagcatg	600
gagggtgacga	atgtgatctt	cctaggagtc	ccgggttctgt	tcatctcttt	ctcctatgtc	660
ttcatcatca	ccaccatcct	gaggatcccc	tcagctgagg	ggaggaaaaa	ggtcttctcc	720
acctgctctg	cccacctcac	cgtgggtgatc	gtcttctacg	ggaccttatt	cttcatgtat	780
gggaagccta	agtctaagga	ctccatggga	gcagacaaag	aggatctttc	agacaaactc	840
atcccccttt	tctatgggg	ggtgaccccg	atgctcaacc	ccatcatcta	tagcctgagg	900
aacaaggatg	tgaaggctgc	tgtgaggaga	ctgctgagac	caaaaggctt	cactcag	957

<210> 739

<211> 653

<212> DNA

<213> Unknown (H38g588 nucleotide)

<220>

<223> Synthetic construct

<400> 739

ctgcctgaca	tcggttttcac	ctccaccacg	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcatctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	tgtgatagcc	tatgagcgg	ttgtagccat	180
ctgtcaccct	ctatatcatt	cagccatcat	gaacccatgt	ttctgtggct	ttctagtttt	240
gttgtctttt	tttttctcag	tcttttagac	gccagctgc	acaacttgat	tgctttacaa	300
aggacctgct	tcaaggatgt	ggaaattcct	aatttcttct	gtgaccttc	tcaactcccc	360
atcttgcata	ttgtggcacc	ttcaccaata	acataatcat	gtatttccct	gccgccatat	420
ttggttttct	tcccatctcg	gggacctttt	tctcttacaa	taaaattggt	ttctccattc	480
taagggtttc	atcatcaggt	gggaagtata	aggccttctc	cacctgtggg	tctcacctgt	540
cagttgtttg	ctgattttat	ggaacaggca	ttggaggcta	cctcggttca	gatgtgtcat	600
cttccccgag	aaaggctgca	gtggcctcag	tgatgtacac	ggtgggtcatc	ccc	653

<210> 740

<211> 648
 <212> DNA
 <213> Unknown (H38g589 nucleotide)

<220>
 <223> Synthetic construct

<400> 740
 tttgtggatg tctgcttctc ctctaccact gtcctaaag ttctggccaa ccatatactt 60
 gggagtcagg ccatttcctt ctctgggtgt ctcaccacg tgtattttct cgctgtgtgt 120
 ggtaacatgg acaatttcct gctgggtgtg atgtcctatg accgatttgt ggccatatgc 180
 caccctttac actacacaac aaagatgacc cgacagctct gtgtcctgct tgttgtgggg 240
 tcatgggttg tagccaacat gaattgtctg ttgcacatac tgctcatggc tcgactctcc 300
 ttctgtgcag acaacatgat cccccacttc ttctgtgatg gaactcccct cctgaaactc 360
 tcctgtctcag acacacatct caatgagctg atgattctta cagagggagc tgtggtcatg 420
 gtcaccccat ttgtctgcat cctcatctcc tacatccaca tcacctgtgc tgtcctcaga 480
 gtctcatccc ccaggggagg atggaaatcc ttctccacct gtggctccca cctggctgtg 540
 gtctgcctct tctatggcac cgtcatcgtc gtgtatttca acccatcatc ctctcactta 600
 gctgggaggg acatggcagc tgcagtgtat tatccagtgg tgacccca 648

<210> 741
 <211> 988
 <212> DNA
 <213> Unknown (H38g590 nucleotide)

<220>
 <223> Synthetic construct

<400> 741
 atggcagaag aaaataagat tctgggtgact cactttgtcc tcacaggact cacagatcat 60
 ccagggtcgc aggcgcccct gttcctgggtg ttcttgggtca tctacctcat caccctgggtg 120
 ggcaaccttg gcctgatggc tctcatctgg aaggaccccc accttcacac ccccatatac 180
 ttattttctg gcagtttagc ctttgcagat gcatgcactt catcctctgt aacttctaag 240
 atgcttatca atttttttat caaagaatca tatgctatcc atggctaagt gtgccacca 300
 gttttacttt tttggttcca atgcaaccac agaatgcttc ctgctggtag tgatggccta 360
 tgaccgctat gtagccatat gcaatccctt gctttatcca gtggtgatgt ccaatagcct 420
 ctgtactcag tttataggta tttcatattt tattggtttt ctgcattcag cgattcatgt 480
 gggtttgtta tttagattaa ctttctgcag gtccaatatt atacattatt tctactgtga 540
 aattttacag ctgttcaaaa tttcttgac caatcctaca gttaatatac ttctgatttt 600
 catcttttca gcatttatac aagtcttcac ttttatgact cttatcgtct cttactccta 660
 tattctctct gccatcctga aaaagaagtc tgagaagggt agaagcaaag ccttctctac 720
 ttgcagtgcc catctgctct ctgtctcttt gttctacggc accctcttct tcatgtatgt 780
 gagttctagg tctggatcag ctgcagatca ggccaaaatg tattctttat ttacacaat 840
 aataattcct ttactaaatc cttttattta cagcctaagg aacaaagagg ttatagatgc 900
 cctgagaaga atcatgaaga aataaatagt tgtcagacaa cattcaaacc atttcttctt 960
 tatattctgc tgaagaaaac cccaagtc 988

<210> 742
 <211> 636
 <212> DNA
 <213> Unknown (H38g591 nucleotide)

<220>
 <223> Synthetic construct

<400> 742
 tgtcactccc agggtcacgg ctagcagggc taggttactt agagggtagg aggctaagtt 60
 cctcgtacaa tgcttgtgct gctcagatgt tcttttttgt agccttggcc acagtggaaa 120
 atatcgctgt tgacatcaat ggcctatgac cactatatag cagtgtgcaa acccctacac 180
 tacactacca ccacgatagc cagtgtatgt gctcatctgg tcataggctc ctatgtctgt 240
 ggctttctaa atgcctccct ccgcattgtg gacatattca gtctctcttt ctgtaagtcc 300

aatcttgtcc atcacctttt ctgtgatgtt ccaccagtea tggetgtgtc ttgctctggt	360
aaacacatta gcaagaagat tctgggtttt atgtcaagct tcaatgtctt tttggctctt	420
ctagttatct tgacctccta cctgttcata ttcatcacca tcttgaagat gcaactcagct	480
cagggacact taaaagcttt gtccacctgt gcctctcacc tcattgcagt ctccatcttc	540
tatggaacta ctatctttat gtacttacag cctagtcca gccattccat ggacacagat	600
gaaatggcat ccttgttcta tgetgtgttc atctcc	636

<210> 743

<211> 942

<212> DNA

<213> Unknown (H38g592 nucleotide)

<220>

<223> Synthetic construct

<400> 743

atgggggaca accaatcacg ggtcacagaa ttcatcctgg ttggattcca gctcagtgtg	60
gagatggaag tgctcctctt ctggatcttc tccctgttat atctcttcag cctgctgggg	120
aatgggggtca tctttgggct catctgcctg gactctaagc ttcacacccc catgtacttc	180
ttcctctcac acctggccgt cattgacatg tcctatgctt ccaacaatgt tccaagatg	240
ctggcaaac tagtgaacca gaaaagaact atctcgttca tctcttgc ataatgcagact	300
tttttgtatt tggcttttgc tgttacagtg tgcttgattt tgggtggtgat gtcctatgac	360
agatttgtgg ccactctgcca tccctgcat tacactgtca tcatgagctg gagagtgtgc	420
actgtcctgg ctgtggcttc ctgggtgttc agcttcctcc tggctctggt ccatttagtt	480
ctcattctga ggctgccctt ctgtgggccc caggaggtga accacttctt cggtgaaatc	540
ctgtctgtcc tcaagtgggc ctgtgtgac acctggctca accaggtggt catctttgca	600
gctgtcatgt tcatcctggt aggggtgactc tgcctgggtc tggctctcta cttgcacatc	660
ctggcgccca tcttgaggat ccagtctggg gagggccgca gaaaggcctt ctctacctgc	720
tcctccacc tctgcgtggt ggggcttttc ttggcagcg ccattgtcat gtacatggcc	780
cccaagtcaa gccattctca agaacggagg aagatccttt cctgtttta cagccttttc	840
aaccgatcc tgaaccccct catctacagc cttaggaatg cagaggtgaa aggggctcta	900
aagagagtcc tttggaaaca gagatcaatt gaagaatcat tt	942

<210> 744

<211> 648

<212> DNA

<213> Unknown (H38g593 nucleotide)

<220>

<223> Synthetic construct

<400> 744

ttctctgacc tctgcttctc ttccgtgacc attcccaagt tgttacagaa catgcagaac	60
caggacccat ccattccccta tgcggactgc ctgacccaaa tgtacttctt cctgttattt	120
ggagacctgg agagcttctt ccttgtggcc atggcctatg accgctatgt ggccatctgc	180
ttccccctgc actacaccgc catcatgagc cccatgctct gtctcgccct ggtggcgctg	240
tcctgggtgc tgaccacctt ccattgccatg ttacacactt tactcatggc caggttgtgt	300
ttttgtgcag acaatgtgat cccccacttt ttctgtgata tgtctgctct gctgaagctg	360
gccttctctg aactcagat taatgaatgg gtgatattta tcatgggagg gctcattctt	420
gtcatcccat tctactcat ccttgggtcc tatgcaagaa ttgtctctc catcctcaag	480
gtcccttctt ctaagggtat ctgcaaggcc ttctctactt gtggctccca cctgtctgtg	540
gtgtcactgt tctatggaac cggtattggt ctctacttat gctcatcagc taatagttct	600
actctaaagg acactgtcat ggctatgatg tacactgtgg tgacccc	648

<210> 745

<211> 936

<212> DNA

<213> Unknown (H38g594 nucleotide)

<220>

<223> Synthetic construct

<400> 745

atggatggag	agaatcactc	agtgggtatct	gagtttttgt	ttctgggact	cactcattca	60
tgggagatcc	agctcctcct	cctagtgttt	tcctctgtgc	tctatgtggc	aagcattact	120
ggaaacatcc	tcattgtgtt	ttctgtgacc	actgacctc	acttacactc	ccccatgtac	180
tttctactgg	ccagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
atgatttatg	acctgttcag	aaagcgcaaa	gtcatctcct	ttggaggctg	catcgctcaa	300
atcttcttca	tccacgtcgt	tgggtggtgtg	gagatgggtgc	tgctcatagc	catggccttt	360
gacagatatg	tggccctatg	taagccccctc	cactatctga	ccattatgag	cccaagaatg	420
tgcttttcat	ttctggctgt	tgctgggacc	cttgggtgtca	gtcactccct	gttccaactg	480
gcatttcttg	ttaatttagc	cttctgtggc	cctaattgtgt	tggacagctt	ctactgtgac	540
cttctctggc	ttctcagact	agcctgtacc	gacacctaca	gattgcagtt	catggtcact	600
gttaacagtg	ggtttatctg	tgtgggtact	ttcttcatac	ttctaattctc	ctacgtcttc	660
atcctgttta	ctgtttggaa	acattcctca	gggtgttcat	ccaaggccct	ttccactctt	720
tcagctcaca	gcacagtggg	ccttttgttc	tttgggtccac	ccatgtttgt	gtatacacgg	780
ccacacctta	attcacagat	ggacaagtgt	ctggctatgt	ttgatgcagt	tctcactcct	840
tttctgaatc	cagttgtcta	tacattcagg	aataaggaga	tgaaggcagc	aataaagaga	900
gtatgcaaac	agctagtgat	ttacaagagg	atctca			936

<210> 746

<211> 384

<212> DNA

<213> Unknown (H38g595 nucleotide)

<220>

<223> Synthetic construct

<400> 746

atgaactcag	agaacctcac	ccggggccg	gttgccctg	ctgaattcgt	cctcctgggc	60
atcacaaatc	gctgggacct	gcgtgtggcc	ctcttctga	cctgcctgcc	tgtctacctg	120
gtgagcctgc	tgggaaacat	gggcatggcg	ctgctgatcc	gcattggatgc	ccgggtccac	180
acacctatgt	acttcttctc	ggccaacctc	tccctgtctg	atgcctgcta	ttcctccgcc	240
atcggcccca	agatgctagt	ggacctgctg	ctgccccgag	ccaccatccc	ttacacagcc	300
tgtgccctcc	agatgtttgt	ctttgcaggt	ctggctgata	ctgagtgttc	aatgcaatta	360
atgccaaaag	tgaacaaaaa	tgtat				384

<210> 747

<211> 810

<212> DNA

<213> Unknown (H38g596 nucleotide)

<220>

<223> Synthetic construct

<400> 747

atgaccattg	tcttgctttc	agctctggat	tcccggctgc	acacaccaat	gtatttcttt	60
ttggcaaac	tctcattcct	ggacatgtgt	ttcaccacag	gttccatccc	tcagatgttc	120
tacaaccttt	gggtccaga	taagaccatc	agctatgtgg	gttgtgccat	ccagctgtac	180
tttgcctcgg	ccctgggagg	ggtggagtgt	gtcctcctgg	ctgtcatggc	atatgaccgc	240
tatgctgcag	tctgcaaac	cctgcactac	accatcatca	tgcacccacg	tctctgtgga	300
cagctggcct	cagtggcatg	gctgagtggc	tttggaatt	ctctcataat	ggcaccaccg	360
acattgatgc	taccccgctg	tgggcacaga	cgagtggacc	actttctctg	tgagatgcca	420
gcactaattg	gtatggcctg	tgtagacacc	atgatgcttg	aggcactggc	ttttgcctg	480
gcaatcttta	tcactcctgg	accactcatc	ctcattctca	tttcttatgg	ttacgttgga	540
ggaacagtgc	ttaggatcaa	gtcagctgct	gggcgaaaga	aagccttcaa	cacttgcagc	600
tcgcatctaa	ttgttgtctc	tctcttctat	ggtacaatca	tatacatgta	cctccagcca	660
gcaaatactt	attcccagga	ccagggcaag	tttcttacct	ttttctacac	aattgtcact	720
ccagtggtta	acccctgat	ctatacacta	agaaacaaag	atgttaaaga	ggccatgaag	780
aagtgctag	ggaaggggag	tgcaaaata				810

<210> 748

<211> 342
 <212> DNA
 <213> Unknown (H38g597 nucleotide)

<220>
 <223> Synthetic construct

<400> 748
 atttgctttc ctctccacta tcccatccgt ataagcaaaa gagtgtgtgt gatgatgata 60
 acaggatctt ggatgataag ctctatcaac tcttgtgctc acacagtata tgcactctgt 120
 atcccatatt gcaagtccag agccatcaat cattttttct gtgatgttcc agctatgttg 180
 acgctagcct gcacagacac ttgggtctat gagagcacag tgtttttgag cagcaccatc 240
 tttcttgtgc ttcttttcac tggattgca tgttcctatg gccgggttct ccttgctgtc 300
 taccgcatgc actctgcaga agggaggaag aaggcctatt ca 342

<210> 749
 <211> 635
 <212> DNA
 <213> Unknown (H38g598 nucleotide)

<220>
 <223> Synthetic construct

<400> 749
 tttgtggaca ttgcctgttc ctcagccaca gcaccaaga tgattgtaga ctctgtttct 60
 gagaaaaaga ctatttccta ctggggctgt ataactcaga tgtttacctt ccactttttt 120
 ggttgtgctg acatttttgt ttgactgtc atggcttttg atcgctatgc tgctatctgc 180
 caaccctcc gttacactgt catcatgagt gctaagtctt atactgtgct ggcactactg 240
 tcctggttgg gggccctggg tcattccttt gtccagaccc tcctgacctt ccagctgccc 300
 ttctgtaatg ctcaggttat agaccattac ttttgtgatg tccaccagt cctaaaaactt 360
 gcctgtgctg atacaactct ggtaagtatg ttgggtgttg ccaacagtgg tctcatctcc 420
 ctgggggtgt tcctcattct ttggccctcc tacacagtca ttctgttttag tcttcaaaaa 480
 cagtctgcag agagctgaca caaagtcttc tctacctgtg gatctcatct gactatagta 540
 actttcttct ttgttccgtg tacctttatt tatctccatc cactactttc ccattggata 600
 aagctgtgtc tgtgttctat accaccatca cccca 635

<210> 750
 <211> 633
 <212> DNA
 <213> Unknown (H38g599 nucleotide)

<220>
 <223> Synthetic construct

<400> 750
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 gaagatagaa ctatctcctt cacaggatgc accatgcagt tattctttgt ctgcatattt 120
 gtagtaacag aaacatgcat gctggcagt atggcctatg accgatatgt ggcggtgtgt 180
 accctcttct ctacacagtt gcaatgtacc agaggctttg ctccttggtta gtggctacat 240
 catactgctg ggggatagtc tgttccctga cacttaccta gtttctactg gagttatcct 300
 tcagaggaaa taatatcatt aataactttg tctgtgagca cgctgccatt gttgctgtgt 360
 cttgctctga cccctgtgtg agccagtaga tcactttagt ttctgccaca ttcaatgaaa 420
 taagcagcct gcttccatg ctttcatttt tatcactgtc atgaagacgg cttccactgg 480
 ggggcgcaag aaagcgttct ccacgtctgc ctccactga cggccattac cattttccat 540
 gggactattc ttttctcta ctgtgttct aacgccaaaa gttcgtggct catggtcaag 600
 gtggcctctg gcttttacac agtggtcatg ccc 633

<210> 751
 <211> 646
 <212> DNA
 <213> Unknown (H38g600 nucleotide)

<220>

<223> Synthetic construct

<400> 751

tttgtagaca	tctgtgttac	ctccaccaca	gtcccaaaga	cactgtcaaa	catccggaca	60
cagagtaaag	tcatcaccta	tgcagggtgc	atcaccacaga	tgtacttttt	tgtactcttt	120
atagtgttgg	acagcttact	cttgaccgtg	atgggcctatg	accagtttgt	ggccatctgt	180
cacccctgc	actacacggc	catcgtgaac	cctcggtct	gtggactgct	ggttctggcg	240
tcttgatca	tgagtgcct	gaattccttg	atagaaagct	taatgggtgt	gccactgctc	300
ttttgtacag	acttgaaaat	ccccacttt	ttctgtgaac	ttaatcagat	aatccgcagt	360
gcctgttctg	acacctttct	taatgacatg	gtgatgtatt	tgtagctgt	gcttctaggt	420
aggggatgtt	tactgggat	cctgtactct	tactttaaga	cagtttctc	catacgtgca	480
atctcatcag	ctcaggggaa	gtacaaggca	ttttccacct	gtgcatcgca	cctctcagtt	540
gtctccttat	tttattgtat	gggccttggg	gtgtacctta	gtgctgctgc	aaccacaac	600
tcactctcaa	gtgcaacagc	ctctgatgta	cactgtggtc	accccc		646

<210> 752

<211> 342

<212> DNA

<213> Unknown (H38g601 nucleotide)

<220>

<223> Synthetic construct

<400> 752

atttgctttc	ctctccacta	tcccatccgt	atgagaaaaa	gagtgtgtgc	actgatgata	60
acaggatctt	ggatgatagg	ctccatcaac	tcttgtgctc	acacggtata	tgcactccgt	120
atcccatatt	gcaagtccag	agccatcaat	cattttttct	gtgatgttcc	agctatgttg	180
accctagcct	gcacggatac	ctgggtctat	gagtgcacgg	tgtttttgag	caccaccatt	240
tttcttgtgt	ttcccttcat	ttgtattgca	tgttcctatg	gccggattct	ccttgtctgc	300
taccacatgc	actctgcaga	agggaggaag	aaggcctatt	cg		342

<210> 753

<211> 648

<212> DNA

<213> Unknown (H38g602 nucleotide)

<220>

<223> Synthetic construct

<400> 753

cttgtcgatg	tctcctatgc	cacaagtgtg	gtccctcagc	tgctggcaca	ttttcttgca	60
gaacataaag	ccatcccat	ccagagctgt	gcagcccagt	tatttttctc	cctggccttg	120
gggtggattg	agtttgttct	cctggcggtg	atgggctatg	accgctatgt	ggctgtgtgt	180
gatgccctgc	gatactcggc	catcatgcat	ggagggctgt	gtgctagggt	ggccatcaca	240
tcttgggtca	gtgggttcat	cagctctcct	gtgcagactg	ctatcacctt	tcagctgccc	300
atgtgcagaa	acaagtttat	tgatcacata	tcctgtgaac	tcctagctgt	ggtcaggctg	360
gctcgtgtgg	acacctctc	caatgaggtc	accatcatgg	tgtctagcat	tgttcttctg	420
atgacacct	tctgctgggt	tcttttgtcc	tacatccaga	tcactctccac	catcctaaag	480
atccagtcca	gagaagggaag	aaagaaagct	ttccacacgt	gtgcctctca	cctcacagtg	540
gttgccctgt	gctatgggtg	ggccattttc	acttacatcc	agccccactc	cagtcctct	600
gtccttcagg	agaagttgtt	ctctgtcttt	tatgccattt	taacacca		648

<210> 754

<211> 635

<212> DNA

<213> Unknown (H38g603 nucleotide)

<220>

<223> Synthetic construct

<400> 754
 tttgtggaca ttgcctgttc ctcagccaca gcacccaaga tgattgaaga ctttgtttct 60
 gagaaaaaga ctatttccta ctggggctgt ataactcaga tgtttacctt ccactttttt 120
 ggttgtgctg agatttttgt cttgactgtc atggcttttg atcgctatgc tgctatctgc 180
 caacccctcc gttacactgt catcatgagt gctaagtctt atactgtgct ggcactactg 240
 tcctgggttg gggccctggg tcatttcctt gttcagaccg tcctgacctt ccagctgccc 300
 ttctgtaatg ctcagggttat agaccattac ttttgtgatg tccacccagt cctaaaactt 360
 gctgtgctg atacaactct ggtaaatatg ttgggtggtg ccaacagtgg tctcatctcc 420
 ctgggggtgt tcctcattct tttggcctcc tacacagtca ttctgtttag tcttcaaaaa 480
 cagtctgcag agagctgaca caaagttctc tctacctgtg gatctcatct gactatagta 540
 actttcttct ttgttccgtg tatctttatt tatctccatc cactactttc ccattggata 600
 aagctgtgtc tgtgttctat accaccatca cccca 635

<210> 755

<211> 342

<212> DNA

<213> Unknown (H38g604 nucleotide)

<220>

<223> Synthetic construct

<400> 755
 atatgcaaac ctttacttta tccagccatt atgaccaatg gactgtgcat ccggctatta 60
 atcttgtcat atgtagggtg tcttcttcat gctttaatcc atgaaggatt tttattcaga 120
 ctaaccttct gtaactccaa catagtacat cacatttact gtgacattat ccattgtct 180
 aagatttctt gtactgattc ttctattaat tttctaattg tttttatttt ctcaggttca 240
 attcaggtat tcagcattgt gactattctt gtatcttata catttggtct cttcgcaatc 300
 taaaaagga aatctgataa aggtgtaagg aaagcctttt cc 342

<210> 756

<211> 333

<212> DNA

<213> Unknown (H38g605 nucleotide)

<220>

<223> Synthetic construct

<400> 756
 atttgtaacc ctctgagata ccccatcatc atgagcaggg acgtctgtgt gcagatggcc 60
 gccatctcct gggtagacagg ctgtctgact gctctgctgg taactagtgt tgccctgcag 120
 atccccctct gtgggaatgt catcgaccat ttcacatgtg aaatccttgc agtgctaaaa 180
 ctagcttgtg tgagttccct gctcgtggac atggttatgc tgggtggcag tattctcctg 240
 ctgcccaccc caatgctttt gatttgcac tcgtatggct tcatectttc tacaattctg 300
 aggatcggct caacagaggg aagaacaaaa gct 333

<210> 757

<211> 665

<212> DNA

<213> Unknown (H38g606 nucleotide)

<220>

<223> Synthetic construct

<400> 757
 ttgcctgaca tcggttttcac ctccaccacg gtccccaaga tgattgtgga catccagtct 60
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 ggaggcatgg aagagagaca tgctcctgag tgtgatggcc tatggccggg ttgtagccat 180
 ctgtcaccct ctatatcgtt cagecatctt gaacccatgt ttctgtggct tcctagattt 240
 gttgtcttcg ttttgttttg ttttgttttt ctcagtcttt tagactccca gctgcacaac 300
 ttgattgcct tacaatgac cggcttcaag gatgtggaat tcctaatttc ttctgggaac 360


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cttctcaact ccccatcttg catgttgtga caccttcacc aggaacatca acctgtattt 420
ccctgctgcc gtatttggtt ttcttcccat cttggggacc ttttctctta ctgtaaaatt 480
gtttcctcca ttctgagggg ttcacatca ggtgggaagt ataaaccttc tccacctgtg 540
gggtcacct gccagttggt tgctgatttt gtggaacagg tgttgagggt taccttggtt 600
cagatgtgtc atcttcccca agaaagagtg cagtgccttc agtgatgtac cgggtgtgca 660
cctcc

```

<210> 758

<211> 646

<212> DNA

<213> Unknown (H38g607 nucleotide)

<220>

<223> Synthetic construct

<400> 758

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tttgtagaca tctgtgttac ctccaccaca gtcccaaaga cactgtcaaa catccggaca 60
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atagtgttgg acagcttact cttgaccgtg atggcctatg accagtttgt ggccatctgt 180
caccocctgc actacacggt catcgtgaac cctcggctct gtggactgct ggttctggcg 240
tcctggatca tgagtgcctt gaattccttg atagaaagct taatggtgtt gccactgtct 300
ttttgtacag acttgaaaat cccccacttt ttctgtgaac ttaatcagat aatccgcagt 360
gcctgttctg acacctttct taatgacatg gtgatgtatt tgtcagctgt gcttctaggt 420
aggggatgtt tcactgggat cctgtactct tactttaaga cagtttcttc catacgtgca 480
atctcatcag ctcaggggaa gtacaaggca tttccacct gtgcacgca cctctcagtt 540
gtctccttat tttattgtat gagccttggg gtgtacctta gtgctgctgc aaccacaac 600
tcactctcaa gtgcaacagc ctctgatgta cactgtggtc accccc 646

```

<210> 759

<211> 834

<212> DNA

<213> Unknown (H38g608 nucleotide)

<220>

<223> Synthetic construct

<400> 759

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atggcaatta ggaaccattc caccctccac aaaccatgt actttttttt agctaataatg 60
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ggatccaaac aggatcatgg acagctaata tcctttgagg gatgcatgac acagctttac 180
tttttctctg gcttgggctg cactgagtgt gtcttctctg ctgttatggc caatgatcgc 240
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cagatggctg ctggctcttg ggctggaggt tttggcatct ccatgggtcaa agtttttctt 360
atttcgggcc tctctaacgg tggccccaac atcatcaacc actttttctg tgatgtctct 420
ccattgtcga acctctcatg cactgatatg tccacagcag agcttacaga tttcatcctg 480
gccattttta ttcttctagg gccactctct gtcactgggg cctcctatgt ggccattact 540
gggtgctgtg tgcacattcc ttgggctgct ggacggtata aggccttttc cacctgtgcc 600
tctcatttca atgttgtgat aattttttat gcagccagta tcttcattta tgctcggcca 660
aaggcacttt cagcttttga caccaacaag ttggtctctg tactgtatgc tgtcattgta 720
ccattgtcga atcccatcat ttactgctg cgcaatcaag aggtcaagag agccctatgc 780
tgtattttgc acctgtacca gcaccaggat cctgacccca agaaaggtag caga 834

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<210> 760

<211> 942

<212> DNA

<213> Unknown (H38g609 nucleotide)

<220>

<223> Synthetic construct

<400> 760

atggaattta	cagatagaaa	ctacacgttg	gtcactgagt	ttattctatt	aggttttcca	60
actcgccctg	aactgcagat	tgtcctgttc	ctcatgtttc	tgacattgta	tgctataatt	120
ctgatagggg	acattggatt	gatgctgttg	atcaggattg	atcctcacct	tcaaaccccc	180
atgtattttt	tccttagcaa	cctatcattt	gtagaccttt	gctatttttc	agacattggt	240
cccaaatgc	tggtaattt	cctctcggag	aacaaatcta	tttctatta	tgggtgtgcc	300
ctgcagtttt	atttttctg	tacttttgca	gatacagaat	ccttcacct	ggccgccatg	360
gcctatgac	gctatgtcgc	catctgtaac	cctttattgt	acacagttgt	gatgtctagg	420
ggcatctgta	tgcggttgat	tgtcttgta	taccttgagg	gcaacatgag	ttccctgggt	480
cacacatcct	ttgcctttat	tctgaaatat	tgtgacaaaa	atgttattaa	tcattttttc	540
tgtgacctcc	ctccccctgt	taaactatcc	tgcactgaca	caacaattaa	tgagtggctc	600
ctctccacat	acggcagctc	agtggaaatc	atttgtttta	tcacatcat	catctcctac	660
tttttcatte	ttctctcagt	cttaaagatc	cgctctttca	gtgggaggaa	gaagaccttt	720
tctacatcgc	cctctcacct	gacttcagtg	acgatctacc	aagggactct	cctctttatt	780
tactcacggc	ccagctacct	gtattctcca	aacactgata	aaattatctc	agtgttctac	840
accattttca	ttccagtgct	gaatccgttg	atttatagtt	tgagaaataa	agatgtaaag	900
gatgcagctg	agaaagtctt	aagatcaaa	gtagattctt	ca		942

<210> 761

<211> 948

<212> DNA

<213> Unknown (H38g610 nucleotide)

<220>

<223> Synthetic construct

<400> 761

atggataacc	aaagctccac	accgggcttc	ctccttctgg	gcttctctga	acacccaggg	60
ctgggaagga	ctctcttcgt	ggatgtcatc	acttctacc	tcctaaccct	agtgggcaac	120
acactcatca	tctgtctgtc	tgcgctggac	accaagctcc	actctccaat	gtactttttc	180
ctctccaacc	tctccttctt	ggacctctgt	ttcaccacga	gttgtgttcc	ccaaatgctg	240
gccaacctct	ggggcccaaa	gaagaccatc	agcttctctg	actgctctgt	ccagatcttc	300
atcttctctg	ccctggggac	aactgagtgc	atcctcatga	aagtgatggc	ttttgatcgc	360
tacgtggcgt	tctgccagcc	cctccactat	gccaccatca	tccaccccg	cctgtgctgg	420
cagctggcat	ctgtggcctg	ggtcattggg	ctagtggggg	cagtgggtcca	gacaccatcc	480
accctgcacc	tgccttctg	ccccgatcgg	cagggtggatg	attttgtctg	tgagggtccca	540
gctctaattc	gactctcctg	tgaagacacc	tcctacaatg	agatccagg	ggctgttgcc	600
agtgtcttca	tcttggttgt	gcctctcagc	ctcatccttg	tctcttacgg	agccattacc	660
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tcccatctca	ctgtggtcac	cctcttctac	agctcagtc	ttgctgtcta	cctccagccc	780
aaaaatccgt	atgccaaagg	gaggggcaag	ttctttgggc	tcttctatgc	agtgggcact	840
ccttcaacta	accctctcgt	atacacctg	aggaacaagg	agataaagcg	agcactcagg	900
aggttactag	ggaaggaaa	agactccagg	gaaagctgga	gagctgct		948

<210> 762

<211> 927

<212> DNA

<213> Unknown (H38g611 nucleotide)

<220>

<223> Synthetic construct

<400> 762

atgaaaagag	agaactttac	tctcatcact	gactttgttt	tccaaggttt	ctctagcttc	60
catgagcagc	agatcacctt	ttttggcgtg	ttccttgca	tatacatctt	aaccttagca	120
ggcaatatca	tcattgtgac	catcatccga	attgatcttc	atcttcacac	acccatgtac	180
ttcttctctga	gcatgctgtc	cacttcagag	actgtatata	cattgggtcat	tctcccaaga	240
atgctctcca	gcctcgtagg	tatgagccag	cccatgtcat	tggcaggggtg	tgccacacag	300
atgttctttt	ttgtaacctt	tggcatcact	aactgcttcc	tgctcacagc	aatgggatat	360
gaccgctatg	tggccatctg	caacccctg	agatacatgg	ttattatgaa	caagaggctg	420
cgtatccaac	ttgtcctggg	ggcctgcagc	attggcgtga	ttgtagcaat	aacgcaagtg	480
acatctgtat	tcaggttacc	cttctgtgct	agaaaggtgc	cccacttctt	ctgtgacatc	540

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cgccctgtga tgaagctctc ctgcattgac accactgtca atgaaatcct gactttgatt 600
atcagtgtgc tgggtgctgt tgtacctatg ggtctggttt tcatttctta tgttctcatt 660
atctctacaa tcctcaagat tgcttcagtt gagggccgga agaaggcttt tgccacctgt 720
gcatcccacc tcaactgtgtt cattgtccac tacagctgtg cctccattgc ctacctcaag 780
cccaagtcag agaaccaccag agaacatgac cagctgatct cggtgacctc cactgtcatc 840
actcccctac tgaaccctgt ggtatacacc ctgagaaata aagagggtcaa agatgctctg 900
tgcagggctg ttgggtggaa gttttcc 927

```

<210> 763

<211> 650

<212> DNA

<213> Unknown (H38g612 nucleotide)

<220>

<223> Synthetic construct

<400> 763

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cataggagag ccattctctca tgggggctgt ctgacgcaga tgtctttctt gttcctttgt 120
gcatgtgtag aaggcatgct cctgactgtg atggcctatg actgctttgt agacatctgt 180
cgccctctgc actaccacgt catcggaat cctcacttct gtgtcttctt cgtgggggtg 240
tcctttctcc ttagcctgtg ggattcccag ctgcacagtt ggattgtgtt acaatatcac 300
catcttcaag aatgtggaaa tctctaattt tgtctgtgac ccctctcaac ttctcaaact 360
tgcctgttct gacggcgta tcaatagcat attcatatat ttgatagta ctatgtttgg 420
tttcttccc atttcaggga tcctatggtc ttactataaa atcgtcccct ccattctaag 480
gatttcacg tcagatggga agtataaagc cttctccacc tgtggctcct caccaggcag 540
ttgtttgctg attttataga acaggcattg gcattgacct gacttcagct gtgtcaccac 600
ccccaggaa tgggtgtggtg gcattcattga tatacgtctt tgtcactccc 650

```

<210> 764

<211> 641

<212> DNA

<213> Unknown (H38g613 nucleotide)

<220>

<223> Synthetic construct

<400> 764

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ttcactgacc tcttctttgt caccaacaca atccccaaga tgctggtgaa cctccagtc 60
cagaacaaag ccattctcta cacagggtgt ctgacacagc tctacttctt ggtctccttg 120
gtggcccttg acaacctcaa cctggccgtg atggcgatg atcgctatgt ggccatctgc 180
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tctgtgggtc tcaaaagatc cactacctct tctgtgagat gtacttctg ctaaggctgg 360
catgttccaa catccacgtc aaccacacag tactggttgc cagggtctgc ttcattctcc 420
tcattcccct aggttctatg atcacatcca acgcccgcac tgtcagagcc atcctccaaa 480
taccctcagc cactgggaag taaaaagcct tcctccactg tgcttcccat ttggctgtgg 540
tctccctctt ctatgggact ctgggtatgg tgtacctgca gccctccaa acctactcca 600
tgaaggactc agtagccaca gtgatgcatg cgggtggtgac g 641

```

<210> 765

<211> 635

<212> DNA

<213> Unknown (H38g614 nucleotide)

<220>

<223> Synthetic construct

<400> 765

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tttgttgatt tctgttatc caccacaatt acacccaaac tgctggagaa cttggtgtg 60
gaagatagaa ctatctcctt cacaggatgc accatgcagt tattctttgt ctgcatattt 120

```

gtagtaacag	aaacattcat	gctggcagtg	atggcctatg	accgatatgt	ggcgggtgtg	180
aaccctcttc	tctacacagt	tgcaatgtac	cagaggcttt	gtcccttggt	agtgggtaca	240
tcatactgtt	gggggatagt	ctgttccctg	acacttacct	agtttctact	ggaattatcc	300
ttcagaggaa	ataatatcat	taataacttt	gtctgtgagc	acgctgcat	tggtgctgtg	360
tcttgctctg	acccctgtgt	gagccaggag	atcactttag	tttctgccac	attcagttaa	420
ataagcagcc	tgcttccctat	gctttcattt	ttatcactgt	catgaagacg	ccttccactg	480
gggggcgcaa	gaaagcggtc	tccacgtctg	cctccactt	gacggccatt	accattttcc	540
atgggactat	ccttttcctc	tactgtgttc	ctaactccaa	aagttcgtgg	ctcatggtca	600
aggtggcctc	tgtcttttac	acagtgtgtca	ttccc			635

<210> 766

<211> 635

<212> DNA

<213> Unknown (H38g615 nucleotide)

<220>

<223> Synthetic construct

<400> 766

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gaagatagaa	ctatctcctt	cacaggatgc	accatgcagt	tattctttgt	ctgcatattt	120
gtagtaacag	aaacattcgt	gctggcagtg	atggcctatg	accgatatgt	ggcgggtgtg	180
aaccctcttc	tctacacagt	tgcaatgtac	cagaggcttt	gtcccttggt	agtgggtaca	240
tcatactgtt	gggggatagt	ctgttccctg	acacttacct	agtttctact	ggaattatcc	300
ttcagaggaa	ataatatcat	taataacttt	gtctgtgagc	acgctgcat	tggtgctgtg	360
tcttgctctg	acccctgtgt	gagccaggag	atcactttag	tttctgccac	attcaatgaa	420
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gggggcgcaa	gaaagcggtc	tccacgtctg	cctccactt	gacggccatt	accattttcc	540
atgggactat	ccttttcctc	tactgtgttc	ctaactccaa	gagttcgtgg	ctcatggtca	600
aggtggcctc	tgtcttttac	acagtgtgtca	ttccc			635

<210> 767

<211> 936

<212> DNA

<213> Unknown (H38g616 nucleotide)

<220>

<223> Synthetic construct

<400> 767

atgtccattt	ccaacatcac	agtctacatg	ccctctgtgt	tgacactagt	agggatccca	60
ggcctagaat	ctgtgcagtg	ctggattggg	attccattct	gtgccattta	tctcattgct	120
atgattggaa	attccttgct	tctgagcatc	atcaaatctg	agcgagctct	ccatgagccc	180
ttgtacattt	tcttaggcat	gctaggagcc	acagacattg	cacttgctag	cagcattatg	240
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gccctggacc	gttatgtggc	catctgttat	ccactaagac	atgccaacat	cttccccac	420
cagcttgtca	ttcagatagg	aactatggtc	gtactcaggg	ctgctattct	tgtagcccca	480
tgccctagtag	tgataaagtg	ccggtttcaa	ttttatcaca	caacagtcac	ctcccactcc	540
tactgtgagc	atatggccat	tgtgaaacta	gcagcagcaa	atgttcaagt	caacaaaatc	600
tatggtttgt	ttgtggcctt	cactgtagca	ggatttgacc	tcacattcat	cacattgtcc	660
tacatccaga	tatttatcac	agtttttcgt	ttgcccaga	aggaggctag	gtttaaagca	720
ttcaataacct	gcattgtcca	catctgtgtc	ttcctccagt	tctacctcct	tgcccttctc	780
tccttcttca	cacataggtt	tgggtctcac	atccccctt	atatccatat	tctcttttct	840
agcatttact	tgctggctcc	tccatttctc	aatccacttg	tctatggtgc	aaagaccaca	900
cagattcgca	ttcatgtggt	aaaaatgttc	tgttca			936

<210> 768

<211> 954

<212> DNA

<213> Unknown (H38g617 nucleotide)

<220>

<223> Synthetic construct

<400> 768

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atgtggcaga agaatcagac ctctctggca gacttcatcc ttgaggggct cttcgatgac      60
tcccttacct acccttttct tttctccttg accatgggtg tcttccttat tgcgggtgagt    120
ggcaacaccc tcaccattct cctcatctgc attgatcccc agcttcatac accaatgtat      180
ttcctgctca gccagctctc cctcatggat ctgatgcatg tctccacaat catcctgaag      240
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gaccgctatg ttgccatctg tcatccactg cgctatgctg tgctcatgaa caagaagggtg      420
ggactgatga tggctgtcat gtcatgggtg ggggcatccg tgaactccct aattcacatg      480
gcgatcttga tgcacttccc tttctgtggg cctcggaaag tctaccactt ctactgtgag      540
ttcccagctg ttgtgaagtt ggtatgtggc gacatcactg tgtatgagac cacagtgtac      600
atcagcagca ttctcctcct cctccccatc ttctgattt ctacatccta tgtcttcac      660
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cccaggctcc agtgcaactc attgcagaac aaagttgggt ctgtgttcta cagcatcatt      840
acgccacat  tgaattctct gatttatact ctccggaata aagatgtagc taaggctctg      900
agaagagtgc tgaggagaga tgttatcacc cagtgcattc aacgactgca attg          954

```

<210> 769

<211> 881

<212> DNA

<213> Unknown (H38g618 nucleotide)

<220>

<223> Synthetic construct

<400> 769

```

gccacgtaca attccagcaa tactgtgggt acagagtttg tgtttctgag cttcccagag      60
ctgcaccatc ttcaagggtc gctatttggg cactcctcat catctatgtg gtgaccatcc    120
tagaggacct ggctgtcgtg gggaccatca gagccagcca ccacctgcac atatccacac      180
acctcttctc ggccaaactc tcgggtgctg agactctgta cacctcggtc accgtcccaa      240
agctgttggc cggactccca gcacgagcga cgaccatcta tctccttctc ggggcacctc      300
acctggctgc tctcttctc ctcactcagc tctcttgagt gcgtcctccc ggccaacatg      360
gactgtgact ggcaccagtc catctgccac ctgtgcact acccagccca tcatggactc      420
catgcagctg gctctgcctg cacctggcca tcagcgccta gctcagcagc ttcccagcct      480
cctttgtgtc cagggtcttc aactccagcc tgaggctccg cagccccgat gtctcaacc      540
acttctgtga tatccaccc ccgctagggc tctcttgctc cagcaccact accatagaaa      600
tgcggaactc ggcagccagc gtgatccttg cggtctccct gcaggcaacc acggtctcct      660
acaccacat  cctggccaga tcgctgagga ttccagaaag gcccagcagc taaaggcctt      720
ccccacctat gcctcccacc tgggtgggct gctcctctaa cctcatcaag ctggtgttca      780
ggggtctact tgggtgggat cctctgctc aaacctca tctactgcct gggaactgca      840
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```

<210> 770

<211> 880

<212> DNA

<213> Unknown (H38g619 nucleotide)

<220>

<223> Synthetic construct

<400> 770

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gccacataca attccagcaa tactgtgggt acagagtttg tctttctgag cttcccagag      60
ctgcgccatc ttcaagggtc gctatttggg cactcctcat catctatgtg gtgaccatcc    120
tagaggacct ggctgtcgtg gggaccatca gagccagcca ccacctgcac atatccacac      180
acctcttctc ggccaaactc tcgggtgctg agacctgta cacctcggtc accgtcccaa      240
agctgttggc cggactccca gcacgagcga cgaccatcta tctccttctc ggggcacctc      300

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acctggctgc	tctcttccct	ctcactcagc	tctcttgagt	gcacccctcc	ggccaacatg	360
gactgtgact	ggcaccgggt	catctgccac	ctgetgcact	acccagccca	tcatggactc	420
catgcagctg	gctctgcttg	cacctggcca	tcagcgccca	gctcagcagc	ttcccagcct	480
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tgcggaactc	ggcagcccag	gtgatccctg	cggtctccct	gcaggcaacc	acgggtctcct	660
acaccacat	cctggccaga	tcgctgagga	ttccagaaa	gcccagcagc	ttaaaggcctt	720
ccccacctat	gcctcccacc	tgggggtggc	gctcctctaa	cctcatcaag	ctgggtgtcag	780
gggtctactt	ggttggggtc	cctctgctca	aacctcatcat	ctactgcctg	ggaactgcaa	840
catcagggag	gccctggcca	aactcctcca	ggcccttccc			880

<210> 771

<211> 524

<212> DNA

<213> Unknown (H38g620 nucleotide)

<220>

<223> Synthetic construct

<400> 771

ctcctaattg	cagcagacaa	ccacacagcg	tagaggcggt	tgtcctgcag	ggtttctctg	60
aagaccttcc	actccagggc	tgtctgcttg	cttttttccct	cctttacctg	atggcacttg	120
taggaaacat	cctcatggtc	atggccatca	gtctgaatcc	aggcctccac	acgccagtgt	180
acttctttct	caccaacctg	gcccttttag	acatcgtctg	cacatccatg	gacaacagca	240
gagtgggtgc	tgtgctgtac	acagtggcca	gccccaccct	gaaccctca	cctactccct	300
gcggaacaag	gacttatcag	tagcactgag	gagagtgttt	tcttgcatca	ggtaaaaagga	360
agggaaagttt	ctagtgtgaa	atgttccagg	tgtaacaaa	ctaatttcaa	catatgactt	420
tgagaatctc	atgcaagcag	caaggaacaa	gaaagtaatt	aatgccacat	atttataaat	480
aatgtgctcc	cgcacggggc	tgccatcatt	caatgtggaa	ctcc		524

<210> 772

<211> 951

<212> DNA

<213> Unknown (H38g621 nucleotide)

<220>

<223> Synthetic construct

<400> 772

atggaaagga	ccaacgattc	cacgtcgaca	gaatttttcc	tggtagggct	ttctgcccac	60
ccaaagctcc	agacagtttt	cttcgttcta	attttgtgga	tgtacctgat	gatcctgctt	120
ggaaatggag	tccttatctc	agttatcatc	tttgattctc	acctgcacac	ccccatgtat	180
ttcttctctc	gtaatctttc	cttcctcgac	gtttgctaca	caagttcctc	tgteccacta	240
attcttgcca	gctttctggc	agtaaagaaa	aaggtttccct	tctctgggtg	tatgggtgcaa	300
atgtttattt	cttttgccat	ggggggccag	gagtgcata	tcttaggcac	gatggcactg	360
gaccgctatg	tggccatctg	ctaccactg	agataccctg	tcacatgag	caagggtgcc	420
tatgtggcca	tggcagctgg	gtcctgggtc	actgggcttg	tggactcagt	agtgcagaca	480
gcttttgcaa	tgcagttacc	attctgtgct	aataatgtca	ttaaaccattt	tgtctgtgaa	540
attctggcta	tcttgaaact	ggcctgtgct	gatatttcaa	tcaatgtgat	tagtatgaca	600
gggtcgaatc	tgattgttct	ggttattcca	ttgttagtaa	tttccatctc	ttacatattt	660
attgttgcca	ctattctgag	gattccttcc	actgaaggaa	aacataaggc	cttctccacc	720
tgctcagccc	acctgacagt	ggtgattata	ttctatggaa	ccatcttctt	catgtacgca	780
aagcctgagt	ctaaagcctc	tgttgattca	ggtaatgaag	acatcattga	ggccctcatc	840
tcctttttct	atggagtgat	gactcccatg	cttaatcctc	tcacttatag	tctgcgaaac	900
aaggatgtaa	aggctgctgt	caaaaacata	ctgtgtagga	aaaacttttc	t	951

<210> 773

<211> 954

<212> DNA

<213> Unknown (H38g622 nucleotide)

<220>

<223> Synthetic construct

<400> 773

atggaatggg	aaaaccaaac	cattctggtg	gaattttttc	tgaaggagaca	ttctgttcac	60
ccaaggcttg	agttactctt	ttttgtgcta	atcttcataa	tgtatgtggt	catccttctg	120
gggaatggta	ctctcatttt	aatcagcadc	ttggaccctc	accttcacac	ccctatgtac	180
ttctttctgg	ggaacctctc	cttcttggac	atctgtctaca	ccaccacctc	tattccctcc	240
acactagtga	gcttcctttc	agaaagaaaag	accatttcct	tttctggctg	tgcaagtgcag	300
atgttccttg	gcttggccat	ggggacaaca	gagtgtgtgc	ttctgggcat	gatggccttt	360
gaccgctatg	tggctatctg	caaccctctg	agatatccca	tcacatgag	caagaatgcc	420
tatgtaccga	tggctgttgg	gtcctgggtt	gcagggattg	tcaactctgc	agtacaaact	480
acatttgtag	tacaattgcc	tttctgcagg	aagaatgtca	tcaatcattt	ctcatgtgaa	540
attctagctg	tcataagtt	ggcctgtgct	gacatctcag	gcaatgagtt	cctcatgctt	600
gtggccacaa	tattgttcac	attgatgcc	ctgctcttga	tagttatctc	ttactcatta	660
atcattttcca	gcacccctca	gattcactcc	tctgagggga	gaagcaaagc	tttctctacc	720
tgctcagccc	atctgactgt	ggtcataata	ttctatggga	ccatcctctt	catgtatatg	780
aagcccaagt	ctaaagagac	acttaattca	gatgacttgg	atgctaccga	caaaattata	840
tccatgttct	atggggtgat	gactcccatg	atgaatcctt	taatctacag	tcttagaaac	900
aaggatgtga	aagaggcagt	aaaacaccta	ccgaacagaa	ggttcttttag	caag	954

<210> 774

<211> 369

<212> DNA

<213> Unknown (H38g623 nucleotide)

<220>

<223> Synthetic construct

<400> 774

ttctctcttt	aggccaacta	cagcgcagag	gagcgctttc	tcctgctggg	tttctccgac	60
tggccttccc	tgcagccggt	cctcttcgcc	cttgctctcc	tgtgctacct	cctgaccttg	120
acgggcaact	cggcgctggt	gctgctggcg	ggctcgaccg	cgcctgcaca	cgcccatgta	180
ctacttcttc	tccacctggc	cttggttagac	gcgggcttca	ctactagcgt	ggtgcccggc	240
ctgctggcca	acctggcgga	ccagcgtctc	cgtgcgcgca	gccactgcac	ggcccagctg	300
tgcgcacgc	tggctctggg	ttccgccgaa	tgcgtccatc	tggcggtgat	ggctctgggc	360
cgcgcggtc						369

<210> 775

<211> 945

<212> DNA

<213> Unknown (H38g624 nucleotide)

<220>

<223> Synthetic construct

<400> 775

atgagacaga	ataacaatat	tacagaattt	gtcctcctgg	gcttttctca	ggatcctggt	60
gtgcaaaaag	cattatttgt	catgttttta	ctcacatact	tggtagacgt	ggtggggaac	120
ctgctcattg	tggtagatat	tattgccagc	ccttccttgg	gttccccaat	gtatttcttc	180
cttgccctgc	tgtcatttat	agatgctgca	tattccacta	ccatttctcc	caagttaatt	240
gtaggcttat	tctgtgataa	aaagactatt	tccttccaag	gttgcatggg	ccagctattt	300
atagaccatt	tcttgggtgg	ggctgaggtc	ttccttctgg	tggtagatggc	ctgtgatcgc	360
tatgtggcca	tctgtaagcc	actgcactat	ttgaccatca	tgaatcgaca	ggtttgtctc	420
cttctgttgg	tggtagccat	gattggaggt	tttgtacatt	ctgcgtttca	aattgttgtg	480
tacagtctcc	ctttctgtgg	tccaatgtc	attgttcatt	tcagttgtga	catgcaccca	540
ttactggaac	tggcatgcac	tgacacctac	tttataggcc	tcactgttgt	tgtcaatagt	600
ggagcaatct	gtatggatcat	tttcaacctt	ctgttaatct	cctatggagt	catcctaagc	660
tcccttaaaa	cttacagtca	ggaaaagagg	ggtaaagcct	tgtctacctg	cagctccggc	720
agtaccgttg	ttgtcctctt	ttttgtacct	tgtaatttca	tatatgttag	acctgtttca	780
aactttccta	ctgataagtt	catgactgtg	ttttatacca	ttatcacaca	catgctgagt	840

cctttaatat atacgttgag aaattcagag atgagaaatg ctatagaaaa actcttgggt 900
 aaaaaggttaa ctatatttat tataggagga gtgtccgtcc tcatg 945

<210> 776

<211> 352

<212> DNA

<213> Unknown (H38g625 nucleotide)

<220>

<223> Synthetic construct

<400> 776

cgctgtgagc cccgcctgct ggaccacttc atctgtgagc tgccggcggt gctcaagctg 60
 gcctgcggag gcgacggaga cactaccgag aaccagatgt tcgccgcccg cgtgggtcatc 120
 ctgctgtgct cgtttgccgt catcttggcc tcctacggtg ccgtggcccc agactgtctg 180
 ttgcatgcgg ttcagcggag gccggcagag aggcggtggg cacgtgtggg tcccacctga 240
 cagcgtctctg cctgttctac ggctcggcca tctacaccta cctgcagccc gcgcagcata 300
 caaccaggca cggggcaagt tcgtatcgct cttctacacc gtggtcacac ct 352

<210> 777

<211> 937

<212> DNA

<213> Unknown (H38g626 nucleotide)

<220>

<223> Synthetic construct

<400> 777

ggactgagta ataatgttac agaatttgtc ctcttgggca acactcagtg tcctgatgtg 60
 caaaatgcat tatttgtcat ggttttactc acatacgttg tgagtatggc gggaaacttg 120
 cttgctgtgg tggctattat ttccagccct tcctttggct ccccaatgta cttcttcctc 180
 acagcctggt atttatatat gctgcataatt ccaataccat ttctcccaa ttgattatag 240
 gcttactcca tgataaaaag actattttct tcacagcatg catggggcag ctatttatag 300
 accacttatt tgggtgtgct gaggtcttcc tacttgtggg gatgtcctac gatttctatg 360
 tggccatctc taagccactg cactatttga ccatcatgaa tcaacagggt tgtatccttc 420
 tgttgggtgt ggctgtgact ggaggttttg tgagtgtgtg gtttcaaatt gttgtgtgtg 480
 acactctctc gttctgtgyc caaatgtcac tgaccacttt gtctgtgaca tgtaccatt 540
 attggaactg gtttgcactg atacctactt tataggtctc actgttgttg ccaatgggtc 600
 agcaatctgt atggtcgtct tcacccttct actaatctcc tatggagtca tcctaaacaa 660
 ctttaaaact tatagtcagg aagggaggct taaagccctg tctgcctgca tctcctacat 720
 aacagtcact gtctgtttc ttgttcctg tattttcctt ttcgttagac ctgtttcgaa 780
 ctttctatt gataaattca tgactgtgtt ttatacagtt atcatacaca tgttgaatcc 840
 attaataac acactgagaa atttagagat gagaattgct gtaaaatcca atgtaaaaaa 900
 actctggcat taaaaactta actatagtta gaatgag 937

<210> 778

<211> 970

<212> DNA

<213> Unknown (H38g627 nucleotide)

<220>

<223> Synthetic construct

<400> 778

atgagactga gtagcgatgt tacagcattt gtctctcctag gccttactca ggatcctgat 60
 gtgtaaaaatg cattatttgt cgtacattta ctcacataca ttatgactat ggtggggaac 120
 ctgcccattg tggtgactat tattgccacc cccaccttag gctcccaggt gtacttcttc 180
 attgtctgct tgtcatttat agatgttgtg tattccacca ccattcctcc caaattgatt 240
 gtaagctatc tccatgataa aaagactatt tccttccgag cttgcatggg tcagcccttt 300
 tatagaccac ttagttgggt gtgtgaggc cttcattctg ttggtgatgg cctataatcg 360
 ctatgtagcc atctgtaagc cactgcacta tttcaccatc atgaattgac aggtttgcat 420


```

ccttctgttg gtggtggctg tcaactgctg ttttgtgcat tctgtgttcc aaatttttagt 480
tgcgtacagt ctccttttct gtggtcccaa tatcattgac cactttttct gtgacatgta 540
cccattattg gaactggcac acactgacac ctactttata ggcctcactg ttgttgccaa 600
tggtggagga atctgtatgg tcttgttcat ccttctacta atctcctgtg gggtcacct 660
aatctccctt aaaacttata gtcaggaagg gaggcataaa gccctgtcta cctgcagctc 720
ccacattacc gtggttgctc tgttttttgt tccctgtatt ttcctgtatg ttagacctgt 780
ttcaaacttt cctattaata aattcattac tgtgttttat acagttatca caccatgtt 840
gaatccatta atatacacat tgagaaactg agagatgaaa aatgctatag gaaacctctg 900
gtgtaaatat taactctaga tagaataaga ggttacattt tcatgtaggt acagggtaat 960
gcaggtaaag 970

```

<210> 779

<211> 704

<212> DNA

<213> Unknown (H38g628 nucleotide)

<220>

<223> Synthetic construct

<400> 779

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cccatgtact tgttcctcgg caatttgtcc ttcattgac tctgttattc atttgtcttt 60
acccccaaaa tgctgatgag ctttatttca gagaggaaca tcatctcctt tccaggatgc 120
ataactcagc tcttttttct ctgctttttt gtccactctg agtgctatgt gctgacagcc 180
atggcctatg atcgctatgt ggccatctgc aaacccttcc tgtacatggt caccacgtcc 240
ctcagatctg ttctctactg atgcttgggt catatgtgat ggggtttgct ggggccatgg 300
tccacacaga gtgtatgatg aagctcatct tttgtgactc caacgtcatc aaccataaca 360
tgtgtgacat cttcccaactg ctccagctct cctgcagcag cacctaggcc aatgagctgg 420
tgatgtctgt tattgttagc acagttgtta tagtatcaag cctcattatc ttaatctctt 480
atgctttgat tcttttcaat atccttcaca tgtcctcagc cgagggttgg ttcaaagcca 540
tcggtacctg tggctccac ataataactg ttggcctatt ctatgaattt gggctgatca 600
ctcatgttaa gttatcatct gatttgtata tgggtcaggg gaagtttctc tcagtgtttt 660
atacaaatgt ggttcccatg ctgaaccctc tcatctactg tctg 704

```

<210> 780

<211> 924

<212> DNA

<213> Unknown (H38g629 nucleotide)

<220>

<223> Synthetic construct

<400> 780

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atgaggcaga ataacaatat tacagaattt gtcctcctgg gcttctctca gtatcctgat 60
gtgcaaaatg cattatttgt catgttttta ctcatatata ttgtgactat ggtggggaac 120
ctgctcattg tgggtgtctat tattgccagt cccttttttg gctccccagt gtacttcttc 180
cttgccctgcc tgtcatttat agatgctgtg tattccacca ccatttctcc tgtattgatt 240
gtagacttac tctgtgataa aaagactatt tccctccag cttgcatggg tcagctattt 300
atagagcact tgtttgggtga tactgacgtc ttcttcttgg tgggtgatggc ctatgatcgc 360
tacgtggcca cctgtaagcc actgcgctat ttgaccatca tgaattgaca ggtttgcac 420
cttctgttgg tgggtggctgt gactggagggt tttctgcatt ctgtgtttca aatttttagtt 480
gtgtacagtc tccctttctg tggccccaat gtcatttctc actttttctg taacatatac 540
cctttattgg acctggaatg cactgacacc tacttcgtag gcctcgctgt ggttttcaat 600
gggtggagcaa tctgtatggc catcttcacc ctctactaa tctcctatgg ggtcatccta 660
aactccctta aaacttatag tccggaaggg aggcataaag ctccgtttat ctgcagctcc 720
cactttatca tgggttatctt gttttttgtt ccctgtattt tcttatatgt tagaccggtt 780
tcaaacttcc ctattgataa attcctgact gtgttttatt cagttatcac acccaagtgt 840
aatcctttta tatacatgtt gagaaattca gagatgagaa atgctataga aaatctcttg 900
ggataccaaa gtgggaagac agga 924

```

<210> 781

<211> 690

<212> DNA

<213> Unknown (H38g630 nucleotide)

<220>

<223> Synthetic construct

<400> 781

```

cccatgtact tgttcctcgc caacttgctc ttgcctgaca tcggtttcac ctccagcatg      60
gtccccaaga tgattgtgga catctaactc cacagcagac tcatctccta ggcaggctgc      120
ctgactccca tgtctctctt tgccattttt ggaggcatgg aagagagaca tgctcctgag      180
tgtgatccct atgaccggtt tgtagccatc tgtcaccctc tatatcattc agccatcatg      240
aaccgctggt tctgtggcct tctagttttg ttgtcttttt tttctcagtc tcttttagac      300
gcccagggtgc acaacttgat tgccttacaa atgacctgct tcaaggatgt ggaaattcct      360
aatttcttct gggaaccttc tcaactcccc catcttgcat gttgcgacac cttcaccaat      420
aacataatca tgtattcccc tctgtccata tttgggtttt tcccatctc ggggaccctt      480
ttctcttact ataagattgt ttctccatt cggagggttt catcatcagg tgggaagtat      540
aaggcctgct ccacctgtgg gtctcacctg tcagttgttt gctgatttta tggaacaggc      600
ttttgggggt acctcagttc agatgtgtca tcttccccgg gaaaggctgc agtggcctca      660
gtgatgtaca cggtggtcac ccccatgctg

```

<210> 782

<211> 681

<212> DNA

<213> Unknown (H38g632 nucleotide)

<220>

<223> Synthetic construct

<400> 782

```

tctttcctgg agattggctt caacctagtc attgtgcca aaatgctggg gacctgctt      60
gcccaggaca caaccatctc cttccttggc tgtgccactc agatgtattt cttcttcttc      120
tttggggtag ctgaatgctt cctcctggct accatggcat atgaccgcta tgtggccatc      180
tgcagtccct tgcactaccc agtcatcatg aaccaaagga cacgggcca actggctgct      240
gcttcctggt tcccaggctt tctgtagct actgtgcaga ccacatggct cttcagtttt      300
ccattctgtg gcaccaacaa ggtgaaccac ttcttctgtg acagcccgcc tgtgctgaag      360
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gtcatgatcc cctgcttget gatcttgtgt tctatactc gcattgctgc tgctatcctc      480
aagatcccat cagctaaagg gaagcataaa gccttctcta cgtgctcctc acacctcctt      540
gttgtctctc ttttctatat atcattaagc ctcacgtact tccggcctaa atcaaataat      600
tcacctgagg gcaagaagct gctatcattg tcgtacactg ttatgactcc catgctgaac      660
ccctttcatc tactgtcctg g

```

<210> 783

<211> 576

<212> DNA

<213> Unknown (H38g633 nucleotide)

<220>

<223> Synthetic construct

<400> 783

```

atggtcacag agttcctcct actgggattt ctcctgggcc caaggattca gatgctcctc      60
tttgggctct tctccctggt ctatgtcttc accctgctgg ggaatgggac catcctgggg      120
ctcatctcac tggactccag actccacacc cccatgtact tcttctctc acacctggcg      180
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ccagccaagc ccatctcctt tgcggggccg atgatgcaga cttttctgtt ttccactttt      300
gctgtcacag aatgtctcct cctgggtggt atgtcctatg atctgtacgt ggccatctgc      360
caccacctcc gatatttcat catcatgacc tggaaagtct gcactactct ggccatcact      420
tctggacatc tgggctccct cctggctatg gtccatgtga gcctcatcct aagactgccc      480
ttttgtgggc ctcgtgaaat caaccactty ytctgtgaaa tcctkkctgt cctcaggctg      540
ggctgtgctg atacctggct caaccagggt gtcac

```

<210> 784
 <211> 924
 <212> DNA
 <213> Unknown (H38g634 nucleotide)

<220>
 <223> Synthetic construct

<400> 784
 tatgcagacc cacagaatct aacagatgtc tcwatattcc tcstcctaga actctcagag 60
 gatccagaac tgcagccagt ccttgctggg ctgttcctgt ccatgtgcct ggtcacgggtg 120
 ctgggggaacc tgetcatcat cctggccatc agccctgact cccacctcca ccccccatg 180
 tactttcttcc tctccaacct gtcttgcct gacatcggtt tcacctccac cacgggtcccc 240
 aagatgattg tggacatcca gtctcacagc agagtcatct cctatgcagg ctgcctgact 300
 cagatgtctc tctttgccat ttttgaggc atggaaagaga gacatgctcc tgagtgtgat 360
 ggcctatgac tggttttag ccattctgtca cccgctatat cattcaccat catgaacccg 420
 tgtttctgtg cctttctagt tttgtgtct tttttttct cagtcttta gactcccagc 480
 tgcacaactt gattgcctta caagtaccc gcttcaagga tgtggaaatt cctaatttct 540
 tctgtgaccc ttctcaactc ccccatcttg catgttgtga caccttcacc aataacataa 600
 tcatgtattt cctgtgtgcc atatttggtt ttcttcccat ctgggggacc cttttctctt 660
 actataaaat tgtttcctcc attctgaggg ttcatcatc aggtgggaag tataaagcct 720
 tctccacctg tgggtctcac ctgtcagttg tttgctgatt ttatggaaga ggtgttgag 780
 ggtacctcag ttcagatgtg tcatcttccc ccagaaaggg tgcagtggcc tgcagtgatg 840
 tacacgggtg tccactccat gctcaacccc tttatctaca gcctgagaaa cagggatatt 900
 aaaagtgtct tgcggcgccc gcaa 924

<210> 785
 <211> 714
 <212> DNA
 <213> Unknown (H38g635 nucleotide)

<220>
 <223> Synthetic construct

<400> 785
 atgtacttgt tcttgaggaa tctgtccttg cctgacatcg gtttcacctc caccattgtc 60
 cccaagatga ttgtggacat ccagtctcac agcagagtga tctcctatgc aggcgcctg 120
 actcagatgt ctctctttgc catttttgga ggcattggaag acaacatgct cctgagtgtg 180
 atggcctatg accggtttgt agccatctgt caccctctat atcattcagc catcatgaat 240
 ccgtgtttct gtggcttctt acttttgggt tcttttttt tttttctcag tcttttagac 300
 acccagctgc acaacttgat tgctttacaa atgacctgct tcaaggatgt ggaaattcct 360
 aatttcttct gtgaccttc tcaactcccc catcttgcac gttgtgacac cttaccaat 420
 aacatcatcg tgtatttccc tgcgtgcata tttgttttcc ttcccatctc ggggacctt 480
 ttctctttta aactgtttgt ttctccatt ctgagggtt catcatcagg cgggaagtat 540
 aaaaccttct ccacctgtg gtctcacctg tcagtatttt gcttatttta tggaaagggt 600
 gttggagggt acctcagttc agatgtgtca tcttccctga gaaaggctgc agtggcctca 660
 gtgatgtaca agatggtcac ccccatgctg aaccttcca tttacacct gcgg 714

<210> 786
 <211> 962
 <212> DNA
 <213> Unknown (H38g636 nucleotide)

<220>
 <223> Synthetic construct

<400> 786
 ttcaaacggt ccataacatt cacacctaca acattcactc tcgttggcat cccgggactg 60
 gaggcagaac attatgtgga tatccatccc cttctgcctg atatacacca tcatctttcc 120
 gggaaatggc atcattcttc acatcatccg aattgactct tccttgacc aacctatgta 180

ctatcttctg gccatgccgg cctttgttga acttggtgtc tctgcttcca ccatgcccac	240
tgtgttaagc atattcctct ttggcattaa cgatgtcagt tttggtggtt gcctgtcca	300
gatgtttct atgactctt tcaactctat ggagtcagggt gtccttctgg caatgtcagt	360
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catttctggg atgggtgccg ccattgcctt gcgcagtgtg atgcttatgc tcccactgct	480
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ccactcagat ctgatcaaat tgccctgtgg agacacacgc cccaatagca tcctggctct	600
atttgtcatt accttcacat ttggactgga cttattgttc attgtggttt cttatgtgct	660
gattcttcat acagtactgg aaatagcttc tggagcaggg cgtggcaggc actcaacaca	720
tgtgtgtgc acatatgtgc tgtgcttgtg tactatgtgc ccatgatcag cctctcctga	780
tgcaccgctt tggacggcat ttacctccac ttttcagac tgtcacggcc aatgcttacc	840
tcttctttcc tcctgtgggc aaccaccttg tctatagtat caaaatcaaa gaaattgca	900
acagcgttgt tcttacacta tccaggaaga ggggtgagtt ctaatggaga ccgaagatac	960
cc	962

<210> 787

<211> 872

<212> DNA

<213> Unknown (H38g637 nucleotide)

<220>

<223> Synthetic construct

<400> 787

acctcagagg atccagaacg gcagctgggc cttgctggac tgttcctgtc catgtgcctg	60
gtcatgggtg tggggaacct gctcatcacc cggccatgag cctgactcc cacctccaca	120
cctccatgta cttcttctc tccaacctgt cttgcctga catcggtttc acctccacca	180
cgggtcccca gatgactgtg gacatccagt ctgcagcag agtcactctc tatgcaggct	240
gcctgactca gaagtctctc tttgccattt ttggaggcac ggaagagaga catgctcctg	300
agtgtgatgg cctatgaccg gttttagacc atctgtcacc ctctatatca ttcagccatc	360
atgaacctgt gtttctgtgg ctctcctagt ttgctgtctt tttttttct cagtctttta	420
gactcccagc tgtacaactt gattgcctta ctaatgacct gcttcaagga ggtggacatt	480
cctaatttct tctgtgacct ttctcaactc ccccatcttg ccgttgtgac accttcatca	540
ataacataat catgtatttc cctactgcca tatttgggtt tcttcccacc tcggggaccc	600
ttttctctta ctataaaatt gtttcccca ttctgagggt ttcatcatca ggtgggaagt	660
ataaagcctt ctccacctgt ggggtctacc tgtcagttgt ttgctgattt tatggaagag	720
gtgttggagg gtacctcagt tcagatgtgt catcttcccc cagaaagggt gcagtggctg	780
cagtgatgta cacggtgggc acctccatgc tcaaccctt tatctacagc ctgggaacaa	840
gggatattaa aagtgtcttg cggcgccgc aa	872

<210> 788

<211> 646

<212> DNA

<213> Unknown (H38g638 nucleotide)

<220>

<223> Synthetic construct

<400> 788

ctagtggact tttgttactc ttcagctgtc actcccacag tcatagctgg gctcgttata	60
ggagacaagg tcatctctta caatgcatgt gctgtcaca tgttctttt tgcagccttt	120
gccactgtgg aaaatttctt cttggcctca atggcctatg accgctatga tgcagtgtgc	180
aaaccctac attacaccac caccatgaca acaagtgtgt gtgcatgtct ggctataatc	240
tgttatgtct gtggtttctt gaatgcctcc atacacattg gggaaacatt gtctctcttt	300
ctgtatgtcc aatgaagtcc attgctttt ctgtgatgtt ccaccagtca tggctctgtc	360
ttgctgtgat agacatgtga atgagctagt tctattttat gtaggcagtt tcaatatctt	420
ttctgccatc ctagttatct tgatctccta cctattcata ttatcacca tcctaaagat	480
gcactcagct tcaggatacc agaaggcttt gtccacctgt gcctcccacc tcaatgcagt	540
catcatcttc tatgggacta ttatcttcat gtacttacag ccagctctg gtcactccat	600
ggacacagac aaactggcat ctgtgttcta tactatgatc atcccc	646

<210> 789
 <211> 648
 <212> DNA
 <213> Unknown (H38g639 nucleotide)

<220>
 <223> Synthetic construct

<400> 789

tttgtggaca tctgcttctc ctgcaccacc gtccccaaga tgctggccaa tcacatactc	60
gagactcaga ccatctcctt ctgtggctgt ctcacacaga tgtatttcgt tttcatgttc	120
gtggacacgg acaatttcct cctagctgtg atggcctatg accactttgt cgccgtgtgc	180
caccccttac attacacagc aaagatgacc catcagctct gtgccctgct gggtgtgtga	240
ttatgggtgg ttgccaacct gaatgtcctt ctgcacaccc tgctgatggc tccactctca	300
ttctgtgcag acaatgccat cactcacttc ttctgcatg tgactcccct actgaaactc	360
tcctgtctag acacacacct caatgaggtc ataatcctta gtgaggggtgc cctgggtcatg	420
atcaccccat ttctttgcaa cctggcgtct tatatgcaca tcacctgcac tggcctgaag	480
ggcccatcca caaaggaag gtggaaagcc ttctccacct gtggctctca cctggctgtg	540
ggctctctct tctacagcac catcactgct gtgtatttta accctctgtc ctccactca	600
gctgcgaaag acactatggc tactgtgttg tatacagtag tgactccc	648

<210> 790
 <211> 471
 <212> DNA
 <213> Unknown (H38g640 nucleotide)

<220>
 <223> Synthetic construct

<400> 790

atctgcagcc ccttgcgtga caatgtcatc atgtcctatc accactgctt ctggctcaca	60
gtgggagttt acattttagg catccttggg tctacaattc acaccggctt tatgttgaga	120
ctctttttgt gcaagactaa tgtgattaac cattattttt gtgatctctt ccctctcttg	180
gggtctctct gctccagcac ctacatcaat gaattactgg ttctggctct gagtgcattt	240
aacatcctga cgctgcctt aaccatcctt gcttcttaca tctttatcat tgccagcatc	300
ctccgcatte gctccactga gggcaggctc aaagccttca gcacttgag ctccacatc	360
ttggctgttg ctggtttctt tgggtctgca gcattcatgt acctgcagcc atcatctgtc	420
agctccatgg accaggggaa agtgcctctt gtgttttata ctattgttgt g	471

<210> 791
 <211> 975
 <212> DNA
 <213> Unknown (H38g641 nucleotide)

<220>
 <223> Synthetic construct

<400> 791

atgaagactt tgtgttcctt tcttcagatc agcagaaata tgcatcaaga aaaccaaacc	60
accatcactg aattcattct cctgggactc tccaaccagg ctgaacatca aaacctcctc	120
tttgtgcttt tcctgagtat gtatgtggct actgtggttg ggaacgggct catcattgtg	180
gctatcagct tggatatata ccttcacacc cccatgtatc tcttccttgc ctacctatcc	240
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aacagccaat ccatctctta tgagagctgc atcacacaga tgtacttttc tattgtgttt	360
gtcgtcactg acaatttgct ttgggggacc atggccttcg accactttgt ggcgatctgc	420
cacctctga actatacaac ttcatgcgg gccagggtcg gcactttgct cacagtcatc	480
tcgtggttcc tcagtaatat tattgtctct acacacaccc ttctgtcatc tcaattgtc	540
ttctgtgacc acaacactct cccacacttc ttctgtgact tggccctctc gctcaaactg	600
tcctgttcag atacaatgat caatgagctt gtgtgtttta ttgtgggttt atcagttatc	660
atcttccctt ttgtactcat cttctctccc tatgtctgca tcatcagagc tgtcctggga	720
gtatcatcca cacagggaaa gtggaaagcc ttctccactt gtggctctca cctgacaatt	780

gcattactgt	tctacggaac	cactgtaggc	gtgtactttt	tccccctcctc	cactcaccct	840
gaggacactg	ataagattgg	tgctgtccta	ttcactgtgg	tgacacccat	gatgaacccc	900
ttcatctaca	gcttgaggaa	taaggatatg	aaaggtgccc	tgagaaagct	catcaataga	960
aaaatttctt	ccctt					975

<210> 792

<211> 943

<212> DNA

<213> Unknown (H38g642 nucleotide)

<220>

<223> Synthetic construct

<400> 792

atgagaccta	ataacagcat	tacagaattt	gtcctcctgg	gattctctca	ggatcctggg	60
atgcaaaaag	aattatttgt	catgttttta	ttcacatacg	ttgtgactgt	gttggggaac	120
cagctcattg	tgggtgactat	cattgccagc	ccttccttgg	gtcccccaat	gtacttcttc	180
cttgccctgcc	tgctatttat	agatgctgca	tatttcaactg	tcatttctcc	caaattgatt	240
gtggacttac	tctgtgataa	aaagactatt	tccttccaaa	cgttcatggg	ccaactattt	300
atagaccact	tctttgggtg	tgagaggcc	ttccttctgg	tggtgatggc	ctatgatcgc	360
tatgttgcca	tctgtaagac	attgactat	ttgaccatca	tgactcgaca	ggtttgatc	420
cttgcatcgc	tgggtggctgc	gacaggcggg	tttgtgcatt	ctgtgtttca	aattgttggt	480
gtgtacagtc	tccttttctg	tggcgccaat	gtcattgatc	atttcagttg	tgacatgtat	540
ccattattgg	aactggcatg	aactgacacc	tactttatag	gcctcactgt	tgttttcagt	600
ggtggagcac	tctgtatggg	catcttcacc	cttctaataa	tttctatag	ggtcaccta	660
aactccctta	aaacttacac	tcaggaaggg	agcataaagc	cctgtctacc	tgagctccc	720
acatcactgt	gattgttctc	tttttattcc	ctgtatttcc	atatatgtga	gacctgttcc	780
aaacttttct	attgacacat	tcatgactgt	cttttataca	gttatcacac	ccaagttgaa	840
tcctttaata	tacactttca	gaaattcaga	gatgagaaat	gttatagaaa	aactcttggt	900
gaaaaaggta	actatattta	gaataacagg	gtccatcctc	atg		943

<210> 793

<211> 942

<212> DNA

<213> Unknown (H38g643 nucleotide)

<220>

<223> Synthetic construct

<400> 793

atgagacaga	ataaaaaataa	tacagaattt	gtcctcttgg	gcttctctca	ggatcctgat	60
gtgcaaatgc	attattttgtc	atgttttact	cacataattg	gtgacaacag	tggggaacct	120
gctcattgtg	gtgactatta	ttgccagccc	ttccttgggc	tcctccagtgt	atttctgact	180
tgccctgtctg	tcatgtatag	atgctgcata	ttccactacc	atttctccca	aactgattgt	240
agagttactc	attgataaaa	agactatttc	cttccgagct	tgcatgggcc	agctatttat	300
agaacacttg	tttgggtgta	ctgagatctt	cattctgatg	atgatggcct	gtgatcgcta	360
tgtggacatc	tgtaagccac	tgactatttt	gaccatcatg	aattgacagg	tttgcacctc	420
tctgttgggtg	ttggctgtga	caggagggtt	tgtacattct	atgtttcaaa	ctgttggtgt	480
gtacaatctc	ccttttctctg	gccccaatgt	cattgacatt	gaccactttg	tctgtgacat	540
gtacccatta	ttggaactgg	cgttcactga	tacctacttt	ataggcctca	ctgttggtgt	600
caatggttga	gcaatgtgta	tgggtcatctt	caccattcta	ctaatacctc	acggaatcat	660
cctaaactct	cttaaaactt	atagtcagga	agggaggtgt	aaagccctgt	ctacctgcag	720
ccccacata	accgtggttg	tcctcttttt	tggtccctgt	attttcatat	atgttagacc	780
tgtttcaacc	tttctatttg	ataaattcat	gactgtgttt	tatacagtta	tcacacccat	840
gttgaatcct	ttaatatata	cgttgagaaa	ttcagagatg	agaaactcta	tagaaaatct	900
cttgtgtaaa	aaagctatct	gtagttagaa	taagagtgtc	cc		942

<210> 794

<211> 945

<212> DNA

<213> Unknown (H38g644 nucleotide)

<220>

<223> Synthetic construct

<400> 794

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cctgatgtgc	aaaatgcgct	atttgatcatg	tttttactga	catacattgt	gacaatgggtg	120
gggaacctac	tcattgtggt	gactattatt	gccagccctt	ccttgggctc	cccaatgtac	180
tttttccttg	cccacctgtc	atttatagat	gctgtgtatt	ccaccaccat	ttctcctgta	240
ttgattgtag	acttactctg	tgacaaaaag	acgatttcct	tctgagcttg	catgggacaa	300
ctgtttatag	accacttatt	tggtgggttct	gaggtcttcc	ttctgggtgt	gatggcctgt	360
gacgcgtgtg	tgcccatctg	taagccactg	cactatttga	ccatcatgaa	tcgacagggt	420
tgcatctctc	tttggtgtt	ggctgtgact	ggaggttttg	tgcatcctgt	atttcaagtt	480
gttgttgtgt	acagtctccc	tttctgtggc	cccaatgtca	ttgaccactt	tttctgtgac	540
atataccctt	tatttggaac	tgcatgcac	tgacacctac	tttataggcc	tcactgtgggt	600
tttcaatggg	ggagcaatgc	gtatgggtcat	cctcaccctt	ctactagtct	tctatggagt	660
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cagctcccat	gttaccgtgg	ttatcttgtt	ttttgcttcc	tgtattttca	tatatgttag	780
acctgtttca	aattttctgt	tgataaatte	atgactgtgt	tttatacggt	tatcacaccc	840
atgttgaatc	cttttatatg	catgttgaga	aattcagaga	tgagaaatgc	tatagaaaaa	900
ctcctgtgta	aaatgaactg	tagttagaat	aagagtgttc	cttcc		945

<210> 795

<211> 939

<212> DNA

<213> Unknown (H38g645 nucleotide)

<220>

<223> Synthetic construct

<400> 795

atgggactga	gtaacaatgt	tacagaactt	ttcctcctgg	gcctcactca	ggatctcgat	60
gtgcaaaatg	cattatttgt	catgttttta	ctaacataca	ttgtgactat	ggtgggggaa	120
ctgctcattg	tggtgactat	tattgccacc	ccatccttgg	gtcctccaat	gtacttttct	180
cttgccctgcc	tgtcatttat	agatgctgtg	tattccacca	ccatttatcc	caaattgggt	240
gtagactaac	tccataatta	aaagactatt	ttgttcccaa	cttgcattgg	ccagccactt	300
acagaccact	tatttggtgg	tggtgaggtc	tttttttctg	ttggtgatgg	cctgtgatcg	360
ctatgtggcc	atctgtaagc	cactgcacta	ttttaccatc	atgaatcgac	aggttttcat	420
ccttctgttg	gtagtggctg	tgactggagt	tttgtgcgtt	ctgtgttcca	aattgttgtt	480
gtgtacagtc	tccctttctg	tgccccaat	gtcattgacc	actttttctg	taacatgtac	540
ccattaatgg	aaatggcatg	aactgacacc	tactttatag	gcctcactgt	ggttttcaag	600
gttgaagcaa	tctgtgtggt	catcttcacc	cttctactaa	tctcctctgg	cgtcactcta	660
atctccctta	aaacttacag	tcaggaaggg	aggcataaag	ccctgtttac	ctgcagctcc	720
cgcattactg	tagttgtcct	cttttttgtt	ccctgtattt	tcatgtatgt	tagacctgtt	780
tttaacttcc	ccattgataa	atattattatt	gtgttttata	cagttatcac	acccatgctg	840
aatcctttta	tatacatgtt	gagaaattca	tagacgagaa	atgctataga	aaacccttag	900
tgtaaaaaat	taactgtaga	tagaataaga	gtgtacatc			939

<210> 796

<211> 945

<212> DNA

<213> Unknown (H38g646 nucleotide)

<220>

<223> Synthetic construct

<400> 796

atgagacctt	ataacagtat	tacagaattt	gtcctcctgg	gctttttcaca	ggatcctgat	60
atgcaaaaca	cattatttgt	catgttttta	ctcacataca	ttgtgacagt	ggtgggggaa	120
ctactcgttg	cgggtgactat	tattgtcagc	ccttccttga	gtcctccaat	gtaattcttc	180
cttgcttgcc	tgtcattaat	agatgctgta	ttatccacca	ccatttctcc	catattgatt	240

gtagacctac	tctgtgacaa	aaagactatt	tccttcccag	cttgcattggg	ccagctatatt	300
acagaccact	tggttggtgg	aactgagatc	ttccttcttg	tggtgatggc	ctatgatcgc	360
tacgtggcca	tctgtaagcc	actgcactat	ttaccatca	tgaatcgaca	ggtttccatc	420
cttctgttgg	tggtggccat	gactggaggt	ttccttcatt	ctgtgtttca	aattgtctgt	480
ctgtacagtc	tccctttctg	tggtcccaat	gtcattgacc	actttttctg	tgacatgtac	540
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gggtggagcaa	tgtgtatggg	catcttcgcc	cttctactaa	tctcctatgg	agtcagccta	660
aactccctta	aaacttatag	tcaggaaggg	aggcgtaaag	ccctgtctac	ctgcagctcg	720
cacatcaccg	tggttgctct	cttttttgtt	ccctgtatatt	tcatgtatgt	tagacctgtc	780
tcaaaattcc	ctattgataa	attcgttact	gtgttttata	cagttaatcac	acccatgctg	840
aatccttttt	tatacacgtt	gagaaattca	gagatgataa	atgctataaa	acacctgttg	900
tgtaagaagc	taactatagt	tagaataaga	gtgtccctcc	tcattg		945

<210> 797

<211> 967

<212> DNA

<213> Unknown (H38g647 nucleotide)

<220>

<223> Synthetic construct

<400> 797

atgggatcta	gtaacaatgt	tacagaattt	gtcctcctgg	ccctcactca	ggctcctgat	60
gtgcaaaaag	tattatttgt	aatgttttta	ttcacatata	ttgtgactat	gggtggcaac	120
ctgctcactg	tggtgaccat	ttttgccctc	cctcttttgg	ctccccagtg	taactcttcc	180
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tagacttact	ctgcgataaa	aaagactggt	tccttcccgg	cttgcattggg	ccagctatatt	300
gcgaccacc	tatttggtgg	tggtgaggtc	tttcttttctg	tggtgatggc	ctatgatcac	360
tatgtggcca	tctctaagcc	actgcactat	ttgatcatcg	tgaatcgact	ggtttgcatc	420
cttctgttgg	tggtggccgt	gactggagga	ttttgaattc	tatgtttctt	tttttttaaa	480
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tctgtggctc	caatgtcatt	gaccacattg	tctgtgacat	gtaccatta	ctggaactgg	600
catgcgctga	cacctacttt	atagggtca	ctgtgattgc	caatgggtgga	gcaatctgta	660
tggtcatctt	ctgccttcta	ctaaccctct	atggagtcac	cctaaacttc	cttaaaactt	720
atagtcaaga	agggaggcat	agaaccctgt	ctacctgcag	ctcccacatt	actgtggttg	780
tcctcttttt	tggtccctgt	attttcatgt	atgttagacc	tgtttcaaac	ttccctattg	840
ataaatcat	tactgagttt	tatacagtta	tcaccccaa	gttgaatcca	ttaatccaac	900
cactgagaaa	ttgagaaatg	agaattacta	tgaagaaact	ctggtgttaa	acctgaacta	960
tagttag						967

<210> 798

<211> 930

<212> DNA

<213> Unknown (H38g648 nucleotide)

<220>

<223> Synthetic construct

<400> 798

atgaaaaata	agaacaatgt	gactgaattt	atcctcttag	ggctcacaca	gaaccctgag	60
gggcaaaaag	ttttatttgt	cacattctta	ctaacttaca	tggtgacgat	aatgggcaac	120
ctgcttatca	tagtgaccat	catggccagc	cagtccttgg	gttcccccat	gtactttttt	180
ctggcttctt	tatcatctat	agataccgtc	tattctactg	catttgctcc	caaaatgatt	240
gttgacttgc	tctctgagaa	aaagaccatt	tcctttcagg	gttgatggc	tcaacttttt	300
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tacatggcca	tctgtaagcc	tcttcatgaa	ttgatcacca	tgaatcgctg	agtcctgtgt	420
cttatgtctg	tggtggcctg	gattggaggg	tttcttcaact	cattgggttca	atttctcttt	480
atttatcagc	tccctttctg	tggtaccaat	gtcattgaca	acttcctgtg	tgatttgat	540
cccttattga	aacttgcttg	caccaatacc	tatgtcactg	ggctttctat	gatagcta	600
ggaggagcga	tttggtctgt	caccttcttc	actatcctgc	tttcttatgg	ggatcatatta	660
cactctctta	agactcagag	tttggaaggg	aaacgaaaag	ctttctacac	ctgtgcatcc	720

cacgtcactg	tggtcatttt	attctttgtc	ccctgtatct	tcttgtatgc	aaggcccaat	780
tctacttttc	ccattgataa	atccatgact	gtagtcttaa	cttttataac	tcccatgctg	840
aaccactaa	tctataccct	gaagaatgca	gaaatgaaaa	gtgccatgag	gaaactttgg	900
agtaaaaaag	taagcttagc	tgggaaatgg				930

<210> 799

<211> 825

<212> DNA

<213> Unknown (H38g649 nucleotide)

<220>

<223> Synthetic construct

<400> 799

atgggtggaa	acctcctcat	ttgggtgact	actattggca	gcccctcctt	gggctcccta	60
atgtacttct	tccttgccta	cttgtcactt	atggatgcca	tatattccac	tgccatgtca	120
cccaaattga	tgatagactt	actctgtgat	aaaatcgcta	tttccttgtc	agcttgcatg	180
ggtcagctct	tcatagaaca	cttacttggt	ggtgcagagg	tcttcctttt	ggtgggtgatg	240
gcctatgata	gctatgtggc	tatctctaag	ccgctgcact	atttgaacat	catgaatcga	300
ctggtttgca	tccttctgtt	ggtgggtggc	atgattggag	gttttgtgca	ctctgtggtt	360
caaattgtct	ttctgtacag	tctaccaatc	tgtggcccca	atgttattga	ccactctgtc	420
tgtgacatgt	accattgtt	ggaactgtt	tgccttgaca	cctactttat	aggactcact	480
gtggttgcca	atgggtggaat	aatttgtatg	gtcatcttta	cctttctgct	aatctcctgt	540
ggagtcaccc	taaacttcct	taaaacttac	agtcaggaag	agaggcataa	agccctgcct	600
acctgcatct	cccacatcat	tgtgggtgcc	ctcgtttttg	ttccctgtat	ttttatgtat	660
gttagaccgc	tttccaaact	tccctttgat	aaattaatga	ctgtgtttta	ttcaattatc	720
acactcatgt	tgaatccttt	aatatactcg	ttgagacaat	cagagatgaa	aaatgctatg	780
aaaaatctct	ggtgtgaaaa	gttaagtata	gttagaaaaa	gagta		825

<210> 800

<211> 654

<212> DNA

<213> Unknown (H38g650 nucleotide)

<220>

<223> Synthetic construct

<400> 800

ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagac	tcattctccta	ggcaggctgc	ctgactccca	tgtctctctt	tgccatcttt	120
ggaggcatgg	aagagagaca	tgctcctgag	tgtgatccct	atgaccggtt	tgtagccatc	180
tgtcaccctc	tatatcattc	agccatcatg	aaccggtgtt	tctgtggctt	tctagttttg	240
ttgtcttttt	tttctcagtc	tcttttagac	gcccagggtg	acaacttgat	tgccctacaa	300
atgacctgct	tcaaggatgt	ggaaattcct	aatttcttct	gggaaccttc	tcaactcccc	360
catcttgcac	gttgcgacac	cttcaccaat	aacataatca	tgtattcccc	tgctgccata	420
tttggttttc	ttcccatctc	ggggaccctt	ttctcttact	ataagattgt	ttcctccatt	480
ctgagggttt	cttcatcagg	tgggaagtat	aaagccctct	ccacctgtgg	gtctcgctg	540
tcagttgttt	gctgagttta	tggaaacagg	gttggagagt	acctcggttc	agatgtgtca	600
tcttccccga	gaaagggtgc	agtggcctca	gtgatgtaca	cggtggtcac	cccc	654

<210> 801

<211> 648

<212> DNA

<213> Unknown (H38g651 nucleotide)

<220>

<223> Synthetic construct

<400> 801

tcaatggccc	tcattgtcat	ctgcaccacc	ggacccaaga	ggccttcaac	tacctgtctg	60
gcagcaagtc	ccatttctat	ggctgttgtg	ccacacaaat	tttcttctat	acatcactgc	120

ttggctctga	gtgctttctt	ttggctgtta	tggttatga	ccgctacact	gccatttgcc	180
accctctaag	atacaccaat	ctcatgagcc	ctaaaatttg	tggtactatg	actgcctttt	240
cctggatcct	gggtctctacg	gatggaatta	ttgatgttgt	agcaacattt	tccttctcct	300
actgtgggtc	tgggaaata	gcccacttct	tctgtgactt	ccccctccct	actaatcctc	360
tcatgcagt	acacatcaat	atttgaaaag	attcttttca	tctgctgtat	agtaatgatt	420
gttttccctg	ttgcaatcat	cattgcttcc	tatgctcgag	ttatcctggc	tgctattcac	480
atgggatctg	gagagggtcg	tcgcaaagct	tttactactt	gttcctctca	cctcttggtg	540
gtgggaatgt	actatggagc	agctttgttc	atgtacatac	ggccacacac	tgatcgctcc	600
ccaacacagg	acaagatggt	gtctgtattc	tacaccatcc	tcactccc		648

<210> 802

<211> 635

<212> DNA

<213> Unknown (H38g652 nucleotide)

<220>

<223> Synthetic construct

<400> 802

tttgtggaca	ttgcctgttc	ctcagccaca	gcaccaaga	tgattgaaga	ctttgtttct	60
gagaaaaaga	ctatttccta	ctggggctgt	ataactcaga	tgtttacctt	ccactttttt	120
ggttgtgctg	agatttttgt	tttgactgtc	atggcttttg	atcgctatgc	tgctatctgc	180
caaccctcc	gttacctgt	catcatgagt	gctaagtctt	atactgtgct	ggcatcactg	240
tcctgggttg	gggccctggg	tcattccttt	gttcagaccc	tcctgacctt	ccagctgccc	300
ttctgtaatg	ctcaggttat	agaacattac	ttttgtgatg	tccaccaggt	cctaaaactt	360
gcctgtgctg	atacaactct	ggtaaatag	ttggtggttg	ccaacagtgg	tctcatctcc	420
ctggggtgtt	tcctcattct	tttggcctcc	tacacagtca	ttctgtttag	tcttcaaaaa	480
cagtctgcag	agagctgaca	caaagttctc	tctacctgtg	gatctcatct	gactatagta	540
actttcttct	ttgttccgtg	tatctttatt	tatctccatc	cactactttc	ccattggata	600
aagctgtgtc	tgtgttctat	accaccatca	cccca			635

<210> 803

<211> 670

<212> DNA

<213> Unknown (H38g653 nucleotide)

<220>

<223> Synthetic construct

<400> 803

ttgcctgaca	tgggtttcac	ctccacacgg	tccccaagat	gattgtggac	atccagtcctc	60
acagcagagt	catctcctat	gcaggctgcc	tgactcagat	gtctctcttt	gccatttttt	120
gaggcagga	agagagacat	gtcctgagt	gtgatggcct	acgaccagtt	tgtagccatc	180
tgtaaccctc	catatcggtc	agccatcttg	aaccctgtgt	tctgtggctt	cctagatttg	240
ttgtccttgt	ttttttttct	tttttttttt	tctcagctct	ttagactccc	agctgcacaa	300
cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	tcttctggga	360
accttctcaa	ctcccccatc	ttgcatgttg	tgacatcttc	accaggaaca	tcaacctgta	420
tttccctgct	gccatatttg	gttttcttcc	catctcgggg	acctttttct	cttactctaa	480
aattgtttcc	tccattctga	gggtttcatc	gtcagggtgg	aggtataaag	ccctctccac	540
ctgtgggtct	cacgtgtcag	ttgtttgctg	agtttatgga	acaggcgttg	gagggtacct	600
cagttcggat	gtgtcatttt	ccccagaaa	gggtgcagtg	gcctcagtga	tgtacgcggt	660
tgtcaccccc						670

<210> 804

<211> 648

<212> DNA

<213> Unknown (H38g654 nucleotide)

<220>

<223> Synthetic construct

<400> 804
 ctctctggatc tttgtttacac cacatgtaca gtcccacaaa tgctagtaaa tttatgcagc 60
 atcaggaaaag taatcagtta tcgtggctgt gtagcccagc ttttcatatt tctggccttg 120
 ggggctactg aatatcttct cctggccgtc atgtcctttg ataggtttgt agctatttgt 180
 cggcctctcc attactcagt tatcatgcac cagagactct gcctccagtt ggcagctgca 240
 tccagggtta ctgggttttag taactcagtg tggttgtcta cctgactct ccagctgcca 300
 ctctgtgacc cctatgtgat agaccacttt ctctgtgaag tccctgcact gctcaagtta 360
 tcttgtgttg agacaacagc aaatgaggct gaactattcc ttgtcagtga gctcttccat 420
 ctaatacccc tgacactcat ccttatatca tatgctttta ttgtccgagc agtattgagg 480
 atacagtctg ctgaagggtcg acaaaaagca ttgtggacat gtgggttccca tctaattgtg 540
 gtgtctcttt ttaatagtac agccgtctct gtgtacctgc aaccaccttc gccagctcc 600
 aaggaccaag gaaagatggt ttctctcttc tatggaatca ttgcaccc 648

<210> 805
 <211> 655
 <212> DNA
 <213> Unknown (H38g655 nucleotide)

<220>
 <223> Synthetic construct

<400> 805
 ttgcctgaca tcgggtttcac ctccaccatt gtcccacaaga tgattgtgga catccagtct 60
 cacagcagag tgatctccta tgcaggccgc ctgactcaga tgtctctctt tgccattttt 120
 ggaggcatgg aagacagaca tgcctctgag tgtgatggcc tatgaccggt tcgtagccat 180
 ctgtcaccct ctatatcatt cagccatcat gaatccgtgt ttctgtggct tcctactttt 240
 gttgtctttt ttttttctca gtcttttaga cgcccagctg cacaacttga ttgccttaca 300
 aatgacctgc ttcaaggatg tggaaattcc taatttcttc tgtgaccctt ctcaactccc 360
 ccatcttgca tgttgtgaca ccttcaccaa taacataatc atgtattttt ctgctgccat 420
 atttggtttt ctteccatct cggggaccct ttctctttac gataaaattg tttcctccat 480
 tctgagggtt tcatcatcag gtgggaagta taaagccttc tccacctatg ggtctcacct 540
 gtcagatggt tcctgatttt atggaacagg cggttgaggg tacctcagtt cagatgtgtc 600
 atcttccccg agaaagactg cagtggcctc agtgatgtac acagtgggtca ccccc 655

<210> 806
 <211> 662
 <212> DNA
 <213> Unknown (H38g656 nucleotide)

<220>
 <223> Synthetic construct

<400> 806
 tttcctgaca tcgggtttcac ctccaccaca gtcccacaaga tgattgtgga catccagtct 60
 cacagcagag tcatctccta tgcaggctgc ccgactcaga tgtctctctt tgccattttt 120
 ggagacacgg aagagagaca tgttcctgag tgtgggtggc tatgaccggt ttgtagccat 180
 ctgtcaccct ctatatcgtt cagccatctt aaacctgtgt ttctgtggct tcctagattc 240
 gttgtccttg gttttttttt ttttctcagt ctttttagact ccagctgca caacttgatt 300
 gccttataaa tgacctgctt caaggatgtg gaaattccta atttcttctg ggaaccttct 360
 caactcccc atcttgcagt ttgtgacatc ttcaccagga acatcaacct gtatttccct 420
 gctgccatat ttgggtttct tcccatctcg gggacgcttt tctcttgcta taaaattggt 480
 tccttcattc tgagggtttc atcatcagg gtggaagtata aaccttctcc gcctgtgggt 540
 ctcactgtgc agttgtttac tgattttatg gaacaggctt tggagggtac ctcagttcag 600
 atgtgtcatc ttccccgaga aagactgcag tggcctcagt gatgtacgca gtgggtcaccc 660
 cc 662

<210> 807
 <211> 647
 <212> DNA
 <213> Unknown (H38g657 nucleotide)

<220>

<223> Synthetic construct

<400> 807

gtgctggatg	tcggatgtat	cactgtcact	gttcctgcaa	tgttgggtcg	tctcttgtec	60
cacaagtcca	caatttccta	tgacgcctgc	ctctcccagc	tcttcttctt	ccaccttctg	120
gctgggatgg	actgcttctt	gctgaccgcc	atggcctatg	accgactcct	ggccatctgc	180
cagccctca	cctacagcac	ccgcatgagt	cagacagtcc	agaggatggt	ggtggctgcg	240
tcctgggctt	gtgccttcac	caacgcactg	acccacactg	tggccatgtc	cacgctcaac	300
ttctgtggcc	caaatgaggt	caatcacttc	tactgtgacc	ttccacagct	cttccagctc	360
tcctgtctta	gcacccaact	caatgagctg	ctgctctttg	tagcagcagc	cttcatggct	420
tgggcaccct	tggctctcat	cagtgtgccc	tatgcccattg	tggtagctgc	tgtgctgcaa	480
atcgctccgc	tgagggcaga	aagaaggcct	tctccacatg	tggctccac	ctcactgtgg	540
tgggcatctt	ctatgggaca	ggtgtcttca	gctacatgag	gctgggttca	gtggaatctt	600
cagacaagga	taaggggggt	ggggttttca	tgactgtgat	caacccc		647

<210> 808

<211> 635

<212> DNA

<213> Unknown (H38g658 nucleotide)

<220>

<223> Synthetic construct

<400> 808

tttgtggaca	tagcctgttc	ctcagccaca	gcacccaaga	tgattgaaga	ctttgtttct	60
gagaaaaaga	ctatttccta	ctggggctgt	ataactcaga	tgtttacctt	ccactttttt	120
ggttgtgctg	acatttttgt	tttgactgtc	atggcttttg	atcgctgtgc	tgctatctgc	180
caaccctcc	gttacactgt	catcatgagt	gctaattgctt	atactgtgct	ggcatcactg	240
tcctgggttg	gggcccctgg	tcattccttt	gttcagaccc	tcctgacctt	ccagctgccc	300
ttctgtaatg	ctcaggttat	agaccattac	ttttgtgatg	cccaccaggt	cctaaaactt	360
gcctgtgctg	atacaactct	ggtaaatatg	ttgggtgggtg	ccaacagtgg	tctcatctcc	420
ctgggggtgt	tcctcattct	tttggcctcc	tacacagtca	ttctgtttag	tcttcaaaaa	480
cagtctgcag	agagctgaca	caaagttctc	tctacctgtg	gatctcatct	gactatagta	540
actttcttct	ttgttccgtg	tatctttatt	tatctccatc	cactacttcc	ccattggata	600
aagctgtgtc	tgtgttctat	accaccatca	cccca			635

<210> 809

<211> 648

<212> DNA

<213> Unknown (H38g659 nucleotide)

<220>

<223> Synthetic construct

<400> 809

ttctctgacc	tctgcttctc	ttccgtgacc	attcccaagt	tgttacagaa	catgcagaac	60
caggacccat	ccatccccta	tgcggactgc	ctgacccaaa	tgtacttctt	cctgttattt	120
ggagacctgg	agagcttctt	ccttgtggcc	atggcctatg	accgctatgt	ggccatctgc	180
ttccccctgc	actacaccgc	catcatgagc	cccatgctct	gtctcgccct	ggtggcgctg	240
tcctgggtgc	tgaccacctt	ccatgccatg	ttacacactt	tactcatggc	caggttgtgt	300
ttttgtgcag	acaatgtgat	ccccactttt	ttctgtgata	tgtctgctct	gctgaagctg	360
gccttctctg	acactcgagt	taatgaatgg	gtgatattta	tcatgggagg	gctcattctt	420
gtcatcccat	tcctactcat	ccttgggtcc	tatgcaagag	ttgtctcctc	catcctcaag	480
gtcccttctt	ctaagggtat	ctgcaaggcc	ttctctactt	gtggctccca	cctgtctgtg	540
gtgtcactgt	tctatggaac	cgttattggt	ctctacttat	gctcatcagc	taatagtctt	600
actctaaagg	acactgtcat	ggctatgatg	tacactgtgg	tgaccccc		648

<210> 810

<211> 438

<212> DNA

<213> Unknown (H38g660 nucleotide)

<220>

<223> Synthetic construct

<400> 810

actttgcaga	atatcacctc	cacttccatc	attttctctg	tcactgggtg	tcctgggctg	60
gaagccttcc	acacctggat	ctccattccc	ttctgcttcc	tctctgtaac	tgctctcttg	120
ggaaacagcc	tgatcctctt	cgctaccatc	actcagccca	gcctccacga	accaatgtac	180
tatttctctt	ccatgctgtc	cgccactgac	ctcggcctgt	ccatatccac	tctggtcacc	240
atgctgagta	tattctgggt	caatgtgagg	gaaatcagct	ttaatgcctg	cttgtcccac	300
atgttcttta	ttaaattctt	cactgtcatg	gaatcctcag	tgctgttggc	catggctttt	360
gacgttttgg	tgccgtctct	atccccttag	tatgccatga	tttaactgac	tcagatagct	420
aaaatgagtg	cagtgtat					438

<210> 811

<211> 1002

<212> DNA

<213> Unknown (H38g661 nucleotide)

<220>

<223> Synthetic construct

<400> 811

gcagggtgtg	aaaacgataa	tacaagttct	ttcgaaggct	tcatacctggt	gggcttctct	60
gacgttcccc	acctagagct	gacgtctctt	gtgggtgtcc	tcatacttta	tctgctgact	120
cttcttggca	acatgacat	tgtcttgcct	tcagctctgg	attcccggct	gcacacacca	180
atgtatttct	ttttggcaaa	cctctcattc	ctggacatgt	gtttcaccac	aggttccatc	240
cctcagatgc	tctacaacct	ttgggggtcca	gataagacca	tcagctatgt	gggttgtgcc	300
atccagctgt	actttgtcct	ggccctggga	gggggtggagt	gtgtcctcct	ggctgtcatg	360
gcatatgacc	gctatgctgc	agtctgcaaa	cccctgcact	acaccatcat	catgcaccca	420
cgtctctgtg	gacagctggc	ttcagtgcca	tggtctgagt	gctttggcaa	ttctctcata	480
atggcaccct	agacattgat	gctaccccg	tgtgggcaca	gacgagttga	ccactttctc	540
tgtgagatgc	cagcactaat	tggtatggcc	tgtgtagaca	ccatgatgct	tgaggcactg	600
gcttttgccc	tggcaatctt	tatcatcctg	gcaccactca	tcctcattct	catttcttat	660
ggttacgttg	gaggaacagt	gcttaggatc	aagtcagctg	ctgggcgaaa	gaaagccttc	720
aacacttgca	gctcgcact	aattgttgct	tctctcttct	atgggtacaat	catatacatg	780
tacctccagc	cagcaaatac	ttattcccag	gaccagggca	agtttcttac	ccttttctac	840
acaattgtca	ctcccagtg	taacccctg	atctatacac	taagaaacaa	agatgttaaa	900
gaggccatga	agaaggtgct	aggggaaggg	agtgcagaaa	tatagtaagg	gggtgattaaa	960
ctttgggatt	gtattttgac	ccatcttcta	tatatgttgt	ta		1002

<210> 812

<211> 827

<212> DNA

<213> Unknown (H38g662 nucleotide)

<220>

<223> Synthetic construct

<400> 812

ctctacctca	tcaagcatga	ccacagtctt	catgagccca	tgtactactt	cctcaccatg	60
ctggcaggca	cagacctcat	ggtgacattg	accacgatgc	ctactgtaat	gggcataccta	120
tgggtgaatc	acagggaaga	ttagcagtgt	gggctgcttc	ctacaggctt	actttattca	180
ctccctttct	gttgtggaat	caggttccct	cctggcaatg	gcatatgatc	gtctcattgc	240
catccgcaat	cctttgagat	atgctctcca	ttccaccaa	tactagagtc	atagcggttag	300
gagtgggatt	gttcctaagg	ggtttggtat	ccatcctgcc	tgtaattttg	cgtctttttc	360
catttccata	tggcaaatct	catgttatca	cacgttgctt	tctgcctcca	ccaagaaatc	420
atgagactgg	cttgtgctga	cataacttcc	aataaacttt	accctgtaat	tttgatctct	480
ttaacaatct	ccctaaactc	tctgatcacc	ccctcctcct	atataccta	ccttaatact	540
gtcataggca	ttgcctctgg	tgaaaaaaaa	ccaaagccct	caatacctgt	atctcccaca	600

taagttgtgt	ccttatctcc	tatgttacgg	tgatgggttt	gacattcatt	tacaaatttg	660
ggaagaatgt	gccaaagggt	gtccacatta	tcataagtta	catctacttc	ctctttcccc	720
ctttaatgaa	ccctgtcatc	tacagcatca	aaaccaagca	aatacaatat	ggcattatcc	780
gcctttttatc	taaacatagg	tttagtaggt	aaactcggat	ctggaaa		827

<210> 813

<211> 657

<212> DNA

<213> Unknown (H38g663 nucleotide)

<220>

<223> Synthetic construct

<400> 813

ttggccgaca	tcggtttcac	ctccaacacg	gtccccaaga	tgattgtgga	catccaatct	60
cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgctgttttt	120
ggaggcatgg	aagaaagaca	tgctcctgag	tgtgagggcc	tatgaccggt	ttgtagccat	180
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gttgtctttt	tttttttttt	ttctcagtct	ttcagactcc	cagctgcaca	acttgattgc	300
cttacaaatg	acctgcttca	aggatgtgga	aattcctaata	ttcttctggg	aaccttctca	360
actctcccat	cttgcattgt	gtgacacctt	caccagggaac	atcagtattt	ccctgctgcc	420
atatttggtt	ttcttcccat	ctcggggacc	cttttctctt	acgataaaat	tgttttctcc	480
attctgaggg	tttcatcatc	aggtgggaag	cataaggcct	tctccaccag	ggggctctac	540
ctgtcagttg	tttctgattt	ttatggaaca	ggcattggag	gctacctcag	ttcagatgtg	600
tcattctccc	cgagaaaggc	tgcagtggcc	tcagtgatgt	acacggtggc	catcccc	657

<210> 814

<211> 655

<212> DNA

<213> Unknown (H38g664 nucleotide)

<220>

<223> Synthetic construct

<400> 814

ttgcctgaca	tcggtttccc	ctccccacg	gtccccaaga	tggttgtgga	catccaatct	60
cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagacaca	tgctcctgaa	tgtgatggcc	tatgtccggt	ttgtagccat	180
ctgtcacccct	ctatattcatt	cagccatcat	gaaccctgtt	ttctgtggct	tcttactttt	240
gttgtctttt	ttttttctcg	gtcttttaga	cgcccagctg	cacaacatga	ttgccttaca	300
aatgacctgc	atcaaggatg	tggaatttcc	taatttcttc	tgtgaccttc	ctcaactccc	360
acaccttgcg	tgttgtgaca	ctttcaccaa	taacatagtc	atgtatttcc	ttgtgtccat	420
atttggtttt	cttcttatct	cacggatcat	tttctcttac	tataaaattg	tttctcccat	480
gctgagtgtt	tcattcatcag	gtgggaagta	taaagccttc	tccatctgtg	ggctctccct	540
gtcagttgtt	tgcttatttt	atggaaaagt	cgttgggggg	tacctgagtt	cagatgtgtc	600
atcttcccc	agaaagggtg	cagtggcctc	aatgatgtac	acggtgatca	cccc	655

<210> 815

<211> 646

<212> DNA

<213> Unknown (H38g665 nucleotide)

<220>

<223> Synthetic construct

<400> 815

ctagtggact	tttgttactc	ttcagctgtc	actcccacag	tcattgctgg	gctcgttata	60
ggagacaagg	tcattctcta	caatgcatgt	gctgctcaaa	tgctcttttt	tgacgctttt	120
gccactgtgg	aaaatttcc	cttggcctcg	atggcctatg	accgcatga	tgcatgtgtc	180
aaacccctac	attacaccac	caccatgaca	acaagtgtgt	gtgcatgtct	ggctataatc	240
tgttatgtct	gtggtttctt	gaatgcctcc	atacacattg	gggaaacatt	gtctctcttt	300

ctgtatgtcc	aatgaagtc	attgcttttt	ctgtgatgtt	ccaccagtca	tggtctctgtc	360
ttgctgtgat	agacatgtga	atgggctagt	tctcatttat	gtagccagtt	tcaatatctt	420
ttctgccatc	ctagttatct	tgatctccta	cctattcata	tttatcacca	tcctaaggac	480
gcactcggtc	tcaggatacc	agaaggcttt	gtccacctgt	gcctcccacc	tcactgcagt	540
catcatcttc	tatgggacta	ttatctccat	gtacttacag	cccagctctg	gtcactccat	600
ggacacagac	aaactggcat	ctgtgtccta	tactatgatc	atcccc		646

<210> 816

<211> 649

<212> DNA

<213> Unknown (H38g666 nucleotide)

<220>

<223> Synthetic construct

<400> 816

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gaggcatgga	agagagacat	gtccttgagt	gtgatggcct	atgaccggtt	tgtagccatc	180
tgtcaccctc	tatatcattc	agccatcatg	aaccggtgtt	tctgtggctt	cctagttttg	240
ctgtcttttt	tttctttctt	tttctcagct	gcacaacttg	attgccttaa	aaatgacctg	300
cttcaaggat	gtggaaattc	ctaatttctt	ctgtgacctt	tctcaactcc	cccatcttgc	360
atgttggtac	accttcacca	ataagataat	catgtatttc	cctgctgcca	tatttggttt	420
tcttcccatc	tcagggaccc	ttttctctta	ctctaaaatt	gtttcctcca	ttctgagggt	480
ttcatcatca	ggtgggaagt	ataaagcctt	ctccacctgt	gggtctcacc	tgtcagttgt	540
ttgctgagtt	tatggaacag	gcgttgagg	ttacctcagt	tcagatgatg	tgcatcttc	600
ccccagaaag	ggtgcagtgg	cctcagtgat	gtacacggtg	gtcaccccc		649

<210> 817

<211> 651

<212> DNA

<213> Unknown (H38g667 nucleotide)

<220>

<223> Synthetic construct

<400> 817

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aacaagagaa	aaacaatctc	ctttgtccca	tgacaaatgc	agaccttttt	atacatggct	120
tttgctcaca	ctgagtgtct	catcttggtg	atgatgtcct	acgatcggtg	catggctatc	180
tgccaccctc	tgcaatattc	tgatcatcatg	agatggggag	tgatgcacagt	cctgggtgtc	240
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cccttctgtg	ggcccatga	aatcaaccac	ttcttctgtg	aaatcctgtc	tgctcctcaag	360
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gggatccagt	ctggggagg	cgcagaaaag	gccttctcca	cctgctcctc	ccacctttgc	540
atgggtgggac	tcttctttgg	cagcgccatt	gtcatgtaca	tggtccccc	gtcccgccac	600
cctgaggagc	agcagaaggt	cctttccctg	ttttacagcc	ttttcaaccc	g	651

<210> 818

<211> 646

<212> DNA

<213> Unknown (H38g668 nucleotide)

<220>

<223> Synthetic construct

<400> 818

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ggagacgagg	tcattcttta	cagtgcattg	gctgctcaaa	tggtcttttt	tgacgctttt	120
gccactgtgg	aaaatttcct	cttggcctca	atggcctatg	accgctatga	tgacgtgtgc	180

aaacccctac	attacaccac	caccatgaca	acaagtgtgt	gtgcatgtct	ggctataatc	240
tgttatgtct	gtgggtttctt	gaatgcctcc	atacacattg	gggaaacatt	gtctctcttt	300
ctgaatgtcc	aatgaagtcc	attgcatttt	ctgtgatgtt	ccaccagtca	tggtctgttc	360
ttgtctgtat	agacatgtga	atgagctagt	tctcatttat	gtagccagtt	tcaatatctt	420
ttctgccatc	ctagtaatcc	tggctctccta	cctattccta	tttatcacca	tcctagagat	480
gcactcagct	tcaggatacc	agaaggcttt	gtccaactgt	gcctcccacc	tcactgcagt	540
catcatcttc	tatgggacta	ttatcttcat	gtacttacag	cccagctctg	gtcactccat	600
ggacacagac	aaactggcat	ctgtgtttcta	tactatgatc	atcccc		646

<210> 819

<211> 933

<212> DNA

<213> Unknown (H38g669 nucleotide)

<220>

<223> Synthetic construct

<400> 819

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ccgggagtc	agatccccct	cttcttcctg	tttctaggct	tctacgtggt	cactgtgggtg	120
gggaacctgg	gcttgataac	cctgataagg	ctcaactctc	acttgcacac	ccctatgtac	180
ttcttctctt	ataacttgte	cttcatagat	ttctgtctatt	ccagtgttat	cactcccaaa	240
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tgcagctccc	acataattgc	agtttctctg	ttctttgggt	caggagcatt	catgtacctc	780
aaaccctttt	ctcttttagc	tatgaaccag	ggcaagggtg	cttccttatt	ctataccact	840
gtggtgcccc	tgtctaaccc	attaatttat	agcctgagga	ataaggacgt	caaagttgct	900
ctaaagaaaa	tcttgaacaa	aatgcattc	tcc			933

<210> 820

<211> 927

<212> DNA

<213> Unknown (H38g670 nucleotide)

<220>

<223> Synthetic construct

<400> 820

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ggcaacttgg	gcttgatcac	cttaattggg	ataaatccta	gccttcacac	ccccatgtac	180
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cgctatgtgg	ccatctgcaa	ccccctgtc	tacatggtca	ccatgtcccc	aagggtctgc	420
ttctgtctga	tgtttgggtc	ctatgtggta	gggtttgctg	gggccatggc	ccacactgga	480
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acatcttttc	ctggctctat	gaaccatggc	agatttgcct	cagtctttta	caccaatgtg	840
gttcccatgc	ttaacccttc	gatctacagt	ttgaggaata	aggatgataa	acttgcctctg	900
ggcaaaaccc	tgaagagagt	gctcttc				927

<210> 821
 <211> 887
 <212> DNA
 <213> Unknown (H38g671 nucleotid)

<220>
 <223> Synthetic construct

<400> 821
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 cataaatttta tgtccctaaa ttctcacctt cataccccca cacacttttt cctcttcacg 180
 ctatccttca ttgatgtctg ctattcattt gtctgtacca caaaaattcc aatgggcttt 240
 atctcagaga ggaacatcat ctcttttggt ggatggccaa cgtagctata tttcttttgc 300
 atctttgtca aagaacctaa aaatggggtc attgtgggaa taatgttctc agccaagatg 360
 cttgtagccg agagataatg gactagtcgt tgatgtgaaa ctagaaaatg cacatggccc 420
 tagaaaggtc tgattttaga atgggataaa caggatctgc taaaaagaaa catttaatca 480
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 gttccttagc gaagcaagac acactctcta gaattgcaca tgtactttaa aaagtctgtt 600
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 atcatagaaa atggatcttt acaaaatctt catgttttgt gggttactca caagaaaaat 720
 tttctccgct catttctact tctcaaatgg ttcaaggaaa aatgctcctt aaaggatata 780
 tctgattctg gagaatgagc ttacctatgt gtgcaatttt tatctttgtc agaagatact 840
 actaccttct gaaaaagttg aaaacactgc ttataagaa cagctat 887

<210> 822
 <211> 939
 <212> DNA
 <213> Unknown (H38g672 nucleotide)

<220>
 <223> Synthetic construct

<400> 822
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 ggcaaccctg gcttgatcat tcttttcggt ctaaattctc acctccacac accaatgtac 180
 tatttctctt tcaatctctc ctctcattgat ctctgttact cctctgtttt cactcccaaa 240
 atgctaataga actttgtatc aaaaaagaat attatctcct atgttgggtg catgactcag 300
 ctgtttttct ttctcttttt tgtcatctct gaatgctaca tgttgacctc aatggcatat 360
 gatcgctatg tggccatctg taatccattg ctgtataagg tcaccatgtc ccatcaggtc 420
 tgttctatgc tcacttttgc tgcttacata atgggattgg ctggagccac ggcccacacc 480
 ggggtgcatg ttagactcac ctctctgagt gctaatatca tcaaccatta cttgtgtgac 540
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 attgttgggg gtattaatat catggtaccc agttgtacca tctcatttc ttatgttttc 660
 attgtcacta gcattcttca tatcaaatcc actcaaggaa gatcaaaagc cttcagtact 720
 tgtagctctc atgtcattgc tctgtctctg ttttttgggt cagcggcatt catgtatatt 780
 aaatattctt ctggatctat ggagcaggga aaagtcttct ctgttttcta cactaatgtg 840
 gtgcccacgc tcaatcctct catctacagt ttgaggaaca aggatgtcaa agttgcactg 900
 aggaaagctc tgattaaaat tcagagaaga aatatattc 939

<210> 823
 <211> 1071
 <212> DNA
 <213> Unknown (H38g673 nucleotide)

<220>
 <223> Synthetic construct

<400> 823
 atgaattggg taaataagag tgtccacag gagttcatcc tgtagtttt ctcagatcaa 60

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atgtgggttaa acatatgcaa caccaggaaa gtaatcagtt atgggtggctg tgtggcccag 300
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tgcttccagt tggcagctgc atcctggatt agtggcttta gcaattcagt attacagtcc 480
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tttaaaaggt tggttgcaaa gagtcttctt aatcaagaaa taagaaatat gcaaatgata 960
agctttgcta aagacacagt gcttacttac cttactaact tctccgcaag ttgtcctatt 1020
tttgtcatta ctatagaaaa ctattgtaat ctccctcaaa gaaaatttcc t 1071

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<210> 824

<211> 991

<212> DNA

<213> Unknown (H38g674 nucleotide)

<220>

<223> Synthetic construct

<400> 824

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tttggcttgg taactctcgt tgtgtcfaat tcacaccttc atacccccat gtactttttc 180
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atgaacttca taacacagaa ggatattatc tcccacatgg ggtgcatgtc ccagcttttc 300
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catgtccccc aaagtgtact ctcaccttat gcttggttta tacttgctag ctttttctag 480
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ctttctctga gaaaaaac ctagtaggaa aaaattttga ctagaaatag tatctttctg 960
tgcatgtatt ttaggacag ggagcttctg t 991

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<210> 825

<211> 997

<212> DNA

<213> Unknown (H38g675 nucleotide)

<220>

<223> Synthetic construct

<400> 825

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ccagatcttt aactccctct gttcttcatg tttcttgtaa tgtatgttgt cactgtgata 120
agaaactttg tcttggtaat tctaactatg cgaaattcac gtcttcacac tcccaagtac 180
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gacgtcaatg gcctatgatt gctgtgtggc catctgttac ccacttcttt atcacattgc 420

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catgtccct	aaagtgtgtt	tcagccttat	gcttgggtcc	tacttcctat	ccttttctgg	480
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tgtaaatttt	gccatgggaa	aatctctgag	taggagaatg	tttttgccat	aaacaacatt	960
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<210> 826

<211> 939

<212> DNA

<213> Unknown (H38g676 nucleotide)

<220>

<223> Synthetic construct

<400> 826

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gggaacattc	tcattcatcat	tgccacagtc	tttactccaa	gtctccatac	ccccatgtat	180
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ctcttcttcc	tacatctctt	tgcctgtgcc	gagatcttcc	tgtgatcat	tgtggcgtat	360
gatcgttacg	tggctatctg	cactccactc	cactacccca	atgtgatgaa	catgagagtc	420
tgtatacagc	ttgtctttgc	tctctggttg	gggggtactg	ttcactcact	agggcagacc	480
ttcttgacta	ttcgtctacc	ttactgtggc	cccaacatta	ttgacagcta	cttctgtgat	540
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ttgctgaatc	ccttcattta	caccttgagg	aatgaggagg	taaaaagtgc	catgaagcag	900
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<210> 827

<211> 992

<212> DNA

<213> Unknown (H38g677 nucleotide)

<220>

<223> Synthetic construct

<400> 827

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gggaatttgg	gcttggtaac	tctgattgtg	ttcagttcac	actttcatgc	acccatgtac	180
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tttttttctt	tctttttttt	tttttttttg	ttatttctga	atgctatgtt	ttgacgtcaa	360
tggctctctga	tcactagtgg	ccatggccat	ctgtaaccgg	cttctgtata	acattgccat	420
gtccctctaaa	gtgtgttcca	gccatagct	tggttccctac	ttctggccct	tttctggggc	480
catggcccat	accaggtgca	tgtgaaact	gacctcctgt	gaggcaaaca	ccatcaacca	540
ctacttctgt	gacacccttc	atctgtcca	gctctcttgc	accagcacct	acgtcagtga	600
gttgatgggt	ttcattgcag	caggcatcat	tttactgtg	cccagtatca	ccatctttat	660
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acattgatgt	agttcccatg	ataaactcct	caatttacag	cttaagaaac	aatgatgtta	900

aacttgcctg gagaaaaatc ctaagttgga gaaaatttcc atttgaaact atctctctcc 960
atgcatatag ttacaggaca aggagattct gt 992

<210> 828

<211> 966

<212> DNA

<213> Unknown (H38g678 nucleotide)

<220>

<223> Synthetic construct

<400> 828

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ccttctgacc ctcatgggtg acacatccat catctgcgct gtgtgggtcaa gccagaaact	180
ccacacacct atgtacatcc tcttgggttaa tttctcttcc ctggagatct gctgcattag	240
ttctgatgtc ccaaaatgtt ggccaatctc atctcccata tcaagagcat ctcctatgct	300
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ctgaaa	966

<210> 829

<211> 1003

<212> DNA

<213> Unknown (H38g679 nucleotide)

<220>

<223> Synthetic construct

<400> 829

atggaagagg ccactctact caatcaaact tctttagtga catattttcg gcttagaggt	60
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ctgacactga ttgggaatgt tctcattgtc ataactatta tctatgacca ccggctccat	180
actcccatgt atttcttctt cagcaacctg tcctttattg atgtctgcca ctccactgtc	240
actgtcccca agatgtctgag agacgtgtgg tcagaggaaa agctcatctc ttttgatgcc	300
tgtgtgaccc agatgttctt cctgcacctc ttgacctgca cagagatctt cctcctcacc	360
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aactggaagg tatgtgtgct gctggctgtg gccctctgga caggagggac catccactcc	480
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agatcctcat tgtctccaac agtggattga tctccgtggg ctgttttgtg gtcctgggtg	660
tgtcctacgc agtcatcctg gtgagtctga ggcagcagat ctccaagggc aagtggaagg	720
ccctgtccac ctgtgcagcc catctcactg tagttacact gttcctggga cactgcactc	780
tcacttatcc ccgcccaccc accagcctcc cagagacaaa ggcagtatct gtgtttttca	840
ctgcagtcac cccctgtctg aaccccatga tctataccct taggaatgaa gaaatgaaga	900
gtgccttaaa caagttagtg gggagaaaag agagaaaaga agaaaaatga aaatgtctac	960
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<210> 830

<211> 478

<212> DNA

<213> Unknown (H38g680 nucleotide)

<220>

<223> Synthetic construct

<400> 830

acggggactg gatgatggct gtgtcatgcc atgatacctaa ctcccctcac ttccagttac	60
cttactgtgg cctaacaagg tgggctatac ttctgtgata tcctgcagtg tacctctagc	120
ctgtaaggac acatccttag ccagagggt aggttttaca aatgttggtc tttgtctct	180
catttgcttt tttctcatcc ttgtttccta tacttgcatt gggatttcca tatcaaaaat	240
ccgctcagca gagggcaggc agcgggcctt ctccacctgc agcgctcacc tcaactgcaat	300
cctttgtgct tatgggccag tcatcgttat ctatctacaa cccaatcca gtgccttgct	360
tggttccata attcagatat tgaataatct ggtaacccca atgttgaatc cactaatcta	420
tagccttagg aataaggatg taaaatcaga tcagccctga ggaatgtatt tcccaaga	478

<210> 831

<211> 400

<212> DNA

<213> Unknown (H38g681 nucleotide)

<220>

<223> Synthetic construct

<400> 831

ttactatttt taatgttctt tattacttcc ttgggtcata aattccatct gatatcattt	60
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tgataacata cactcacagc attaatattat tgtaaattgt ccttgttcta gggtagagac	180
ctattttagt ggtataccct ttagtcccag agtattgttc ttatttctag ggcgtgggtcc	240
ttctgggttt tcattagaaa gcctaagttt ttaccgaacc tctttcactt ggcagcactt	300
gcatttaaaa ttctattgcc ctagttaggg gtaactgcta aaatcttttc tctcagccat	360
ctggctgctg ttttctactt actttcttag agtcttgtct	400

<210> 832

<211> 933

<212> DNA

<213> Unknown (H38g682 nucleotide)

<220>

<223> Synthetic construct

<400> 832

atggctactt caaaccattc ttcaggggct gagtttatcc tggcaggctt gacacaacgc	60
ccagaacttc aactgccact ctctctctctg ttcttggaa tatatgtggg cacagtgggtg	120
gggaacctgg gcatgatctt cttaatgtct ctcagttctc aactttaccc tccagtgtat	180
tattttctca gtcatttgct tttcattgat ctctgctact cctctgtcat tacccttaag	240
atgctgggtga actttgttcc agaggagaac attatctcct ttctggaatg cattactcaa	300
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gaccgttatg ttgctatctg tcgcccactg ctttacaata ttgtcatgtc ccacaggggc	420
tgttccataa tgatggctgt ggtatactca ctgggttttc tgtggggccac agtccatact	480
acccgcatgt cagtgttgct attctgtagg tctcatacgg tcagtcatta tttttgtgat	540
attctccccct tattgactct gtcttgctcc agcaccaca tcaatgagat tctgctgttc	600
attattggag gagttaatac cttagcaact acactggcgg tccttatctc ttatgctttc	660
attttctcta gtatccttgg tattcattec actgaggggc aatccaaagc ctttggcact	720
tgtagctccc atctcttggc tgtgggcac ttttttgggt ctataacatt catgtatttc	780
aagccccctt ccagcactac tatggaaaaa gagaagggtgt cttctgtgtt ctacatcaca	840
ataatcccca tgctgaatcc tctaattctat agcctgagga acaaggatgt gaaaaatgca	900
ctgaagaaga tgactagggg aaggcagtc tcc	933

<210> 833

<211> 948

<212> DNA

<213> Unknown (H38g683 nucleotide)

<220>

<223> Synthetic construct

<400> 833

atgggtgatcc	tgtcctggga	aaaccaaacg	atgagagtgg	aattcgtgct	tcaaggattc	60
tcttccatca	gacagttaaa	tattttcctc	tttatgataa	ttttagtttt	ctacatctta	120
actgtttctg	gaaacatcct	cattgtcctt	ctagttttag	tcagacatca	tctccacacc	180
cctatgtact	tctcctgggt	gaacttgctc	tgtctggaga	tctgggtatac	ctctaacatc	240
atccccaaaa	tgttgctgat	tatcatagct	gaatagaaga	ctatctctgt	ggctggctgg	300
ctggcacaat	tctacttctt	cggatccctg	gctgccacgg	agtgcctctt	gctcactgtg	360
atgtcctatg	atcgctacct	agccatctgc	cagcctcttt	gctaccgtgt	cctcatgact	420
ggcccccttt	gcacaggct	agctgctggc	tcttggttct	gctgcttctt	ccttacagca	480
atcaccatgg	tcttgctatg	tagactaacc	ttctgtggac	cctatgaaac	tgatcacttc	540
ttttgtgact	tcacccctct	ggttcatctc	tcttgcattg	atacctcagt	gactgagacc	600
attgcctttg	ccacctcttc	tgcagtaact	ctgatcccat	ttctcctcat	tgtagcctcc	660
tactcctgcg	tcctttctgc	tatcctaaga	atccccatct	gcacaggcca	gaaaaaggcc	720
ttctccacct	gctcttccca	cctcactgtg	gtcatagtgt	tttatgggac	actgattggc	780
acataccttg	tgccctcagc	caactcatcc	caactcttgt	gcaaagggtc	ctctctgtct	840
tacatcatcc	tgacacccat	gtttaacccc	atcatttata	gcctgagaaa	tagagacatc	900
catgaagctc	tgaagaagtg	cttgaggaag	aagtcagggt	tttgctt		948

<210> 834

<211> 946

<212> DNA

<213> Unknown (H38g684 nucleotide)

<220>

<223> Synthetic construct

<400> 834

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ggcttcccct	gccgtggga	gatccagatc	ctcctttttg	tggctctctc	tctcatctac	120
cttctgacct	tcctaggtaa	cacatccatc	atctgtgctg	tgtgggtcaag	ccagaaactc	180
cacacaccta	tgtacatcct	actggccaat	ttctccttcc	tggagatctg	ctgtgtcagt	240
tctgacgtgc	ccataatggc	agccaatctc	atctcccaga	cacagagcat	ctcctgtgct	300
ggctgcctgc	tcgggttcta	cttcttctcc	atgtgtgctg	cagagtgtct	atttctgtca	360
gtgatgtctt	ttgatagggt	tctgcccatt	tgtagacctt	tgactatcc	caccttaatg	420
acccatcacg	tttgtgtca	tttttgtgat	cttctgctgg	gtgggtggct	gtctctgggt	480
attgacctt	ttgacactaa	tatctcaggt	gctcttttgt	ggtccaaaca	ctatcgacca	540
ttttttctgt	gatctggcac	ctttgctggc	actgtcttgt	gctccaatac	ctggaattac	600
tctgacttgt	ggtatcatta	gcgctctcat	catctttctt	accttcttgt	atatccttgg	660
gacttatttc	tgtgttctaa	gcacagtgtc	acaggtgcct	tcaggcttag	gaaggcataa	720
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gggtgatgtat	gttagccag	gttctgggga	ctatcatggg	ataaagaaat	ttgcgacctt	840
gttctatact	ttgtcaactc	cattctttta	tcctctgata	tacagtttcc	ggaacaagga	900
tatgaaagag	gcactaaaga	aatttctgag	gaatcgccac	actgtc		946

<210> 835

<211> 946

<212> DNA

<213> Unknown (H38g685 nucleotide)

<220>

<223> Synthetic construct

<400> 835

cttatagcta	caggaaactg	gacaagaata	agtaagttaa	tcctcatgag	cttctcttcc	60
ctgcctactg	aaatacagtc	attactcttt	ctgacatttc	taaccatcta	cctgggtcacc	120
ctgatgggaa	actgcctcat	cattctgggt	accctagctg	accccatgct	acacagcccc	180
atgtacttct	tcctcagaaa	cttatcttct	ctggagattg	gcttcaacct	agtcattgcy	240

cccaacatgc	tgtggaccct	gcttgcccag	gacacaacca	tctccttcct	tggctgtgcc	300
acttagatgt	atttcgtctt	cttctttggt	gtggctgaat	gcctcctcct	ggctaccatg	360
gcatatgacc	gctatgtggc	catctgcagt	ccttgcaacta	cccagtcac	atgaacccaa	420
ggactcttgc	caaactggct	gctacctcct	ggttcccagg	ctttcctgta	gctactgtgc	480
agaccacatg	gctcttcagt	ttccattct	gtggaccacaa	caaggtgaac	cacttcttct	540
gtgacagccc	acctgtgctg	aggctggctc	gtgcagacac	agcactcttt	gagatctacg	600
ccatcgctcg	aaccattctg	gtggctcatga	tcccctgctt	gctgatcttg	tgttcctata	660
ctcacattgc	tgtgcccac	ctcaagatcc	catcagctaa	agggagaagt	aaagcctttt	720
ctacatgttc	ctcacacctc	cttggtgtct	ctcttttcta	tatatcatta	agcctcacct	780
acttccggcc	taaatcaaat	aattcacctg	agggcaagaa	gctgctatca	ttgtcctaca	840
ctgttatgac	tcccatgttg	aaccccata	tctacagcct	gagaaataac	gaggtgaaga	900
atgccctcag	caggacggtc	tctaaggccc	tagccctcag	aaactg		946

<210> 836

<211> 973

<212> DNA

<213> Unknown (H38g686 nucleotide)

<220>

<223> Synthetic construct

<400> 836

atggctgtgg	aaaatgactc	ttcagtgaca	agagtttatt	cttttgggat	taacagacca	60
gcctgagatc	taattgcccc	tgtttttcct	gttcttgggt	aactatatga	ccaccatggt	120
gggcaacttg	agtttaatta	atctaatttg	cctgaattca	caccttcaca	ctcccatgta	180
ttttttcctt	ttcaatctgt	ccttcattga	tctctgttat	tcatttgtct	ttacccccaa	240
aatgctgatg	agctttatct	cagagaggaa	catcatctcc	tttccaggat	gcgtaactca	300
gctctttttc	ttctgctttt	ttgtccactc	tgagtgtcat	gtgctgacag	ccatggccta	360
tgatcgctat	gtggccatct	gcaaaccctc	tctgtacatg	gtcaccacgt	cccctcagat	420
ctgttctcta	ctgatgcttg	gttcataatg	gatgggggtt	gctggggcca	tggtccacac	480
agagtgtatg	atgaagctca	tcttttgtga	ctccaacgtc	atcaaccatt	acatgtgtga	540
catcttccca	ctgtccagc	tctcctgcag	cagcacctag	gccaatgagc	tggtgatgtc	600
tgttattgta	ggcacagttg	ttatagtatc	aagcctcatt	atcttaattc	cttatgcttt	660
gattcttttc	aatatccttc	acatgtcttc	agccgagggt	tggttcaaag	ccatcggtac	720
ctgtggctcc	cacataataa	ctgttggcct	attctatgaa	tttgggctga	tactcatgtt	780
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tgaggtaccc	atgtcgaacc	ccctcattta	tagcctcagg	aacaaggatg	tcaaacttgc	900
tctaaggaa	accctaata	aaattacaaa	ctgagtagag	ccaatggtgc	tgccttagcc	960
cctctccaat	tgc					973

<210> 837

<211> 992

<212> DNA

<213> Unknown (H38g687 nucleotide)

<220>

<223> Synthetic construct

<400> 837

atgagataga	taaatcagac	acaagtgata	gaattcctcc	ttctgggact	ctctgatggg	60
ccacacaccg	agcagctgct	atttatcgta	ttattgggtg	tctacctggt	cactgtgctt	120
ggaaatctgc	ttctaattct	ccttggtcat	gttgactccc	aacttcacac	acccatgtat	180
ttttttctct	gcaacttgtc	tctggctgac	ctctatttct	ctaccaacat	acttctctag	240
gcactagtcc	acctgctttc	cataaacaac	ctcattgcat	tcacactttc	tctaactcaa	300
cttctctttt	tcctcatttt	tggtgacccc	agtgcgcctc	tattgcagtg	atgtcctata	360
atccctatgt	tgcaatctgc	aatcctctgc	attaccctaa	catcatgacc	tggaaagtgt	420
gtgtccagct	ggcaacagga	tcatggacca	gtggcattct	ggtgtctgtg	gtagacacca	480
ccttcacact	gaggctaccc	taccgaggca	gtaacagcat	tgtcattttc	ttttgtgagg	540
ccctctgact	attgatctta	gcataccag	acacccatgc	atcagagatg	gccatttatc	600
ttacgggggt	tgtgattctc	ctcatacctg	tttttctgat	tctggtatcc	tatggccgta	660
tcatagtaac	tgtggtcaag	atgaagtcaa	ctgtggggag	tctcaaggca	ttttctacct	720

gtggctccca	cctcatgggtg	gtcatacttt	taaatggatc	agcaatactc	acttgcata	780
cacccaagtc	ttccaaacag	cagtaaaaat	cggtgtctgt	tttctatgca	atagtaactc	840
ccatgcttaa	ttccctcatc	tatagcctga	gaaacaagga	tgtgaaggca	gctctgagga	900
aagtagccac	aaggaatttc	ccatgaaggc	ttggaatctc	acactgacag	tgagctcaga	960
gaaccttttg	gttcctact	tcaaagactt	gc			992

<210> 838

<211> 549

<212> DNA

<213> Unknown (H38g688 nucleotide)

<220>

<223> Synthetic construct

<400> 838

atggaaaaaa	gcaataatag	cactttgttt	attctcttgg	ggttttccca	aaataagaac	60
attgaagtcc	tctgctttgt	attatttttg	ttttgctaca	ttgctatttg	gatgggaaac	120
ttactcataa	tgatttctat	cacgtgcacc	cagctcattc	accaaccat	gtatttcttc	180
ctcaattacc	tctcactctc	cgaccttgc	tacacatcca	cagtgacccc	caaattaatg	240
gttgacttac	tggcagaaag	aaagaccatt	tcctataata	actgtatgat	acaactcttt	300
accacccatt	tttttgagg	catagagatc	ttcattctca	cagggatggc	ctatgaccgc	360
tatgtggcca	tttgcaagcc	cctgcactac	accattatta	tgagcaggca	aaagtgtaac	420
acaatcatca	tagtttgttg	tactggggga	tttatacatt	ctgccagtca	gtttctcttc	480
accatctctg	taccattttg	tggcccaaat	gatatagatc	actactctcg	cgatgtgtat	540
cctttgctg						549

<210> 839

<211> 670

<212> DNA

<213> Unknown (H38g689 nucleotide)

<220>

<223> Synthetic construct

<400> 839

ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgagcgtgga	catccagtct	60
cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	gtgatggcct	atgacctgtt	tgtagccatc	180
tgtaaccttc	tatatcgttc	agccatcttg	aacctgtttg	tccgtggctt	cctagatttg	240
ttgtctttgt	tgttggtttt	tttttttttc	tctcagtctt	ttagactccc	agctgcacaa	300
cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attccgaatt	tcttctggga	360
accttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	accaggaaac	acaacatgta	420
tttccctgct	gccgtatttg	gttttcttcc	catctcgggg	acctttttct	cttactgtaa	480
aattgtttcc	tccattctga	gggtttcatc	atcaggtggg	aagtacaaac	cttctccacc	540
tgtgggtctc	acctgtcagt	tgtttgctga	ttttatggag	caggcgttgg	agggtacctt	600
ggttcagatg	tgatcatctt	cccagaaaag	ggtgcagtgg	cctcagtgc	gtacgtacac	660
ggtggtcacc						670

<210> 840

<211> 645

<212> DNA

<213> Unknown (H38g690 nucleotide)

<220>

<223> Synthetic construct

<400> 840

atggacgtca	ggctcatctg	caccaccgta	cccaagatgg	ccttcaacta	cttgtctggc	60
agcaagtcca	tttctatggc	tggtgtgcc	acacaaattt	tcttctgtgt	atcactgctt	120
ggctctgaat	gctttctgtt	ggctgttatg	tcttatgact	gctacattgc	catttgccac	180
cctctaagat	acaccaatct	catgagaccc	aaaatttgta	gacttatgac	tgcttctctc	240

tggatcctgg	gctctacaga	tggaatcatt	tatgctgtag	ccacattttc	cttctcctac	300
tgtgggtctc	gggaaatagc	ccacttcttc	tgtgagttac	cttccctact	aatcctctca	360
tgcaatgaca	cgtcaatatt	tgaaaagggt	atttttcattt	gctctatagt	aatgcttggt	420
ttccctgttg	caatcatcat	tgcttccctat	gctggagtta	ttctggctgt	cattcacatg	480
ggatctggag	agggtcgtcg	caaagctttc	acgacctgtt	cctctcacct	catgggtggtg	540
ggaatgttct	atggagcagg	tttgttcatg	tacatacagc	ccacatctga	tcgctcccca	600
acgcaggaca	agctgggtgc	tgtattctac	accatcctca	ctccc		645

<210> 841

<211> 380

<212> DNA

<213> Unknown (H38g691 nucleotide)

<220>

<223> Synthetic construct

<400> 841

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ctccgagaag	caaggcatgt	cctttcccaa	gaaacttttc	cagaatcaca	aacttttctc	120
actcttttga	gggatgaatg	tattttctgca	gactgtgatg	gcctatgacc	actttgtggc	180
catctgtcac	cccctgcact	acagggcat	catgaatcct	gggatctttg	gactgtgggt	240
tctggtgtcc	tggagcatga	gtgccctgaa	ttcctcactg	caaagcagaa	tgtgttgag	300
ctgtccttct	gcacaaactt	ggaaatcccc	ccattttttt	ctgtgaactt	aatcagttga	360
tctgtcttgc	ctgttctaac					380

<210> 842

<211> 648

<212> DNA

<213> Unknown (H38g692 nucleotide)

<220>

<223> Synthetic construct

<400> 842

tttgttgatt	tctgttatcc	caccacgatt	acacccaaac	tgctggagaa	cttgggtgtg	60
gaagatagaa	ctatctcctt	cacaggatgc	atcatgcagt	tattctttgt	ctgcatattt	120
gtagtaacag	aaacattcat	gctggcagtg	atggcctatg	accgatatgt	ggcgggtgtg	180
aaccctcttc	tctacacagt	tgcaatgtac	cagaggcttt	gtcccttgtt	agtggctacg	240
tcatactggt	gggggatagt	ctgttccctg	acacttacct	agtttctact	ggaattatcc	300
ttcagaggaa	ataatatcat	taataacttt	gtctgtgagc	acgctgccgt	cgttgctgtg	360
tcttggtctg	acccctgtgt	gagccaggag	atcactttag	tttctgccac	attcaatgaa	420
ataagcggcc	tggatgatcat	tctcactccc	tatgctttca	tttttatcac	tgtcatgaag	480
acgccttcca	ctggggggcg	caagaaagcg	ttctccacgt	ctgcctccca	cttgacggcc	540
attaccattt	tccatgggac	tatccttttc	ctctactgtg	ttcctaactc	caaaagtctg	600
tggctcatgg	tcaagggtggc	ctctgtcctt	tacacagtgg	tcattccc		648

<210> 843

<211> 643

<212> DNA

<213> Unknown (H38g693 nucleotide)

<220>

<223> Synthetic construct

<400> 843

ttgccagaca	ttggtttcac	cttggccacg	gtccccaaga	tgattgtaga	catgcaatca	60
catagcagaa	tcattctccca	tgagggtgtg	ctgacacaga	tacctttctt	tgtccttttt	120
gtatgtatag	atgacatgct	cctgactgtg	atggcctatg	actgatttgt	ggccatctgt	180
cacccctgc	actacccagt	catcatgaat	cctcacctct	gtgtcttctt	agtgttgatg	240
tctttttcct	tagcctgttg	gattcctagc	tgcaacaactg	gattgtttaca	attcacctgc	300
ttcaagaatg	tggaaatctc	taattttttc	tgtgactgat	ctcaacttct	caaccttgcc	360

tgttctgact	gtcatcagta	acatattcat	acgttttagat	agtactatat	ttggctttct	420
tccattttca	gggatccctt	tgtcttacta	taaaattgtg	ccctccattc	taagaattcc	480
attgtcagat	gggaagtata	aagccttctc	cacctgctgc	tctcacctgg	caattgtttg	540
cttattttat	ggaacaggca	ttggcatgta	cctgacttca	gctgtgtcac	cagccccag	600
gaatggtgtg	gtggcatcag	tggtgtacgc	tatggtcacc	ccc		643

<210> 844

<211> 652

<212> DNA

<213> Unknown (H38g694 nucleotide)

<220>

<223> Synthetic construct

<400> 844

ttgcctgaca	tcggtttcac	ccccaccacg	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcattctatgc	aggctgcctg	actgtgatgt	ctctctttgc	cattttttgga	120
ggcatggaag	agacacatgc	tcctgaatgt	gatggcctat	gtccggtttg	tagccatctg	180
tcaccctcta	tatcattcag	ccatcatgaa	cccgtgttct	tgtggcttct	tacttttgtt	240
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gacctgcttc	aaggatgtgg	aaattcctaa	tttcttctgt	gaccttctc	aactccccca	360
tcttgcatgt	tgtgacacct	tcaccaataa	cataatcatg	tattttctcg	ctgccatatt	420
tggttttctt	cccatctcgg	ggaccctttt	ctcttactat	gaaattgttt	cctccattct	480
gagggtttca	tcataagggtg	ggaagtataa	ggccttcgcc	acctgtgggt	ctcacctgtc	540
agtcgtttgc	tgattttatg	gaacaggcgt	tggagggtac	ctcagttcag	atgtgtcatc	600
ttccccgaga	aagactgcag	tggcctcagt	gatgtacgca	gtggtcaccc	cc	652

<210> 845

<211> 692

<212> DNA

<213> Unknown (H38g695 nucleotide)

<220>

<223> Synthetic construct

<400> 845

ttgcctgaca	tcggtttcac	ctccaccaca	gtcgccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgtcctgag	tgtgatggcc	tatgaccggg	ttgtagccat	180
ctgtcacct	ctatatcggt	cagccatctt	gagcccggtg	ttctgtgcct	tcctagattt	240
gttgtctttg	ttttgttttg	ttttgttttg	ttttgttttg	ttttgttttg	ctcagtcttt	300
tagactccca	gctgcacaac	ttgattgcct	tacaaatgac	ctgcttcaaa	gatgtggaaa	360
ttcctaattt	cctctgggaa	ccttctcaac	tcccccatct	tgcatgttgt	gacaccttca	420
ccaggaacat	caacatgtat	ttccctgctg	ctgtattttg	ttttcttccc	atctcgggga	480
ccttttctct	tacaatggag	taaaattgtt	tcctccactc	tgagggtttc	atcatcaggt	540
gggaagtata	aaccttctcc	acctgtgggt	ctcacctgtc	agttgtttgc	tgattttgtg	600
gaacaggcgt	tggagggtac	ctcggttcag	atgtgtcatc	ttccccgaga	aagagtgcag	660
tggcctcagt	gatgtacacg	gtggtcaccc	cc			692

<210> 846

<211> 939

<212> DNA

<213> Unknown (H38g696 nucleotide)

<220>

<223> Synthetic construct

<400> 846

atgctggcta	gaaacaactc	cttagtgact	gaattttattc	ttgctggatt	aacagatcgt	60
ccagagttcc	ggcaaccctt	ctttttctcg	ttcctagtga	tctacattgt	caccatggta	120
ggcaaccttg	gcttgatcac	tcttttcggg	ctaaattctc	acctccacac	accaatgtac	180

tatttctctct	tcaatctctc	cttcattgat	ctctgttact	cctctgtttt	cactcccaaa	240
atgctaata	actttgtgtc	aaaaaagaat	attatctcca	atgttgggtg	catgactcgg	300
ctgtttttct	ttctcttttt	cgatcatctc	gaatgttaca	tgttgacctc	aatggcatat	360
gatcgctatg	tggccatctg	taatccattg	ctgtataaag	tcaccatgtc	ccatcagggtc	420
tgttctatgc	tcaacttttg	tgtttacata	atgggattgg	ctggagccac	ggccccacacc	480
gggtgcatgc	ttagactcac	cttctgcagt	gctaataatca	tcaaccatta	cttgtgtgac	540
atactccccc	tcctccagct	ttcctgcacc	agcacctatg	tcaacgaggt	ggttgttctc	600
attgttgtgg	gtactaatat	cacggtagcc	agttgtacca	tcctcatttc	ttatgttttc	660
attgtcacta	gcattcttca	tatcaaattcc	actcaaggaa	gatcaaaaagc	cttcagtact	720
tgtagctctc	atgtcattgc	tctgtctctg	ttttttgggt	cagcggcatt	catgtatatt	780
aaatattctt	ctggatctat	ggagcaggga	aaagtttctt	ctgttttcta	cactaatgtg	840
gtgcccattg	tcaatcccc	catctacagt	ttgaggaaca	aggatgtcaa	agttgcactg	900
aggaaagctc	tgattaaaat	tcagaggaga	aatatattc			939

<210> 847

<211> 924

<212> DNA

<213> Unknown (H38g697 nucleotide)

<220>

<223> Synthetic construct

<400> 847

atgaccatgg	aaaattattc	tatggcagct	cagtttgtct	tagatgggtt	aacacagcaa	60
gcagagctcc	agctgcccct	cttcctcctg	ttcctgggaa	tctatgtggg	cacagttagtg	120
ggcaacctgg	gcattgattct	cctgattgca	gtcagccctc	tacttcacac	ccccatgtac	180
tatttctctca	gcagcttgctc	cttcgtcgat	ttctgtctatt	cctctgtcat	tactcccaaa	240
atgctgggtga	acttcctagg	aaagaagaat	acaatccttt	actctgagtg	catgggtccag	300
ctctttttct	ttgtgggtctt	tgtgggtggct	gaggggttacc	tcctgactgc	catggcatat	360
gatcgctatg	ttgccatctg	tagcccaactg	ctttataatg	cgatcatgtc	ctcatgggtc	420
tgtctactgc	tagtgctggc	tgccttcttc	ttgggctttc	tctctgcctt	gactcataca	480
agtgccatga	tgaaactgtc	cttttgcaaa	tcccacatta	tcaaccatta	cttctgtgat	540
gttcttcccc	tcctcaatct	ctcctgctcc	aacacacacc	tcaatgagct	tctacttttt	600
atcattgcgg	ggtttaacac	cttgggtgccc	accctagctg	ttgctgtctc	ctatgccttc	660
atcctctaca	gcattcctca	catccgctcc	tcagagggcc	ggtccaaaagc	ttttggaaca	720
tgcagctctc	atctcatggc	tgtgggtgatc	ttctttgggt	ccattacctt	catgtatttc	780
aagccccctt	caagtaactc	cctggaccag	gagaagggtg	cctctgtatt	ctacaccacg	840
gtgatcccca	tgctgaacct	tttaatatat	agtctgagga	ataaggatgt	gaagaaagca	900
ttaaggaagg	tcttagtagg	aaaa				924

<210> 848

<211> 984

<212> DNA

<213> Unknown (H38g698 nucleotide)

<220>

<223> Synthetic construct

<400> 848

atggcacctg	gaaatggctc	tttcgtgact	gaattcattc	tggcgggatt	aacacatcag	60
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ggaaaacttg	gcttggtaac	tctaattggg	ctgaactcac	accttcatac	ccccatgtac	180
ttcttctctc	ttacttctgc	cttcattgat	ctctgttatt	cttctgtgtt	tacacccaaa	240
atgctaata	actttatttc	agagaagaat	attatctcct	tcaaggggtg	catgacccaa	300
cttttctttt	tctgtttttt	ttgggtcattt	ctgaatgtta	tgtgctgacg	tcaatggcgt	360
atgatcgctg	tggccatctg	taaccactt	ctgtatcaca	ttgccatgtc	tcctacagtg	420
tgtctccagc	ttatgttttg	ttcctatttg	atggcctttt	ctgggtgccat	ggccccacact	480
ggatgcagtc	tgagactgac	tttctgtgat	gcgaacacca	tcgatcacta	cttctgtgac	540
atcctccctc	tgctccagct	ctcctgcacc	agcacctaca	tcaatgagct	ggtgggttttc	600
actgtgggtg	gcataacat	cattgtgccc	actgttacca	tctttatctc	ttatggtttc	660
atcctctcca	gcattcctca	tatcagttcc	aaggagggca	ggtccaaaagc	tttcagcact	720

tgcagttccc atataattgc tgtttctctg ttctttggat caggtgcatt tatgtatctc	780
aacctatctt ctgctgggtc catggataag agaaaaattat cttctgtctt ttatacaaat	840
gtggttccca tgttgaacct cttaatctac agcctgagga acaaagatgt taaatttgcc	900
ctaagaaaaag cctgagtag taggaaactt tgataagtaa tagtatgtgt ctgtgtgtat	960
agtcacaaga caggatatt ctgt	984

<210> 849

<211> 940

<212> DNA

<213> Unknown (H38g699 nucleotide)

<220>

<223> Synthetic construct

<400> 849

atgaaaccag ggaatgagac acaaatttca caattccttc tcctgggact ttcagaggaa	60
ccagaattgc agcccttctt ctttgggcta tttctgtcca tgtacctggt caccgtgctc	120
gggaacctgc tcatcatcct ggccacaatc tcagactccc acctccacac ccccatgtac	180
ttcttctctt ccaacctgtc ctttgcagac atctgttttg tgtctaccac tgtcccaaag	240
atgctggtga acatccagac acagagcaga gtcacacct atgcagactg catcaccag	300
atgtgctttt ttatactctt tgtagtggtg gacagcttac tcctgactgt gatggcctat	360
gaccggtttg tggccatctg tcacccctg cactacacag tcattatgaa ctctgggctc	420
tgtggactgc tggttctggt gtctggatc gtgagcatcc tatattctct gttacaaagc	480
ataatggcat tgcagctgtc cttctgtaca gaattgaaaa tcctcattt tttctgtgaa	540
cttaatcagg tcatccacct tgccgtgtcc gacactttta ttaatgacat gatgatgaat	600
tttacaagtg tgctgtggg tgggggatgc ctgctggaa tattttactt actttaagat	660
actttgttgc atatgttcga tctcatcagc tcaggggatg aataaagcac tttccacctg	720
tgcattctac ctctcagttg tctccttatt ttattgtaca ggcgtagggtg tgtaccttag	780
ttctgtgca acccataact cactctcaaa tgctgcagcc tcggtgatgt acactgtggt	840
cacctccatg ctgaacccct tcatctacag cctgaggaat aaagacataa acagagctct	900
gaatcgattc ttcagagagc agaaacagga gggccatttt	940

<210> 850

<211> 971

<212> DNA

<213> Unknown (H38g700 nucleotide)

<220>

<223> Synthetic construct

<400> 850

cacacagagc caggaatct cacaggtgtc tgagaattcc tcctcctggg actctcagag	60
gatccagaac tgcagtcggt cctcgttttg ctgtccctgt cctgtccctt gaatctgggtc	120
acggtgctga ggaacctgct cagcatcctg gctgtcagct ctgactcccc cctccacacc	180
cccatgtact tcttctcttc caacctgtgc tgggttgaca tcggtctcac ctcgccacag	240
gttcccaagg tgattctgga tatgcagtcg catagcagag tcatctctca tgtgggctgc	300
ctgacacaga tgtctttctt ggtccttttt gcatgtatag aaggcatgct cctgactgtg	360
atggcctatg gctgctttgt agccatctgt cgccctctgc actaccaggt catagtgaat	420
cctcacctct gtgtcttctt cgtttttggt tccttttttc ttaacctgtt ggattcccag	480
ctgcacagtt ggattgtgtt acaattcacc atcatcaaga atgtggaaat ctctaatttt	540
ttctgtgacc cctctcagct tctcaacctt gcctgttctg acagcgatcat caatagcata	600
ttcatatatatt tcgatagtag tatgtttggt tttcttccca tttcagggat ccttttgtct	660
tactataaaa ttgtcccttc cattctaagg atgtcatcgt cagatgggaa gtataaagcc	720
ttctccacct atggctctca cctaggagtt gtttgcgtgt tttatggaaac agtcattggc	780
atgtacctgg cttagccggt gtcaccaccc cccaggaatg gtgtgggtggc atcagtgatg	840
taggctgtgg tcaccccat gctgaacctt ttcattctaca gcctgagaaa caggacata	900
caaagtggcc tgcggagggt gcgcagcaga acagtcgaat ctcatgatct gttccatcct	960
ttttcttggtg t	971

<210> 851

<211> 1014

<212> DNA

<213> Unknown (H38g701 nucleotide)

<220>

<223> Synthetic construct

<400> 851

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cccattgagc agggaaatta caccagggtg aaggaatctc ttttttcaag gactgaccca      60
gtcccaagag ctgagcttgg tcttatttct tttcttattt tttgtgtact cagcaactgt      120
gctgggtaac ctctcatca tggctgtggt gacctgtgag tctcgcttc acacccccac      180
gtacttcctg ctctgcaatc tctctgtgtt gggtatctgc ttctctcca tcaactgctg      240
gaagggtgcta atagaccttt caagcagaaa gaccatctcc ttcaatggtt gcatgacaca      300
gatgtttttc ttccacctcc tcgggtggac agacgttttt tctctctttg tgatggcggt      360
tgaccaatac atggccatct tcaagccctt gcactgtgtg accatcgtga gtaggggaca      420
gtgctccctt acatcgtgag tagggggcgt gagtgaggcg caggcctcat catggcttcc      480
tgggtggggg gtttgtccac tccattgtgc aggtatttct gttgctcca ctcccttctg      540
tggaacatcat atgattgatg gtttctactg tgatgtcccc caggctctca aacttgctg      600
caccacacac tttgctcttg aggtcttaat gatttccaat aatggcttga tctctatgct      660
gtgggtcact tttctctca tatcttacac ggtcatcttg atgatgttga ggtctcacac      720
tgaggaaaggc aggagaaaag ccctgcacac ctgcacctcc cacatcactg tggtagccct      780
gcatttcgtg ccctgcatct atgtgcatgc ccagccttca ctgccctccc caggacaga      840
gctgtctcca tcacctttac agtcattatt cctgtcctga accccatgat ctacaccctg      900
aggaaccagg agatgaagtc agccttgagg aggcggaaga aaagaccttc tggaaaggga      960
tagatgctac gaagtcacaga ttgaaaatc agaactgaaa agtatttctt cata      1014

```

<210> 852

<211> 1004

<212> DNA

<213> Unknown (H38g702 nucleotide)

<220>

<223> Synthetic construct

<400> 852

```

tctacatacc cgcagaatth aacagatgtc tctttattcc tcctcctaga agctcagagg      60
atccagaaca gcagcctgtc ctgctgtggc tgttcctgtc catgtgcctg gtcacggtgc      120
tggggaacct gtcacatcct ctggccgtca gccctgactc ccacctccac acccccatgt      180
acctcttccct ctccaacctg tccttgcttg acatcggttt cactctcagc atgggtccca      240
agatgattgt ggacatctaa tctcacagca gactcatctc ctaggcaggc tgcctgactc      300
ccatgtctct ctttgccatt tttggaggca tgggaagagag acatgctcct gagtgtgatc      360
cctatgaccc gttttagacc atctgtcacc ctctatatca ttcagccatc atgaacctcg      420
gtttctgtgg ctttctagtt ttgttgtctt tttttctca gtctctttta gacgccagg      480
tgcacaactt gattgcctta caaatgacct gcttcaagga tgtggaatt cctaatttct      540
tctgggaacc ttctcaactc ccccatcttg catgttgcca cacttccac aataacataa      600
tcatgtattc ccctgctgcc atatttggtt ttcttcccat ctgggggacc cttttctctt      660
actataagat tgtttctcc attctgaggg ttctcatcag aggtgggaag tataaggcgt      720
gtctccactg tgggtctcac ctgtcagttg tttgctgatt ttatggaaca ggcttttggg      780
ggtacctcag ttcagatgtg tcatcttccc cgggaaaggc tgcagtggcc tcagtgtatg      840
acacggtggt caccctcatg ccgaaccctt tcatctacag cctgagaaac agggatatta      900
aaagcgctct gcggcgcccg caggcgagca cagtctaag tcaatatctc cttatctggt      960
ccatgccttt ttagtgtgtg gttaaaaaag gcagcaaggt caaa      1004

```

<210> 853

<211> 945

<212> DNA

<213> Unknown (H38g703 nucleotide)

<220>

<223> Synthetic construct

<400> 853

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acaagattgg	tcctatttct	tttcctactc	ttgggtgtaca	tgacgactct	gctgggaaac	120
ctcctcatca	tgggtactgt	cacctgtgaa	tcttgccctc	acatgccc	gtattttttg	180
ctccataatt	tatctattgc	cgatatctgc	ttctactcca	tcacagagcc	caagggtctg	240
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ctcttccacc	ttattggagg	ggtggatgca	ttttctctat	cagtgatggc	attggatcaa	360
tatgtggcca	tttccaagtc	cctgcactat	gcgaccatca	tgagtagaga	ccgttgcat	420
gggctcacag	tggctgcctg	gttggggggc	tttgtccact	ccattgtgca	gattaccctg	480
ttgctccac	tccttttctg	tggaacaaat	gttcttgaca	ctttctactg	tgatgttccc	540
caggttctca	aactcgccca	tacagacatt	ttcatacttg	agctgttgat	gatttccaac	600
aatggactgc	tcaccacact	gtgggttttc	ctgtcctcgg	tgctctacat	ggtcataatta	660
tcattactca	agtctcaggc	aggatagggc	aggaggaaag	tcattctccac	ctgcacctcc	720
cacatcactg	tggtgacctc	gcattttgtg	ccctgcactc	atgtctatgc	ccggcctttc	780
actgccctcc	ccacggataa	ggccatctct	gtcaccttca	ctgtcatctc	ccctctgctc	840
aacccttgat	ctacactctg	agaaaccatg	agatgaagtc	aaccatgaag	agactgaaga	900
ctctgacctt	ctgataggaa	atagaccagt	gcttccctcc	ttctc		945

<210> 854

<211> 962

<212> DNA

<213> Unknown (H38g704 nucleotide)

<220>

<223> Synthetic construct

<400> 854

cacacagagc	cacggaatct	cacaggtgtc	tgaaaagtgc	tcctgggact	ctctctgaga	60
ggatccagaa	ctgcagccca	tcctcgctgg	gctgtccctg	tcctatgtatc	tggtcacggt	120
gctgaggaac	gtgctcatca	tcctggctgt	cagctctgac	tcacacctcc	acacccccat	180
gtacttcttc	ctctccagcc	tgtgctgggc	tgacatcgg	ttcacctcgg	ccactgttcc	240
caagatgact	gtggacatgc	agtcgcatag	cagagtcac	tcctatgtga	gctgcctgac	300
acagatatct	ttcttggctc	tttttgcag	tatggaagac	atgctcctgt	gatggcctat	360
gacagagtgt	tgcccatctg	tcacccccctg	cactatccag	tcacatgaa	tcctcacctt	420
cgtgtcttct	tagttttgct	gtcctttttc	cttagcttgt	tggaattccca	gctgcacagt	480
tggaattgtgt	tacaattcac	cttattcaag	aatgtggaaa	actctagttt	tgtctgtgac	540
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gtcaccccc	tgctgaactt	tttcatctac	agcctgagaa	acagggacat	acaaagtgcc	900
ctgcggaggc	tgccgagcag	aacagtcgaa	tctcatgatc	tggtccatcc	tttttcttgt	960
gt						962

<210> 855

<211> 952

<212> DNA

<213> Unknown (H38g705 nucleotide)

<220>

<223> Synthetic construct

<400> 855

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ctcccacacc	tgaggaaac	actcttcacc	ctgttcttcc	ttacctacct	ggtcaccctc	120
ggtggcaacg	tcaccatcat	caccatcacc	catgcggata	ggccccgcca	cactcccattg	180
taccacttcc	tgggtgtgct	gtccctctcg	gagacctgct	atacacgctg	gtcaccatcc	240
ccagcatgct	ggctcatctg	ctgatggaga	ccaggccatc	tcctatccctg	gctgtcaggc	300
tcagatgttt	ttcttctggt	gtctgggatg	cagccactgc	ttctctctta	ccctgatggg	360
ttatgaccgc	tatgtggcca	tctgccacc	cctgcgctac	tctatggtca	tgagaccac	420
cgtttgcctc	tgccctgggg	ccctgggtttt	ctgtctcggg	ttctcgggtg	ccttgatcga	480

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gaccagcatg atcttctcat cgcccttttg cggcgagagac cacgtggagc acttcttctg 540
tgacatcgcc ccggtgctga agctcagctg cgccaagagt gccagcaagg cgctgggcat 600
ctttttctctg agcgctcctg tgggtgctgat gtccttcgtc ccgatcctct tctcctatgc 660
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cacctgtgtg gccacgtca ccgtggctgt agtacatttt gactgcgcct ccatcatcta 780
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ggtggtgatg ccaactgctga accctgtggt gtgcactctg tggacaagg aggtgagagt 900
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<210> 856

<211> 339

<212> DNA

<213> Unknown (H38g706 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(339)

<223> n = A,T,C or G

<400> 856

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ggagacacta ccgagaacca gatgttcgcc gcccgcgctg tcatcctgct gctgccgttt 120
gccgtcatcc tggcctccta cgggtccgtg gcccgagctg tctgttgcat gcggttcagc 180
ggaggccgga gggaggcgcg tgggcacgtg ttgggtccca cctgacagcc gtctgcctgt 240
tctacggctc ggccatctac acctacctgc agcccgcgca gcgctacaac cagcacgggn 300
ncagnttcgt atcgtctctc tacacccgtg gtcacaccc 339

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<210> 857

<211> 939

<212> DNA

<213> Unknown (H38g707 nucleotide)

<220>

<223> Synthetic construct

<400> 857

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atggatcaga gaaattacac cagagtgaag gaatttacct tcctgggaat tactcagtcc 60
cgagaactga gccaggctct atttaccttc ctgttttttg tgtacatgac aactctaattg 120
ggaaacttcc tcatcatggt tacagttacc tgtgaatctc accttcatac gcccatgtac 180
ttcctgctcc gcaacctgtc tattcttgac atctgctttt cctccatcac agctcctaag 240
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cccttcaact ccctcccac agacactgcc atctctgtca ccttcaactgt catctccct 840
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<210> 858

<211> 486

<212> DNA

<213> Unknown (H38g708 nucleotide)

<220>

<223> Synthetic construct

<400> 858

gtagccatat	gtaatccctt	gctttatcca	gtgatgatgt	ccaacaaact	cagcgctcag	60
ttgctaagta	tttcatatgt	aattggtttc	ctgcatcctc	tggttcatgt	gagtttacta	120
ttgcgactaa	ctttctgcag	gtttaacata	atacattatt	tctactgtga	aattttacaa	180
ctgttcaaaa	tttcatgcaa	tggtccatct	attaacgcac	taataatatt	tatttttgggt	240
gcttttatac	aaatacccac	tttaatgact	atcataatct	cttataactcg	tgtgctcttt	300
gatattctga	aaaaaaagtc	tgaaaagggc	agaagcaaag	ccttctccac	atgcggcgcc	360
catctgcttt	ctgtctcatt	gtactacgga	actctgatct	tcatgtatgt	gcgtcctgca	420
tctggcttag	ctgaagacca	agacaaagtg	tattctctgt	tttacacgat	tataattccc	480
ctgcta						486

<210> 859

<211> 774

<212> DNA

<213> Unknown (H38g709 nucleotide)

<220>

<223> Synthetic construct

<400> 859

atgtactact	tcctctgcca	cctggccttg	gtagacgcgg	gcttactac	tagcgtgggtg	60
ccgccgctgc	tgccaacct	gcgcggacca	gcgtctggc	tgccgcgcag	ccactgcacg	120
gccagctgt	gcgcacgct	ggctctgggt	tcggccgaat	gcgtcctcct	ggcggtgatg	180
gctctggacc	gcgcggccgc	agtgtgccgc	ccgctgcgct	atgcggggct	cgtctccccg	240
cgctatgtc	gcacgctggc	cagcgccctc	tggtctaacg	gcctcaccaa	ctcggttgctg	300
caaaccgcgc	tcctggctga	gcggccgctg	tgccgcgccc	gcctgctgga	ccacttcac	360
tgtgagctgc	cgccgttgct	caagctggcc	tgccgaggcg	acggagacac	taccgagaac	420
cagatgttcg	ccgcccgct	ggctcctctg	ctgctgccgt	ttgccgtcat	cctggcctcc	480
tacggtgccg	tgcccgagc	tgtctgttgc	atgcggttca	gcggaggccg	gaggagggcg	540
gtgggcacgt	gtgggtccca	cctgacagcc	gtctgcctgt	tctacggctc	ggccatctac	600
acctacctgc	agcccgcgca	gcgctacaac	caggcacggg	gcaagttcgt	atcgctcttc	660
tacaccgtgg	tcacacctgc	tctcaaccgc	ctcatctaca	ccctcaggaa	taagaaagtg	720
aagggggcag	cgaggaggct	gctgcggagt	ctggggagag	gccaggctgg	gcag	774

<210> 860

<211> 948

<212> DNA

<213> Unknown (H38g710 nucleotide)

<220>

<223> Synthetic construct

<400> 860

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ggcaacctgc	tcacatggc	caccgtctgg	agcgagcgca	gcctccacac	gcccattgtac	180
ctcttctctg	gcgccctctc	cgtctccgag	atcctctaca	ccgtggccat	catccccgcg	240
atgctggccg	acctgctgtc	caccacgcgc	tccatcgctt	tcctggcctg	tgccagtcag	300
atgttctctt	ccttcagctt	cggcttcacc	cactccttcc	tgctcacggt	catggggtac	360
gaccgctacg	tggccatctg	ccaccccctg	cgctacaacg	tgctcatgag	cccgcggggc	420
tgccgctgcc	tggtgggctg	ctcctgggct	ggtggcttgg	tcatggggat	ggtggtgacc	480
tcggccatth	tccacctgcg	cttctgtgga	cacaaggaga	tccaccatth	tgtttgccat	540
gtgccacctc	tggtgaagtt	ggcctgtgga	gacgatgtgc	tggtgtgggc	caaaggcggtg	600
ggcttgggtg	gtatcacggc	cctgctgggc	tgthttctcc	tcactctcct	ctcctatgcc	660
ttcatcgctg	ccgccatctt	gaagatccct	tctgctgaag	gtcggaaaca	ggccttctcc	720
acctgtgcct	ctcacctcac	tgtggtgggc	gtgactatg	gctttgcctc	cgtcatttac	780
ctgaagccca	aaagtcccca	gtctctggaa	ggagacacct	tgatgggcat	cacctacacg	840
gtcctcacac	ccttctctag	ccccatcatc	ttcagcctca	ggaacaagga	gctgaaggtc	900
gccatgaaga	agaccttctt	cagtaaaactc	taccagaaaa	aaaatgta		948

<210> 861
 <211> 674
 <212> DNA
 <213> Unknown (H38g711 nucleotide)

<220>
 <223> Synthetic construct

<400> 861
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 gaagcatgga agagaggcat gctcctgagt gtgatggcat atgaccggtt tgtagccatc 180
 tgtcaccctc tatatcggtc agccatcttg aaccctggtt tctgtggctt cctagatttg 240
 ttgtctttgt tttttttgtt ttgtttgttt tgtttttctc agtcttctag actcccagct 300
 gcacaacttg attgccttac aaatgacctg ctccaaggat gtggaaattc ctaatttctt 360
 ctgggaacct tctcarctcc cccatcttgc atgttgtgac accttcacca ggaacatcaa 420
 catgtatttc cctgctgccg tatttggttt tcttccatc tcagggaacct tttctcttac 480
 tgtaaaattc tttctcccat tctgagggtt tcatcatcag gtgggaagta taaaccttct 540
 ccacctgtgg gtctcacctg tcagttgttt gctgatttta tggaacaggc gttggagggt 600
 acctcggttc agatgtgtca tcttccccga gaaagrgtgc agtggcctca gtgatgtaca 660
 ygggtggtcac cccc 674

<210> 862
 <211> 653
 <212> DNA
 <213> Unknown (H38g712 nucleotide)

<220>
 <223> Synthetic construct

<400> 862
 ttgcctgaca tcgggtttcac ctccaccatg gtccccaaga tgattgtgga atccaatctc 60
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 gaggcatgga agagagacat gctcctgagt gtgatggcct atgaccggtt tgtagccatc 180
 tgtcaccctc tatgtcattc agccatcacg aaccctggtt tctgtggctt tctagttttg 240
 ttgtcttttt tttttctcag tccttttagc gccagctgc acaacttgat tgccttacia 300
 aggacctgct tcaaggatgt ggaaattcct aatttcttct gtgaccttc tcaattcccc 360
 gtcttgcatg ttgtggcacc ttcaccaata acataatcat gtatttccct gctgcatat 420
 ttggttttct tcccatctcg gggacctttt tctcttacga taaaattggt ttctccattc 480
 tgagggtttc atcatcagggt gggaagcata aggccttctc caccaggggg tctcacctgt 540
 cagttgtttg ctgattttat ggaacaggcg ttggagagta cctcggttca gatgtgtcat 600
 cttccccgag aaagggtgca gtggcctcag tgatgtacac ggtggtcacc ccc 653

<210> 863
 <211> 648
 <212> DNA
 <213> Unknown (H38g713 nucleotide)

<220>
 <223> Synthetic construct

<400> 863
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 gaagacaagg tcatctctta caatgcatgt gctgctcaaa tgtatatctt tgtagctttt 120
 gccactgtgg aaaattacct cttggcctca atggcctatg accgctatgc agcagtgtgc 180
 aaaccctac attacaccac aaccatgaca acaactgtgt gtgctcgtct ggccataggc 240
 tcctacctct tgggtttcct gaatgcctcc atccacatg gggacacatt tagtctctct 300
 ttctgtaagt ccaatgaagt ccatcacttt ttctgtgata ttccagcagt catgggttctc 360
 tcttgctctg atagacatat tagcgagctt gttcttattt atgttgtgag cttcaatatc 420
 tttatagctc tcctgggttat cttgatatcc tacacattca tttttatcac catcctaaag 480

atgcactcag	cttcagtata	ccagaagcct	ttgtccacct	gtgcctctca	tttcattgca	540
gtcggcatct	tctatgggac	tattatcttc	atgtacttac	aaccagctc	cagtcactcc	600
atggacacag	acaaaatggc	acctgtgttc	tatacaatgg	tcatcccc		648

<210> 864

<211> 645

<212> DNA

<213> Unknown (H38g714 nucleotide)

<220>

<223> Synthetic construct

<400> 864

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caggaaagca	ccatctcctt	ttttccatgc	ataatgcaga	cattcttgta	tttggctttt	120
gtcacgtag	agtgtctgat	tttgggtgtg	atgtcctatg	atcgctatgc	ggacatctgc	180
caccccttac	gttacaatat	cctcatgagc	tgagagagtgt	gcactgtcct	ggctgtggct	240
tcttggtgt	tcagcttcct	cctgggtctg	gtccctttag	ttctcatcct	gaggctgccc	300
ttctgcgggc	ctcatgaaat	caaccacttc	tgtgaaatcc	tgtctgtcct	caagttggcc	360
tgtgtcgaca	cctggctcaa	ccagggtgtc	atctttgcag	cctgcgtgtt	catcctggtg	420
gggccactct	gcctggtgct	ggtctcctac	ttgcgcaccc	tgcccgccat	cttgaggatc	480
cagtctgggg	agggccgcag	aaaggccttc	tccactgtct	cctccacact	ttgcgtggtg	540
ggactcttct	ttggcagcgc	cattgtcacg	tacatggccc	ccaagtcccg	ccatcctgag	600
gagcagcaga	aagttctttc	cctgtttttac	agccttttca	atcca		645

<210> 865

<211> 486

<212> DNA

<213> Unknown (H38g715 nucleotide)

<220>

<223> Synthetic construct

<400> 865

gtggccatct	gtaaaccctt	tcattatgtg	gtcatcatga	acaacagggt	gtgtacctta	60
ttagtctctt	gctgttgggt	ggctggcttg	atgatcattg	ttccaccact	tagcttaggc	120
ctccagctcg	aattctgtga	ctccaatgcc	attgatcatt	ttagctgtga	tgcaggctct	180
ctcctaaaga	tctcatgctc	agatacatgg	gtaatagaac	agatgggttat	acttatggct	240
gtatttgac	tcattatcac	cccagtttgt	gtgattctgt	cctacttgta	catagtcaga	300
acaattctga	agttcccttc	tgttcagcaa	aggaaaaagg	ccttttctac	ctgttcatcc	360
cacatgattg	tggtttccat	tgccatgga	agctgcatct	tcattctatat	caagccctct	420
gcaaaagatg	aggtggccat	aaataaagga	gtttcagttc	ttactacttc	tgtcgcaccc	480
ttgttg						486

<210> 866

<211> 670

<212> DNA

<213> Unknown (H38g716 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(670)

<223> n = A,T,C or G

<400> 866

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ggaggcatgg	aagagagaca	tgctcctgag	cgtgatggcc	tacgaccagt	ttgtagccat	180
ctgtcacctt	ccatatcggt	cagccatctt	gaacccgtgt	ttctgtggct	tccaagattt	240

gttgtccttg	tntttttt	tttttttt	tttttctca	ggcttttaga	ctcccagctg	300
cataacttga	ttgccttaca	aatgacctgc	ttcaaggatg	tggaaatttc	taatgtcttc	360
tgggaacctt	ctcaactctc	ccatcttgca	tgttgtgaca	ccttcaccag	gaacatcagt	420
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ctgtgggtct	cacctgtcag	ttgtttgctg	attttatgga	acaggtgttg	gagggtagct	600
cagttcagat	gtgtcatctt	ccctgagaaa	ggctgcagtg	gcctcagtga	tgtacaagat	660
ggtcaccccc						670

<210> 867

<211> 654

<212> DNA

<213> Unknown (H38g717 nucleotide)

<220>

<223> Synthetic construct

<400> 867

ttggctgaca	tcggtttcac	ctccaacacg	gtccccaaga	tgattgtgga	catccaatct	60
cacagcagag	tcatctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgctgttttt	120
ggaggcatgg	aagaaagaca	tgctcctgag	tgtgagggcc	tatgaccggt	ttgtagccat	180
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atgacctgca	tcaaggatgt	ggaaattcct	aatttcttct	gtgacccttc	tcaactcccc	360
catcttgcat	gttgtgacac	cttcaccatt	aacatagtea	tgtatttccc	tgccgccata	420
tttggttttc	ttcccatctc	ggggaccctt	ttctcttact	ctaaaattgt	ttcctccatt	480
ctgagggttt	catcatcagg	tgggaagtat	aaagccttct	ccacctgtgg	gtctcacttg	540
tcagttgttt	gctgagttta	tggacacagg	gttggagggt	acctcagttc	agatgtgtca	600
tcttcctga	gaaaggctgc	agtggcctca	gtgatgtaca	cggtgggtcac	cccc	654

<210> 868

<211> 882

<212> DNA

<213> Unknown (H38g718 nucleotide)

<220>

<223> Synthetic construct

<400> 868

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gtgatggcag	aggccagcct	tcacaagcct	gtgtacttct	tcctgataaa	cctctcagcc	120
ctagacatcc	tctccactac	agtcactgtc	cccaagacgc	tgccctgtgt	cttgcttggg	180
gaccacttcc	tcagcttccc	tgccgtcttc	ctacagatgt	acctgttcca	cagcttctcc	240
tgctcagaag	ccttcatact	gggtggtcatg	gcctatgacc	gctatgtagc	tatctgccac	300
ccactgcaat	accctgttct	catgaaccca	cagaccaatg	ctgtcttggc	aaccgggtgcc	360
tggctcactg	cctctctcct	gccattcca	gcagtagtac	agaccctcca	gatggcattt	420
gacagcattg	ctgacatcta	ccactgcttc	tgtgatcata	tggctgtggg	ccaggccctcc	480
tgctctgata	ccacccccag	accttcattg	gtttctgcat	cgccatgggt	gtgtccttcc	540
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actcccaaga	aggacgctcc	aaagccttct	ccacctgcag	ctcccatctc	ccggtagtgg	660
gcacctacta	ctcatccatt	gccatagcct	atgtggccta	cagcgctgac	ctgccccctg	720
acttccacgt	catgggcaat	gttgtacatg	tcttcttctt	cctcttcttc	ttcttcttcc	780
tcttctctct	cttctctctc	ctctctgtct	tctcttctct	cttctctctc	ttctccttcc	840
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<210> 869

<211> 934

<212> DNA

<213> Unknown (H38g719 nucleotide)

<220>

<223> Synthetic construct

<400> 869

atggagatgg	aaaactgcac	cagggtaaaa	gaatttattt	tccttggcct	gacccagaat	60
cggaagtga	gcttagtctt	atttcttttc	ctactcttgg	tgtatgtgac	aactttgctg	120
ggaaacctcc	tcatcatggt	cactgttacc	tgtgaatctc	gccttcacac	gcccattgat	180
tttttgctcc	ataattttatc	tattgccgat	atctgcttct	cttccatcac	agtgcccaag	240
gttctgggtg	accttctgtc	tgaaagaaa	accatctcct	tcaatcattg	cttcaactcag	300
atgtttctat	tccaccttat	tggaggggtg	gatgtatttt	ctctttcggg	gatggcattg	360
gatcgatatg	tggccatctc	caagcccctg	cactatgcga	ctatcatgag	tagagaccaa	420
tgcattgggc	tcacagtggc	tgcctgggtg	gggggctttg	tcactccat	cgtgcagatt	480
tccttggtgc	tccactccc	tttctgcgga	cccaatgttc	ttgacacttt	ctactgtgat	540
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gcccttcaact	gccctcccga	tggataagtc	catctctgtc	accttcaactg	tcatctcccc	840
tctgctcaac	cccttgatct	acactctgag	gaaccatgag	atgaagtcag	ccatgaggag	900
actgaagaga	agacttgtgc	cttctgatag	aaaa			934

<210> 870

<211> 898

<212> DNA

<213> Unknown (H38g720 nucleotide)

<220>

<223> Synthetic construct

<400> 870

acaatgcagc	aaaataacag	tgtgcctgaa	ttcatactgt	taggattaac	acaggatccc	60
ttgaggcaga	aaatagtgtt	tgtaatcttc	ttaattttct	atatgggaac	tgtgggtggg	120
aatatgctca	ttattgtgac	catcaagtcc	agccggacac	taggaagccc	catgtacttc	180
tttctatttt	atttgtcctt	tgcagattct	tgcttttcaa	cttccacagc	ccctagatta	240
attgtggatg	ctctctctga	aaagaaaatt	ataacctaca	atgagtgcac	gacacaagtc	300
tttgactac	atttatttgg	ctgcatggag	atctttgtcc	tcattctcat	ggctgttgat	360
cgctatgtgg	ccatctgtaa	gcccttgcgt	tacccaacca	tcagagcca	gcaggctctgc	420
atcatcctga	ttgttcttgc	ctggataggg	tctttaatac	actctacagc	tcagattatc	480
ctggccttaa	gattgccttt	ctgtggaccc	tatttgattg	atcattattg	ctgtgatttg	540
cagcccttgt	tgaaacttgc	ctgcatggac	acttacatga	tcaacctgct	gttgggtgtct	600
aacagtgggg	caatttgcct	aagtagtttc	atgattttga	taatttcata	tattgtcatc	660
ttgcattcac	tgagaaacca	cagtgcacaa	gggaagaaaa	aggctctctc	cgcttgacag	720
tctcacataa	ttgtagtcat	cttattcttt	ggcccatgta	tattcatata	tacacgcccc	780
ccgaccactt	tcccatgga	caagatgggtg	gcagtatttt	atactattgg	aacacccttt	840
ctcaatccac	tcattctacac	atctgaggaa	tgcagaagtg	aaaaatgccca	tgagaaag	898

<210> 871

<211> 943

<212> DNA

<213> Unknown (H38g721 nucleotide)

<220>

<223> Synthetic construct

<400> 871

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caagaccaga	gtttggtctt	gtttcttttt	ttatgtcttg	tgtacatgac	gactctgctg	120
ggaaacctcc	tcatcatggt	caccgtgacc	tgtgagtctc	gccttcacac	ccccatgtac	180
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atatttctct	tccacctcct	tggtggggca	gacatttttt	ctctctctgt	gatggcggtt	360
gactgctaca	tggccatctc	caagcccctg	cactatgtga	ccatcatgag	tagagggcaa	420

tgactgccc	tcatctctgc	ctcttgatg	gggggctttg	tccactccat	cgtgcagatc	480
tcctgtgtgc	tgccctctccc	tttctgtgga	cccaatgttc	ttgacacttt	ctactgcat	540
gtcccccagg	tcctcaaact	cacttgact	gacacttttg	ctcttgagtt	cttgatgatt	600
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gcccttctact	gccctcccca	cagaaaaggc	catctctgtc	accttctactg	tcatctcccc	840
tctgctgaac	cctttgatct	acactctgag	gaaccaggaa	atgaagtcag	ccatgagaag	900
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<210> 872

<211> 942

<212> DNA

<213> Unknown (H38g722 nucleotide)

<220>

<223> Synthetic construct

<400> 872

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ccccacctcc	aactgatgct	cttctgtctg	ttcctgtctga	tgtacctgtt	cacgtgtctg	120
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gtcctcacgc	ccttctctcag	ccccatcatc	ttcagcctca	ggaacaaaga	actgaagggtt	900
gccatgaaga	ggaccttctc	cagcacactc	tattcctcag	gc		942

<210> 873

<211> 948

<212> DNA

<213> Unknown (H38g723 nucleotide)

<220>

<223> Synthetic construct

<400> 873

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ccccagcagc	tcctgcctgt	cttggtcctg	ctgtacctcc	tgatgttctt	gttcacattg	120
cttggcaacc	ttcttatcat	ggccacagtt	tggattgaac	gcagactcca	cacacccatg	180
tacctcttct	tgtgtgacct	ctccatctct	gagattctgt	tcactgttgc	catcaccctt	240
cgcatgctgg	ctgatctgct	cttcacccat	cgttccatca	cctttgtggc	ttgtgccatt	300
cagatgttct	tctccttcat	gtttggcttc	actcactcct	tccttctcat	ggtcattgggc	360
tatgatcact	acgtgacct	ctgccaccga	ctgcattaca	acatgcta	gagtcctcgt	420
ggctgtgccc	atcttgtggc	ctggacctgg	gctgggtggc	cggcatggg	gatgatggtg	480
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tacctcaaac	ccaagggcct	ccattctatg	tacagtgtatg	ccttgatggc	caccacctat	840
actgtcttca	cccccttctc	cagcccaatc	attttcagtc	taagggaaca	ggagctgaag	900
aatgccataa	ataaaaactt	ttgcagaagg	ttctgccctc	taagctcc		948

<210> 874
 <211> 484
 <212> DNA
 <213> Unknown (H38g724 nucleotide)

<220>
 <223> Synthetic construct

<400> 874
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 tggacttcga gagtggtggc cccttctggt cctgcctctt gtcttcctct ttgtgaccat 120
 catctctgcc aatgccctgg tcatccacac agtggttgcc cggcaaaatc tgcacagcc 180
 tacgtgtatg ctcatcactg tgctcctggc tgtcaatatt cgtgctgcca cagccgtgat 240
 gcctaaaatg ctggagggct ttgtatatta tgctaacccc atatcgctgc atggccgcct 300
 ggcctagggtg ttctttatct acttcaccct cctcctggac tacaacttcc tctggccctg 360
 gccctggact ggttactttg ccatctgcca cccactctgc ttttctgacc tgatgacctc 420
 ccagctgctg ggactgctgg ccattcttgc ctttgaacaa agccctggga gtgaccccg 480
 ccct 484

<210> 875
 <211> 595
 <212> DNA
 <213> Unknown (H38g725 nucleotide)

<220>
 <223> Synthetic construct

<400> 875
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 gctggccatt cttgccttga cacagagctg gggagtgaac gtgccttttg tagtactaac 120
 tgcaaaaagc gatttctgcc ggacagcagt gattcgacac ttcacctgtg agtgcatgtc 180
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 tttggtcact gtaatctctg atatggccct gctggggacc tctacaccc acatcatcta 300
 tgctgccttc cggatctctt cttggggagc ccaagccaag gccttacaca cgtgtggctc 360
 ccacctactg gtcactctct ccatctacgt ctctggtctt tccacttcca tcaccttctg 420
 agtagccaag actgtgtccc agaatgtcca gaatctactc agtgccatat acttgctgct 480
 tccaggagcc ttgaatcctg tcatttatgg ggtgaggact agggagatcc agcaacatgt 540
 agaaaagatg ctctgtgaaa aggaacacag ccagaaggct ggggagaagc caaag 595

<210> 876
 <211> 944
 <212> DNA
 <213> Unknown (H38g726 nucleotide)

<220>
 <223> Synthetic construct

<400> 876
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 ctggaggctc tgcattgctg gctctctgtg cctgtgtgac tgctctacat ggcagctttg 120
 gtagggaatg cccttctagt ggggctgggt ggtcgctgac aaggcactct gggcaccat 180
 gtaccagctg ctgtggcttc tggcagctgc tgattttgtt ctggccacat ccacagtgcc 240
 caaagctctg gctgtacttt ggggcttgtc tagtgagata tcatttggag gctgcttggc 300
 tcaactcttt gttgccatg tgtcaatcat tgccacattg ctgagtcctc agtgctgctg 360
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 ggtctagtgg ctctgactac catgaccctg gatgtctgtg tcatgtacac cctgtgatcc 480
 tgttcaagaa actgccttac tgtggacagt gggccctgcc ccacacctac tgcgaacaca 540
 tgggtgtggc ttgacctgga tgtggagata cgtgccccat catcaggatg ggactggcca 600
 ccacactgct ctccccagcc ctggacctag ggctcatagg tgcttcctat gccctcattt 660
 tccgtgctgt ctgccgtctg ccatcccatg ttgcctgcca caaggctctg ggtaactgag 720

ggacctatgc	tagcatcatt	ggtctcttct	acacacctgc	cctcttctcc	ttccttgctc	780
actgttttgg	gtgtcacaca	gtgcccaccc	atattcacat	cctactggct	aacctctacg	840
cagtgggtgt	cccagcttct	aatcctgtgg	tctatggagt	gcagactcag	cagagctcag	900
aggetcagga	acttgcttca	acttttcttg	gcaggagcag	tgaa		944

<210> 877

<211> 939

<212> DNA

<213> Unknown (H38g727 nucleotide)

<220>

<223> Synthetic construct

<400> 877

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gcttggttac	aaatgccctt	ttttgtggct	ctgttaatat	catacacaa	caccatattt	120
ggcaatgtgt	ccatcatgat	ggtgtgcatt	ctggatccca	aacttcatac	tcccatgtat	180
ttctttctca	ctaattcttc	catcttagat	ctctgtctata	ccacaactac	agtcctctcat	240
atgttggttaa	atattgggtg	caacaaaaag	accatcagct	atgctggctg	tgtggccac	300
ctcatcatct	tcctggccct	aggtgctaca	gagtgtctcc	ttctggctgt	tatgtccttt	360
gacagatatg	tggtgttttg	cagacccctc	cactatgtag	tcacatgaa	ttattggttc	420
tgccaaagga	tgccagcctt	ctcatggctc	attggtttcg	gcaactcagt	gctgcagtct	480
tccttgactc	ttaacatgcc	acgctgtggt	caccaggaag	tggaaccactt	tttctgtgag	540
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ttcttttagtg	tactaattct	tctaattcca	gtgacattga	tcctcatctc	ctatggcttc	660
atagctcaag	cagtattaaa	aatcagggtc	gcagaaggac	ggcaaaaagc	atttgggaca	720
tgtgggtccc	acatgattgt	gggtgtccctc	ttttatggaa	cagccattta	tatgtactct	780
caaccacctt	catccacctc	taaggactgg	ggaaagatgg	tttccctctt	ctatggaatc	840
atcacatcca	tggtgaactc	cctcatctac	agccttagaa	ataaagatat	gaaggaggcc	900
ttcaagaggc	tgatgccaag	aatctttttc	tgtaagaaa			939

<210> 878

<211> 968

<212> DNA

<213> Unknown (H38g728 nucleotide)

<220>

<223> Synthetic construct

<400> 878

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ctggagtggg	tctgcatctg	gatgggaatt	ctctccttta	ccagttacct	tgtctccctt	120
gcagggaatg	tcacctctct	ctaccttatc	actgtggaac	acaacctcca	taaaccatg	180
ttttccttcc	tctctatacc	ggcctctgca	aacctcatat	tatgcattac	atatttcccc	240
aaaacatttg	ggatattcta	gctgaaagct	cagaaaaata	tatttcctgg	atgcttcacc	300
aggttttttt	tttttggctc	acttcacttt	agcttttttt	ctggacttgg	ccatcttgtt	360
gggtctggca	tttgatcatt	acatgaccat	tggtttcctt	ctgagataca	ccagtggctt	420
gacacctcaa	cacttggcaa	gattgtgggtg	agcattgatt	gaaggtttaa	taacattttg	480
cccattgatt	tcctggggaa	gcatttggcc	ttctgcagaa	cacacattaa	ttctaacaca	540
tactgtgagc	acataggtgt	ggccctgctt	tcctatgctg	atatctccat	caatatctgg	600
tatgacttta	ctatattggg	aatgactatt	atctcagatc	tgatcctcac	tgatatttcc	660
tacacctca	cccttcatgc	tgttttccac	cttccatcca	gtgatgccct	tctgaaggcc	720
ctaagcacct	gtgtttctca	tgctcagtgc	attctcatgt	tgtacacacc	aacctgtctt	780
tctgccctta	ctcatcactt	tgccagaggt	atctcttgca	ctttttacat	tatgtttgtg	840
ggcctctata	gggcaatccc	tcctgtactc	aattccataa	ttatggagta	aaaacaaagc	900
agattggaaa	caaggtcata	cttttattct	ttcttaaagg	gatgcagtga	tatgaggatg	960
agaatatg						968

<210> 879

<211> 1011

<212> DNA

<213> Unknown (H38g729 nucleotide)

<220>

<223> Synthetic construct

<400> 879

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catctggaag	tagttctctt	tgtggttatc	ttgatcttct	acttgataac	actgatagga	120
aacctgttca	tcatacatct	gtcatacctg	gactceccatc	tccacactcc	catgtacttc	180
ttcctttcaa	atctctcatt	tctggatctc	tgctacacca	ccagctctat	ccctcagttg	240
ctgggtgaatc	tctggggccc	ggaaaagacc	atctcttatg	ctgggtgtac	agttcaactt	300
tactttgttc	tcgcactggg	aaccgcagag	tgtgtcctac	tgggtgggat	gtcctatgat	360
cgttatgcag	ctgtgtgtag	acctttgcat	tacactgtcc	tcatgcaccc	tcgtttctgc	420
cgcttggttg	ctgcggcttc	ttgggtaagt	ggtttttaca	cctcagcact	tcattcctcc	480
tttactttct	ggataccccc	atgtagacat	cgcttagtgg	atcacttctt	ctgtgaagct	540
ccagcacttc	tgcgattatc	atgtgttgat	acctaggcaa	atgagctgac	cctcatgggc	600
atgagctcca	tttttgttct	catacctctc	atcctcatcc	tcacttccta	tgggtgccatt	660
gcccgggctg	tactgagcat	gcaatcaacc	actgggcttc	agaaagtgc	taggacatgt	720
ggagcccata	ttatggttgt	atctctcttt	ttcattccag	tcatgtgc	gtatctccag	780
ccaccatcag	aaaattctca	agatcaaggc	aagttcattg	ccctctttta	cactgttctc	840
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aagagactaa	tgggggtggga	atgggggatg	tgacagggaa	atcatggttg	ctgttggttt	960
tcctagggtc	ttatccattt	tgaaagggtg	tttccctgct	tctttgtgat	t	1011

<210> 880

<211> 956

<212> DNA

<213> Unknown (H38g730 nucleotide)

<220>

<223> Synthetic construct

<400> 880

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ggacttgagc	agtaccacgt	ctggatcagc	atcccattct	gcttaatcta	tctcatggct	120
gtcgtggcca	agagtatcct	tctctacctc	attgtggtag	agcacagtct	tcatgcaccc	180
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cccaaaacac	ttagcatctt	ctggtttggt	ccccaaacag	tttccctggc	tgtctcaccc	300
aattattctt	tctgcactat	agctttgtgt	tggactcagc	tatactgctg	gccatggcat	360
ttgaccgcta	tatggccatt	tgctcaccct	tgagatacac	tactattctg	actcccaaaa	420
ccattgtcaa	aattgctgtg	ggaatatgtt	tccgaagttt	ctgtgttttt	gtcccgtgtg	480
ttttccttgt	gaatcgttta	cccttctgca	ggacacacat	catttctcac	acatactgtg	540
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cctgtgggtc	ccatgtctgt	gttatcctca	tattctatac	accagcattc	ttctccatcc	780
ttgcccatcg	ctttgggcat	aatgtccctc	atacctttca	tattatgttt	gccaaccttt	840
atgtaatcat	tccacctgct	ctcaacccta	ttgtctacag	aataaagacc	aagcaaatcc	900
agaacagaat	ccttttgctc	tttcccaagg	ggtcccatgt	ataggtgcct	gagctc	956

<210> 881

<211> 933

<212> DNA

<213> Unknown (H38g731 nucleotide)

<220>

<223> Synthetic construct

<400> 881

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tctaattggc	ctcatctgga	agtagttatc	tttgtggttg	tcttgatctt	ctacttgatg	120

acactgatag	gaaacctggt	catcatcacc	ctgtcatacc	tggactccca	tctgcacaca	180
ccaatgtact	tcttcctttc	aaacctctca	tttctggatc	tctgctacac	caccagctct	240
atccctcagt	tgctgggtcaa	tctctggggc	ccggaaaaga	ccatctotta	tgctgggttg	300
atgattcaac	tttactttgt	tctcgcaactg	ggaaccacag	agtgtgtcct	actggtgggtg	360
atgtcctatg	accgttatgc	agctgtgtgt	agacctttgc	attacactgt	cctcatgcac	420
cctcgtttct	gccacctgct	ggctgtggct	tcttgggtaa	gtggttttac	caactcagca	480
cttcattcct	ccttcacctt	ctgggtacct	ctgtgtggac	accgccaagt	agatcacttt	540
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accctcatga	tcacaagctc	catatttgtt	ctcatacctc	tcacctcat	tctcacttct	660
tatggtgcca	tcgtccgagc	tgtactgagg	atgcagtcaa	ccactgggct	tcagaaagtg	720
tttgaacat	gtggagctca	tcttatggct	gtatctctct	ttttcattcc	ggccatgtgc	780
atatactctc	agccaccatc	aggaaattct	caagatcaag	gcaagtccat	tgccctcttt	840
tatactgttg	tcacacctag	tcttaacct	ctaactctaca	ccctcagaaa	caaagttgta	900
agaggggcag	tgaagagact	aatgggggtg	gaa			933

<210> 882

<211> 264

<212> DNA

<213> Unknown (H38g732 nucleotide)

<220>

<223> Synthetic construct

<400> 882

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tatgtggcca	tatgccaccc	actgtgccat	gctgaagtgc	tcaacagtac	agtaacagcc	120
catattggca	tcgtagctgg	ggtacgggga	tccctctttt	tttcccact	ggctctgctg	180
ataaagacgc	tgggcttatg	ccactcctat	gtgctctcgc	actcctattc	gctccaccag	240
gatgtagcga	acttgtccta	tgcg				264

<210> 883

<211> 477

<212> DNA

<213> Unknown (H38g733 nucleotide)

<220>

<223> Synthetic construct

<400> 883

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ttggttcttg	cctgctgggt	tgggggtttt	atccactcta	tcatgcaggt	catactagtc	120
atccagctgc	ctttctgtgg	gccaatgaa	ctggacaact	tctactgtga	tgctctacaa	180
atcatcaagc	tggcctgcat	ggacacctat	gtggtagagg	tgctgggtgat	agccaacagt	240
ggctctgctg	ctcttgtctg	cttcttggtc	ttactattct	cttatgctat	catcctgatc	300
accctgagaa	cacgcttctg	ccagggccag	aacaaggtcc	tctctacctg	tgcttctcac	360
ctgacagtgg	tcagcctgat	cttcgtgcc	tgcgattcca	tctatttgag	gcctttctgc	420
agcttctctg	tggataagat	attctccttg	ttttacacag	tgattacacc	tatggtg	477

<210> 884

<211> 948

<212> DNA

<213> Unknown (H38g734 nucleotide)

<220>

<223> Synthetic construct

<400> 884

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gtgtcaggaa	atggctctct	tgtctgtgtg	gtggcagtgg	agcacagtct	tcatgaacct	180
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cccaaagcct	tgagcatttt	ctggtttgat	gatgtggaca	tctcctttgg	tggtgtgtgc	300
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gctttcgacc	gctatgtggc	catctgctac	ccattgaggt	atagcaccat	acttagccac	420
agtgttattg	gcaaaattgg	gggtgtcgtg	gtgttcagga	gttttgcaac	tgtcttctcc	480
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tgtgaacaca	tggggctggc	aaagctaggt	tgttctgaaa	tcaccatcaa	tatttggtat	600
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attcagaaa	gggttgccct	tgtgttttct	ccaaaaggaa	aatgttgc		948

<210> 885

<211> 1087

<212> DNA

<213> Unknown (H38g735 nucleotide)

<220>

<223> Synthetic construct

<400> 885

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ccttggttag	agcttcctct	gttcactagt	cttcttataa	tgtaccctat	agccgtgatg	120
ggaaacatca	caatcattct	catgtccagg	ttagactctc	gtcttcatag	ccccatgtac	180
tttttcttca	ccaacctctc	ctttttggac	atgtgttata	ccacaagcat	tgtccctcag	240
atgctgttta	acctgggaag	ctctaagaag	accatcagct	atatgggggtg	tgcggttcag	300
ctttatttct	ttcacataat	ggggggaaca	gaatgtttgc	ttttggctat	tatgtccttt	360
gatcgctatg	tggccatctg	cagacctctt	cactacaccc	tcacatgaa	tcagcgctgc	420
tgtatcctta	gtttccaccg	tgtggctaata	tgggaataatc	tatgctgtct	cagaggccac	480
tgccacatta	caattgccac	tgtgtgtctt	aataaactgg	accacttggg	gtgtgagatt	540
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tcctcccatc	ttattgtagt	tttcttattt	tatggcccag	ccatcagcat	gtaccttcag	780
ccccctcct	ccatctcaag	ggatcaaccc	aagtctcatg	ccctcttcta	tggagtgggtg	840
actccctcac	tcaacccttt	tatctacacc	ctgcggaata	agaatgtaaa	gggggcatta	900
cgcaacttgg	tgaggagcat	ttcagcttta	agtgatagt	ggtagacata	aaatgaagtt	960
attgaacagt	tagagttagt	tgtatgggt	ttatctaaca	aattcttgtc	tcataatcaa	1020
atatcgcttt	acatgttctt	gcaaaatatg	ttatgtctcc	gagactcttt	gtaaacatgt	1080
tcagcaa						1087

<210> 886

<211> 498

<212> DNA

<213> Unknown (H38g736 nucleotide)

<220>

<223> Synthetic construct

<400> 886

tttattcatg	ccctctcagc	cattgaatcc	accatcctgc	tggccatggc	ctttgaccgt	60
tatgtggcca	tctgccaccc	actgcgcoat	gctgcagtgc	tcaacaatac	agtaacagcc	120
cagattggca	tcgtggctgt	ggctccgcca	tcctctttt	ttttcccaact	gcctctgctg	180
atcaagcggc	tggccttctg	ccactccaat	gtgctctcgc	actcctattg	tgtccaccag	240
gatgtactga	agttggccta	tgacagacact	ttgcccaatg	tggtatatgg	tcttactgcc	300
attctgctgg	ccatgggctg	ggacgcaatg	ttcatctcct	tgtcctattt	tctgataata	360
cgaacggttc	tgcaactgcc	ttccaagtca	tagcgggcca	aggccttttg	aacctgtgta	420
gtacacattg	gtgtggtact	cggcttgat	gtgccactta	ttggcacttc	aagtggtcac	480
cggtttggga	acaaactt					498

<210> 887
 <211> 936
 <212> DNA
 <213> Unknown (H38g737 nucleotide)

<220>
 <223> Synthetic construct

<400> 887
 atgatgatta aaaaaaatgc aagttcggaa gacttccttta ttctacttgg attttctaata 60
 tggcctcagc tggaagtagt tctctttgtg gttatcttga tcttctacct gatgacactg 120
 acaggaaacc tggtcatcat catcctgtca tacgtggact cccatctcca cacaccaatg 180
 tacttcttcc ttccaaccct ctcatctctg gatctctgcc acaccaccag ctctatccct 240
 cagttgctgg tgaatctccg gggcccggaa aagaccatct cgtatgctgg ttgcatgggt 300
 caactttact ttgttcttgc actgggaatc gcagagtgtg tctactgggt ggtgatgtcg 360
 tatgatcgtt atgtagctgt gtgtagacct ttgcattaca ctgtcctcat gcaccctcgt 420
 ttctgccact tggtggctgc ggcttcttgg gtaattgggt ttactatctc agcacttcat 480
 tctctcttta ctttctgggt accccttctg ggacatcgcc tagtggatca cttcttctgt 540
 gaagttccag cacttctgcg tttatcatgt gttgacacct atgcaaata gctgaccctc 600
 atggctcatg gctccatttt ttgtctcata cctctcattc tgattctcac tgcctatgggt 660
 gccattgccc gggctgtact gagcatgcaa tcaaccactg ggcttcagaa agtggttagg 720
 acatgtggag cccatcttat ggttgtatct ctctttttca ttccagtcac gtgcatgtat 780
 ctccagccac catcagaaaa ttctcctgat cagggcaagt tcattgccct cttttatact 840
 gttgtcacac cgagtcttaa tctctaatc tacactctca gaaacaagca tgtaaaaggg 900
 gcagcgaaga gactattggg gtgggagtgg gggaag 936

<210> 888
 <211> 453
 <212> DNA
 <213> Unknown (H38g738 nucleotide)

<220>
 <223> Synthetic construct

<400> 888
 cggcgcgtgt gcgcgccccg cctgctggac cacttcatct gtgagctgcc ggcgttgctc 60
 aagctggcct gcggaggcga cggagacact accgagaacc agatgttcgc cgcccgcggtg 120
 gtcacatctg tgccgggggt tgccgtcatc ctggcctcct acgggtgccgt ggcccgagct 180
 gtctgttgca tgccgttcaa cggaggccgg aggaggcggt tgggcacgtg tgggtccac 240
 ctgacagccg tctgcctgtt ctacggctcg gccatctaca cctacctgca gcccgcgag 300
 cgctacaacc aggcacgggg caagttcgtg tcgctcttct acaccgtggt cacacctgct 360
 cttaaccgcg tcatctacac cctcaggaat aagaaaatga aaggggcacc gaggaggctg 420
 ctgcggagtc ttgggagagg ccaggctggg cag 453

<210> 889
 <211> 1014
 <212> DNA
 <213> Unknown (H38g739 nucleotide)

<220>
 <223> Synthetic construct

<400> 889
 aaagtcaatg ctagctctga ggggtacttt attttagttg gattttctaa ttggccttat 60
 ctggaagtag ttctctttgt gggtattttg atcttctgct tgatgacact gataggaaac 120
 ctgttcatca tcatcctgac gtacctggac tccatctcc atactccctt gtatttcttc 180
 ctttcaaata tctcatttct ggatctctgc tacaccacca gctctatccc tcagttgctg 240
 gtcagtctct ggggtgtgga aaagaccatt tcttatgtcg gttgcatgggt tcaactttac 300
 ttttttctca cactgggaac cacagagtgt gtcctactgg tggatgatgc ctatgaccgt 360
 tatgcagctg tgtgtagacc tttgcattac actgtcctca tgcactctcg tttctgccac 420
 ttgttggctg tggcttcttg ggtaagtgggt tttacaaacc cagcacttca ttctctcttc 480

accttctggg	tacctctgtg	tggacaccgc	caaatagatc	actttttctg	tgaagttccg	540
gcacttttat	gattatcatt	tgtcaatacc	cgtgaaaata	aactgaccct	catgatcaca	600
agctccattt	ttgttctgct	acttctcacc	ctcattttca	cttcctatgg	tgctattgcc	660
caggctgtac	tgaggatgca	gtcaaccact	gggcttcaga	aagtatttgg	aacatgtgga	720
gctcatcata	tggttgatc	tctcttttcc	attccggcca	tgtgcatgta	tctccagcca	780
ccatcaggga	attctcaaga	tcaaggcaag	ttcattgctc	tcttttatac	tggtgttaca	840
cctagtctta	accctctaata	ctacaccctc	agaaacaaag	atgtaagagg	ggtagtgaag	900
agactaaggg	gggtgggagt	agcctgtgtt	tgtgtgatat	taacaatata	atggagtctt	960
tcctcacaat	gattcatcca	tctgttcatt	tatcaacat	tcttttatcc	actc	1014

<210> 890

<211> 656

<212> DNA

<213> Unknown (H38g740 nucleotide)

<220>

<223> Synthetic construct

<400> 890

ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgattgtgga	catccaatct	60
cacagcagag	tcattctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagacagaca	tactcctgag	tgtgatggcc	tatgaccagt	ttgtagccaa	180
atgtcaccct	ctatatcatt	cagccatcat	gaacccgtgt	tctgtggcct	tctacttttg	240
ttgtcttttt	tttttccctc	agtcttttag	atgccagct	gtacaatttg	attgccttac	300
aaatgacctg	cttcaaggat	gtggaaattc	ctaatttctt	ctgtgaccct	tctcaactcc	360
cccattcttg	atgttgtgac	accttcaaca	ataacataat	cctgtatttc	cctgatgcca	420
tatttgggtt	tcttcccatc	tcggggacac	ttttctctta	cgataaaaatt	gtttcctcca	480
ttctgagggt	ttcatcgta	gggtgggagg	ataaagccct	ctccacctgt	gggtctcacg	540
tgctcagttg	ttgctgagtt	tatggaacag	gcgttggagg	gtacctcagt	tcggatgtgt	600
cattttcccc	cagaaagggt	gcagtggcct	cagtgatgta	cgcggttgct	accccc	656

<210> 891

<211> 971

<212> DNA

<213> Unknown (H38g741 nucleotide)

<220>

<223> Synthetic construct

<400> 891

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ccacatttgg	agaagatact	ttttggatca	tttttatttt	ttattttttg	actcttgacg	120
gaaatatggg	catagttctt	gtgtccttga	aggatccaaa	actccacatc	cctatgtatt	180
tctttctttc	caacctttcc	ttggtagacc	tctgtttgac	cagcagctgt	gttccacaga	240
tggtgattaa	cttctggggc	ccagaaaaga	ccatcagcta	cattggctgt	gccattcaac	300
tctatgtttt	tttgtggctt	ggggccacgg	aatatgtcct	tcttgttgct	atggctgtgg	360
attgttatgt	agcagtgtgt	catccactgc	aaaataccat	gatcatgcac	ccaaaacttt	420
gtctgcagct	ggctatcttg	gcatggggga	ctggcttggc	ccagtctctg	atccagtccc	480
ctgccaccct	ccggttaccc	ttctgtctcc	agcggatggg	ggatgatgtt	gtttgtgaag	540
tcccagctct	gattcagctc	tccagtactg	atactacctc	cagtgaaatt	cagatgtcta	600
tcgccagtgt	tgctctctct	gtgatgcctt	tgatcattat	cctttcctct	tctggtgcta	660
ttgctaaggc	tgtgctgaga	attaagtcaa	ctgcaggaca	gaagaaagca	tttggcacct	720
gcactctctc	ccttcttggg	gtttctctct	tttatggcac	tgtcacaggt	gtctaccttc	780
aacaaaaaaa	tcaactatct	catgaatggg	gcaaatttct	cactcttttc	tacactgtag	840
taaccccaac	tcttaatccc	ctcatctaca	ctctaaggaa	caaggaggta	aaggaggcac	900
taataagatt	ggggaggagg	acctgggatt	cccagaataa	ctaacaagggt	taacatatgt	960
ttacctttgc	t					971

<210> 892

<211> 651

<212> DNA

<213> Unknown (H38g742 nucleotide)

<220>

<223> Synthetic construct

<400> 892

ttgcctgaca ttggtttcac cttggccacg gtccccaaga tgatggagac atgcaatcac	60
atagcagagt catctcccat gcaggctgtc tgacacagat acctttcttt gtcctttttg	120
tatgtataga tgacatgtc ctgactgtga tggcctataa ctgatttgtg gccatctgtc	180
acccctgca ctaccagtc atcatgaatc ctcacctctg tgtcttctta gttttggtgt	240
cctttttcct tagcctgttg gattcccagc tgcacagctg gattgtgtta cacaactcac	300
cttcttcaag aatgtgaaa tctataattt tttttctgtg acctatctca acttctcaac	360
cttgccctgt ctgacagcat catcaataac atattatgta ttttagatat cctatatatt	420
ggttttcttc ccatttcagg gatccttttg tcttactata aaattgtctc ctccattcca	480
agaattccat cgtcagatgg gaagtataaa gccttctcca cctgtggctc tcacctggca	540
gttggttgc tattttatgg aacagggctt gtagggtagc tcagttcagc tgtgttacca	600
ccccccagga agagtatggt ggcttcagtg atgtacactg tggtcacccc c	651

<210> 893

<211> 373

<212> DNA

<213> Unknown (H38g743 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(373)

<223> n = A,T,C or G

<400> 893

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ctggcccttc ctgcagccgg tctctctcgc ccttgtctc ctgtgctacc tctgacctt	120
gacgggcaat tcgggcgctg gtgctgcttg gcngngnngg acctacgcct gcanacncac	180
gatgtatgna ctacttcctc tgccacctgg ccttggtaga cgcgggcttc actactagcg	240
tggtgcccgc gctgctggcc aacctgcgc gaccagcgt gctntgncgc gcagccactg	300
cacggcccga gctgtgcgca tcgctggctc tgggttcggc cgaatgcgct ctctggcggt	360
gatggctctg gan	373

<210> 894

<211> 648

<212> DNA

<213> Unknown (H38g744 nucleotide)

<220>

<223> Synthetic construct

<400> 894

atattagaaa ttctgttcac aaccgtcagt ataccaagt ttctgggtaa cattatttca	60
ggagataaaa ccatttcctt taataattgc atagttcagt tatttttctt cattctcttg	120
ggagtcacag agttttacct tctggctgcc atgtcctatg accgctatgt ggccatctgc	180
aagcctctgc attacttgag tatcatgaat cgaagagtct gcacactgct tgtttttact	240
tcttggtctg tttcattctt aatcatatc ccagcactca tgttgctttt aaagcttgat	300
tactgtagg tctaatattat tgaccatttt acctgtgatt attttccact gctgcaactt	360
gcttggtcag acacaaaatt cttagagggt atgggatttt cttgtgctgc gtttactcta	420
atgttcactt tggcattaat atttctgtcc tacatataca ttatcagaac aattttgaga	480
attccttcta ctagtcagag gacaaaaggcc ttttcacat gttcttccca catggttggt	540
atctccatct cttatggcag ctgcattttt atgtacatta aacctcagc aaaagataga	600
gtgtccttga gcaagggagt ggcaatacta aacacctcag tagccccc	648

<210> 895

<211> 659
 <212> DNA
 <213> Unknown (H38g745 nucleotide)

<220>
 <223> Synthetic construct

<400> 895
 tttcctgaca tcggtttcac ctccaccaca gtccccaaga tgattgtgga catccagtct 60
 cacagcagag tcattctcta tgcaggctgc ctgactcaga tgtctctctt tgccattttt 120
 ggaggcatgg aagagagaca tgctcctgag tgtgatggcc tatgaccggg ttgtagccat 180
 ctgtcaccct ctatatcgct cagccatctt gaaccctgtt ttctgtggct tcctagattt 240
 gttgtctttt ttttttttcc ctcatgtctt tagactccca gctgcacaac ttgattgcct 300
 tacaaatgac ctgcttcaag gatgtggaaa ttcttaattt cttctgtgac cttcttcaac 360
 tcccccatct tgcattgtgt gacaccttca ccaataacat aatcatgtat ttccctgctg 420
 ccatatttgg tttcttccag atctcgggga cccttttctc ttactataaa attgtttcct 480
 ccattctgag ggtttcatca tcagggtggga actataaagc cttctccacc tgtgggtctc 540
 acctgtcagt tgtttgctga ttttatggaa caggcgttgg aggggtacct agttcagatg 600
 tgtcatcttc cctgagaaag gctgcagtgg cctcagtgat gtacatgggtg gtcacacc 659

<210> 896
 <211> 804
 <212> DNA
 <213> Unknown (H38g746 nucleotide)

<220>
 <223> Synthetic construct

<400> 896
 atgatggcac tcattttcac agactcccat ctccaaagcc caatgtattt cttcctcaat 60
 gtccctctctg ttcttgatat ttgttactct tctgtgtgca cacctaagct cttgggtcaac 120
 ttccctggct ctgacaagtc catctctttt gagggctgtg tgggtccagct cgccttcttt 180
 gtagtgcatg tgacagctga gagcttccct ctggcctcca tggcctatga cgccttccca 240
 gccatctgtc aacccctcca ttatggttct atcatgacca gggggacctg tctccagctg 300
 gtagctgtgt cctatgcatt tgggtggagcc aactccgcta tccagactgg aaatgtcttt 360
 gccctgcctt tctgtgggccc caaccagcta acacactact actgtgacat accaccctt 420
 ctccacctgg cttgtgccaa cacagccaca gcaagagtgg tctctatgt cttttctgct 480
 ctggtcaccc ttctgcctgc tgcagtcatt ctacctcct actgcttgggt cttgggtggcc 540
 attggggagga tgcgctcagt agcagggagg gagaaggacc tctccacttg tgcctcccac 600
 tttctggcca ttgccatttt ctatggcacc gtggttttca cctatgttca gccccatgga 660
 tctactaaca ataccaatgg ccaagtagtg tccgtcttct acaccatcat aattcccatg 720
 ctcaatccct tcatttatag cctccgcaac aaggaggtga agggcgctct gcagaggaag 780
 cttcaggtca acatttttcc cggc 804

<210> 897
 <211> 949
 <212> DNA
 <213> Unknown (H38g747 nucleotide)

<220>
 <223> Synthetic construct

<400> 897
 atggacttgg gaaatcaaac aagagtttca gaatttttac tcttgggatt ttcccaagac 60
 ctagaggatc aacagttgct ctttgcactg tttctgtcca tgtacctggt caccgttctg 120
 gggaacctgc tcatcatcct ggccatcagc tctgactccc acctccacac cccaggtac 180
 ttcttctctt ccaatctgtc cctggctgac atcgggttca cctccaccgc agtccccaag 240
 atgctggtga acatccaggt gcagagcaat gccatcagct atgcagactg catcgcccag 300
 atgtatgttt ttcatggttt ttggaggcat ggacacattt ctctcaccg tgatggccta 360
 tgaccgggat tggccatct gtcacccct gtactactgt gtcaccagga accctgcct 420
 ctgtggcctg ctggttcttg tgtcctggtt cctcagcttg tcatactccc tgatccagag 480

tctgttggtg	ctgcgggtgt	ccttctgcac	cagttgagtc	attcagcact	tttactgtga	540
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cgtgggtggcc	ggccttcttg	acttttgtgcc	cttctcaggg	atccttttct	cctacaccca	660
aattgtctcc	tacatcctga	gaatctcatc	cacagatggg	aaacacaaag	ccttttctac	720
ctgtggatct	catctgtttg	tggtttcttt	attctatggg	acaggccttg	gtgtgtatct	780
tagttccaat	gcacgtcct	cttcctgggt	gggcatgggt	gcctcgggtca	tgtacactgt	840
ggtcaccccc	atgctgaacc	ccttcattcta	ttgcttgctg	aacagggaca	tcaagaggac	900
cctagaaaca	ctgcttggga	gaatgctgta	tgtcfaatga	cggggacat		949

<210> 898

<211> 927

<212> DNA

<213> Unknown (H38g748 nucleotide)

<220>

<223> Synthetic construct

<400> 898

atggagaatt	gtacggaagt	gacaaagttc	attcttctag	gactaaccag	tgtcccagaa	60
ctacagatcc	ccctctttat	cttggtcacc	ttcatctacc	tcctcactct	gtgtgggaac	120
ctggggatga	tgttgctgat	cctgatggac	tcttgtctcc	acaccccat	gtacttttct	180
ctcagtaacc	tgtctctggt	ggacttttga	tactcctcag	ctgtcactcc	caagggtcatg	240
gctgggttcc	ttagaggaga	caagggtcatc	tcctacaatg	catgtgctgt	tcagatgttc	300
ttctttgtag	ccttggccac	ggtggaaaat	tacttgttgg	cctcaatggc	ctatgaccgc	360
tatgcagcag	tgtgcaaacc	cctacactac	accaccacca	tgacggccag	tgtaggtgcc	420
tgtctggccc	taggctcata	tgtctgtggc	ttcctaaatg	cctcattcca	cattggggggc	480
atattcagtc	tctctttctg	taaatccaat	ctggtacatc	actttttctg	tgatgttcca	540
gcagtcattg	ctctgtcttg	ctctgataaa	cacactagtg	aggtgattct	ggtttttacg	600
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tctcacttca	ctgcagtcct	cgtcttctat	gggacagtaa	tcttcattcta	cttgacagccc	780
agctccagcc	actccatgga	cacagacaaa	atggcatctg	tgttctatgc	tatgatcatc	840
cccattgctga	accctgtggg	ctacagcctg	aggaacagag	aagtcagaa	tgcattcaag	900
aaagtgttga	gaaggcaaaa	atttcta				927

<210> 899

<211> 938

<212> DNA

<213> Unknown (H38g749 nucleotide)

<220>

<223> Synthetic construct

<400> 899

atgcacacca	tgggtggagaa	ccacacccaa	gtcacctggt	tccgcctgct	gggacttaca	60
gagcaggagg	agctcagagg	catcctcttt	gtgctcttcc	tgtcatgca	ttcagtcact	120
gttatgggca	acctgggaat	gatcactctg	atccatgcag	acccacagct	ccacaccccc	180
atgtatttct	tcctgagcgt	cctatccttc	atagactcct	cgttttccac	agtggacacc	240
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gtccagatgg	ccctcatgat	cctccatggt	actgctgagt	gtctgtcctt	ggccatcatg	360
gcctatgacc	gattcaccgc	catctgccac	cctctcctct	atcacactat	tatatcccaa	420
tgtctgtgtg	ccctgctggg	ggtgacctgc	tatactgttt	ctgttgccaa	ttcagctttg	480
ctgactgggt	gcatctttaa	gctgccctac	tgtggcccca	atgtcattaa	ccactatttc	540
tgtgacatcc	cccctgtgct	ccaacttgcc	ggtgcagata	ctacgagggt	gagaccatta	600
tcttctcatt	gtgtgccttg	ctcatcctct	ttaccatcac	cattatccca	gtctcctatg	660
cctacatcct	cgtgaccatt	tgcaggatgc	gtcccttgca	agcccagagc	aaagctctct	720
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ctgtgttcat	ccgcaggctg	aaccctctga	tctacagcct	gaggaataaa	gatgtaaaat	900
atgctttgaa	gaggagatgc	ctgtgcaagc	tgtcttca			938

<210> 900
 <211> 942
 <212> DNA
 <213> Unknown (H38g750 nucleotide)

<220>
 <223> Synthetic construct

<400> 900
 atggaaaata agacagaagt aacacaattc attcttctag gactaaccaa tgactcagaa 60
 ctgcagggtc ccctctttat aacgttcccc ttcattctata ttatcactct ggttggaac 120
 ctgggaatta ttgtattgat attctgggat tctgtctcc acaatcccat gtactttttt 180
 ctcagtaact tgtctctagt ggacttttgc tactcttcag ctgtcactcc catcgatcatg 240
 gctggattcc ttatagaaga caaggatcct tcttacaatg catgtgctgc tcaaattgat 300
 atctttttag cttttgccac tgtggaaaat tacctcttgg cctcaatggc ctatgaccgc 360
 tatgcagcag tgtgcaaacc cctacattac accacaacca tgacaacaac tgtgtgtgct 420
 cgtctggcca taggctccta cctctgtggt ttcttgaatg cctccatcca cactggggac 480
 acatttagtc tctctttctg taagtccaat gaagtcctac actttttctg tgatattcca 540
 gcagtcattg ttctctcttg ctctgataga catattagcg agcttgttct tatttatgtt 600
 gtgagcttca atatctttat agctctcctg gttatcttga tatcctacac attcattttt 660
 atcaccatcc taaagatgca ctcagcttca gtataccaga agcctttgtc cacctgtgcc 720
 tctcatttca ttgcagtcgg catcttctat gggactatta tcttcatgta cttacaaccc 780
 agctccagtc actccatgga cacagacaaa atggcacctg tgttctatac aatgggtcatc 840
 cccatgctga accctctggt ctatagtctg aggaacaagg aagtgaagag tgcattcaag 900
 aaagttgttg agaaggcaaa attgtctgta ggatggctag tt 942

<210> 901
 <211> 936
 <212> DNA
 <213> Unknown (H38g751 nucleotide)

<220>
 <223> Synthetic construct

<400> 901
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 aatggcatcc taatttgtgt catcctctcc caggcaatcc tgcattgagcc catgtacata 180
 ttcttatcta tgctggccag tgctgatgtc ttgctctcta ccaccaccat gcctaaggcc 240
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 ttcttcatte acttctctt cattcactct gctgtcctgc tggccatggc ctttgaccgc 360
 tatgtggcca tctgtctccc cctgcgatat gtcacaatcc tcacaagcaa ggtcattggg 420
 aagatcgta ctgccaccct gagccgcagc ttcattcata tgtttccatc catctttctc 480
 cttgagcacc tgcactattg ccagatcaac atcattgcac acacattttg tgagcacatg 540
 ggcattgccc atctgtcctg ttctgatata tccatcaatg tctggatagg gttggcagct 600
 gctcttctct ccacaggcct ggacatcatg cttactatg tttcctacat ccacatcctc 660
 caagcagtct tccgcctcct ttctcaagat gcccctcca aggcctgag tacctgtgga 720
 tcccatatct gtgtcatcct actcttctat gtccctgccc ttttttctgt ctttgcctac 780
 aggtttgggt ggagaagcat cccatgctat gtccatattc tcctggccag cctctacgtt 840
 gtcattcctc ctatgctcaa tcccgttatt tatggagtga ggactaagcc aatactggaa 900
 ggggctaagc agatgttttc aaatcttgcc aaagga 936

<210> 902
 <211> 994
 <212> DNA
 <213> Unknown (H38g752 nucleotide)

<220>
 <223> Synthetic construct

<400> 902


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ctacaagtcc ccctccttat catgttcact ctcataatcc ttgtcaatgt gggtggaaac      180
ctgggggatga ttgttttaac ttgttgggac attcatctcc acactcccat gtattttttc      240
ctcagtcacc tgtctctagt ggacttttgt tactcttcag ctgtcactcc cacagtcata      300
gctgggctcg ttataggaga caaggctatc tcttacaatg catgtgctgc tcaaagtgtc      360
ttttttgcag cctttgccac tgtggaaaat ttctctctgg cctcaatggc ctatgaccgc      420
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agtcatggct ctgtcttgct gtgatagaca tgtgaatgag ctagtcttca tttatgtagc      660
cagtttcaat atcttttctg ccattcctagt tatcttgatc tctacctat tcatatttat      720
caccatccta aagatgcact cagcttcagg ataccagaag gctttgtcca cctgtgcctc      780
ccacctcact gcagtcacat tcttctatgg gactattatc ttcatgtact tacagcccag      840
ctctgggtcac tccatggaca cagacaaact ggcattctgt ttctatacta tgatcatccc      900
catgctgaac cccctggtct atagcctgag gaacaacgaa gtgaagagcg cattcaagaa      960
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```

<210> 903

<211> 954

<212> DNA

<213> Unknown (H38g753 nucleotide)

<220>

<223> Synthetic construct

<400> 903

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gcactggttg gaaatgctgc cctcatcctg gtcattgccca tggacaatgc tcttcattgca      180
cctatgtacc tcttctctg ctttctctca ctcacagacc tggctctcag ttctaccact      240
gtgcccagaag tcttgcccat tttgtggctc catgctgggt agatttcctt tgggtggatgc      300
ctggcccaga tgttttgtgt ccattctatc tatgctctgg agtcctcgat tctacttgcc      360
atggcctttg ataggtatgt ggctatctgt aacccattaa ggtacacaac cattctcaac      420
catgctgtca taggcagaat tggctttgtt gggctattcc gtagtggtgc tattgtctcc      480
cccttcatct tcttgctgag gcgactcccc tactgtgggc accgtgtcat gacacacaca      540
tactgtgagc atatgggcat cgcccgactg gcctgtgccca acatcactgt caatattgtc      600
tatgggctaa ctgtggctct gctggccatg ggactggatt ccattctcat tgccatttcc      660
tatggcttta tcttccatgc agtcttccac cttccatctc atgatgccca gcacaaagct      720
ctgagtacct gtggctccca cattggcacc atcttggttt tctacatccc tgccttcttc      780
tcttctctca cccaccgctt tggtcaccac gaagtcccca agcatgtgca catctttctg      840
gctaactctc atgtgctggt gcctcctgta ctcaatccta ttctctatgg agctagaacc      900
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```

<210> 904

<211> 989

<212> DNA

<213> Unknown (H38g754 nucleotide)

<220>

<223> Synthetic construct

<400> 904

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cacatagaac cagggaaatga tacacagatt tcagaatttc ttcttctggg actttcagat      60
aaaccagaat tgcagccctt cctctttggg ctgttcttct ccatgtacct ggctactgtg      120
cttgggaatc tgctcatcat cctggccaca atctcagact cccacctcca caccctcatgt      180
acttcttctc ctccaacctg tcttttgagg acatctgttt catctctact acaatcccaa      240
agatgctcgt aaacatccag acacagagca gagtcatcac ttatgcaggc tgcacaccc      300
agatgtgctt ttttgtactc ttagaagcac tggacagctt actcctgacc gtgatggcct      360
atgaccagtt tgtggccatc tgtcaccctc tgcactacat ggtcatcatg agccctggt      420
tctgtggact gctggttctg gcacccctga tcatcatgag cccctggctc tgtggactgc      480

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tggttctggc	atcctggatt	atcagtgatc	tggtttcctc	attacatagc	ttgatgggtgc	540
tgctactgcc	cttctgcaca	gattttccaa	ttccacattt	tgtctatgaa	cttaatcagg	600
tcacccgcct	tgccggttct	gataccttct	ttaatgacat	ggcgatgtat	tttgcagtag	660
ggccactggg	tggagttccc	ctcgctggga	tctgtactt	gtactgtaag	atagttttct	720
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tgctgaaccc	cttcatctgc	agtctgagga	ataaagacat	aaagagagct	ctgaatcaat	960
tcacagggt	agtgcattc	ttcaggaag				989

<210> 905

<211> 932

<212> DNA

<213> Unknown (H38g755 nucleotide)

<220>

<223> Synthetic construct

<400> 905

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gccccagaac	tacaggtcca	cctctttgtc	ttattttaact	tcactctacct	cttcactctg	120
agtgggaacc	tggggatgat	gctgctgac	ctgctggact	ctcgtctcca	cacttccatg	180
tactttttcc	tcagtaacct	gtctctgggt	gacttttgct	actcagaaac	tgctactcca	240
aagatgatgg	ctgggttgct	gatagctcac	aaggctcatct	cctacaatgt	atgtgctgct	300
cagatgttct	ttttgacgt	ctttgctact	gtggaaagt	acttcttgac	ttcagtggcc	360
tatgattgct	acagagtaat	gtgtaaacc	ctacattaca	ccaccaccat	gacaacaaat	420
gtgtgtgctt	ctctggccat	acatgcatgt	cttaggttta	ctgactgctg	ctgttgacat	480
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actctgactt	gctctaataa	acatattaat	gagttgatcc	ttgttcctac	ttcaagctat	600
attttttacc	ctcctagtta	tcttgatttc	ctgcttggtt	gtatttgat	ttgtcaccat	660
tttaaagatg	ctctctttaa	gtatacaaga	agggtttatc	tacctatggt	tctcacctca	720
ctgcagttcc	tttattttat	gagactgtcc	tcatacacata	tgtgcagcca	agttctatca	780
tttcatgaac	acagaaaaaa	ttgtatctgt	gtttcatatt	atggttatcc	ccatgctaata	840
ccctgtgggt	tatagcctga	gaaacaacga	ggtcaagagt	gcattcaaga	ctgtttgttg	900
aggaaacaaa	atattttctg	ggtttagtct	tt			932

<210> 906

<211> 945

<212> DNA

<213> Unknown (H38g756 nucleotide)

<220>

<223> Synthetic construct

<400> 906

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ttcctgggca	acatcctcat	cctctttatc	ataaagggaag	agcagagctt	gcaccagcca	180
atgtactact	tcctgtctct	tttttctgtt	aatgacctgg	gtgtgtcctt	ttctacattg	240
cccactgtac	tggtgctgt	gtgttttcat	gccccagaga	caacttttga	tgctgctctg	300
gcccagacgt	ctttcatcca	cttttctctc	tgacagagt	ttggcatcct	actggccatg	360
agttttgacc	actatgtggc	catctgtaac	ccgctgcgct	atgccacagt	gctcactgat	420
gtccgtgtgg	cccacaatgg	catatccatt	gtcatccgca	gcttctgcat	ggtattccca	480
cttcccttcc	tctgaagag	actgccttcc	tgtaaggcca	gtgtggtaact	ggcccatcc	540
tactgtctgc	atgcagacct	gattcggtcg	ccctgtggag	acactaccat	caacagcatg	600
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tcgaacacat	gtgtgtcaca	tatctatgca	gtgtgatct	tctatgtgcc	tatggttagt	780
gtgtccatgg	ttcatcgatt	tgggagtcgt	gctctggaat	atgtgcacaa	gttcatgtct	840
ctttgtacct	gccaatgtct	taccgcaatt	atctattcca	tcaagactaa	ggagattcgc	900
aggagactac	acaagatggt	attgggagct	aagtctctgat	cgaag		945

<210> 907
 <211> 989
 <212> DNA
 <213> Unknown (H38g757 nucleotide)

<220>
 <223> Synthetic construct

<400> 907
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 gtatttggaa acttgcttat catcctgggt atcattttat gctccacct ccacacctcc 180
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 caactctgtg gattgcttgt tctggatcc tggatcacia gtgtcttgca ttccttatta 480
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 cactgtgggc acccccatgc tgaaccctt catctacagc ctgaggaata aggacataaa 900
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 aagctatatc catgattgca aggtcaaa 989

<210> 908
 <211> 960
 <212> DNA
 <213> Unknown (H38g758 nucleotide)

<220>
 <223> Synthetic construct

<400> 908
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 ggaaacctgc tcatcatcct gaccatcagt tcagactccc acctccacac ccccatgtac 180
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 tgtggactgc tggttctggg gtccctgggtc atcagtgtca tgggttctt gcttgagacc 480
 ttgaccattt tgaggctgtc ctccctgcaca aatatggaaa ttccgcaact tttttgtgat 540
 ccttccgaag tcctgaagct ggcctgttct gacaccttca tcaataacat cgtgatgtgt 600
 tttgtgacca ttgtcctggg tgttttctct ctctgtggaa tcctattctc ttattctcag 660
 attttctcct ccgtcctaag agtatcatct gccagaggcc agcacaagc ctttaccacc 720
 tgtggttccc acctctcagt ggtcagcttg ttctatggca ctggccttgg ggtctatctc 780
 agttctgcag ttacaccacc ttctaggaca agtctggcag cctcgggtgat gcacaccatg 840
 gtcaccccca tgetgaacct ctcatctac agcctgagga acaaggacat gaaggggtca 900
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<210> 909
 <211> 981
 <212> DNA
 <213> Unknown (H38g759 nucleotide)

<220>
 <223> Synthetic construct

<400> 909

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ggaacctgct	cagcatcctg	gccgtcagcc	ctgactccca	cctccacacc	cccatgcact	180
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tgatcgtgga	catccaatct	cacagcagag	tcactctcta	tgcaggctgc	ctgactcaga	300
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ttctgtggct	tcctgggtttt	gttgtctttt	tttttctcag	tcttttagac	tcccagctgc	480
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ataaaattgt	ttcctccatt	ctgagggttt	catcatcagg	tgggagctat	aaagccttcg	720
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acctcagttc	agatgtgtcg	tcttccctga	gaaagcgtgc	agtggcctca	gtgatgtaca	840
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gtgtcctgtg	gcagccgtgc	agccgcacgg	cagcacagtc	tcacttcaat	atcttatctg	960
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<210> 910

<211> 628

<212> DNA

<213> Unknown (H38g760 nucleotide)

<220>

<223> Synthetic construct

<400> 910

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ttgggaaata	gtgctattat	tctggctctc	caactagatt	cccaacttca	tagtctatg	180
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caaagtctgt	tcaatttagg	gggccaaca	agaacatcac	ttaaattaggc	tgtatggccc	300
aggcctatgt	atttcaactg	ctagcctgta	ttgaatgtgt	ccttcttggc	atcgtggcct	360
tagactgcta	tgtggctgtc	tgtaaacctc	caaggtagac	tataatcata	gaccataagg	420
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caacaatcac	aattcagttg	cccctgtaga	ggtgtatagc	tcagatcttc	cttttagttag	540
agtctgtcac	ctaacagtct	ctaactgtaa	caacctttga	gatctgctac	agcattctat	600
ctgaggccaa	cttcatgctg	gggagctc				628

<210> 911

<211> 945

<212> DNA

<213> Unknown (H38g761 nucleotide)

<220>

<223> Synthetic construct

<400> 911

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ggaaatgccc	tcattatcct	ggccatcatc	acggactctc	acctccacac	acccatgtac	180
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cagcccat	ccccagctc	ctcccagaag	gacaaggcag	ccgcccta	gtgtggggtg	840
ttcatcccca	tgtcaaccc	ctttatctac	agcatacgga	acaaggatat	gaaggcagcc	900
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<210> 912

<211> 949

<212> DNA

<213> Unknown (H38g762 nucleotide)

<220>

<223> Synthetic construct

<400> 912

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acagacgccc	acccgctgct	gttccctgctc	tgccttggca	tcctatctgct	caacgccctg	120
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tcacgccgac	cttgaacctt	ttcatcaaca	gccttcgcaa	caaagaggtc	aagggcgccc	900
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<210> 913

<211> 936

<212> DNA

<213> Unknown (H38g763 nucleotide)

<220>

<223> Synthetic construct

<400> 913

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ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	ccagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
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gcatttcttg	ttaatttagc	cttctgtggc	cctaagtgtg	tggacagctt	ctactgtgac	540
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gttaacagtg	ggtttatctg	tgtgggtact	ttcttcatac	ttctaattctc	ctacgtcttc	660
atcctgttta	ctgttttgaa	acattcctca	ggtggttcat	ccaaggccct	ttccactctt	720
tcagctcaca	gcacagtgg	ccttttgttc	tttgggtccac	ccatgtttgt	gtatacacgg	780
ccacacccta	attcacagat	ggacaagttt	ctggctatct	ttgatgcagt	tctcactcct	840
tttctgaatc	cagttgtcta	tacattcagg	aataaggaga	tgaaggcagc	aataaagaga	900
gtatgcaaac	agctagtgtat	ttacaaggag	atctca			936

<210> 914

<211> 954

<212> DNA

<213> Unknown (H38g764 nucleotide)

<220>

<223> Synthetic construct

<400> 914

atgtggcaga	agaatcagac	ctctctggca	gacttcatec	ttgaggggct	cttcgatgac	60
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ggcaacaccc	tcaccattct	cctcatctgc	attgatcccc	agcttcatac	accaatgtat	180
ttctgtctca	gccagctctc	cctcatggat	ctgatgcatg	tctccacaac	catcctgaag	240
atggctacca	actacctatc	tggcaagaaa	tctatctcct	ttgtgggctg	tgcaaccag	300
cacttctct	atttgtgtct	agggtgtgct	gaatgttttc	tcttagctgt	catgtcctat	360
gaccgctatg	ttgccatctg	tcatccactg	cgctatgctg	tgctcatgaa	caagaagggtg	420
ggactgatga	tggctgtcat	gtcatgggtg	ggggcatccg	tgaactccct	aattcacatg	480
gcgatcttga	tgcaactccc	tttctgtggg	cctcggaag	tctaccactt	ctactgtgag	540
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atcagcagca	ttctcctcct	cctccccatc	ttcctgattt	ctacatccta	tgtcttcate	660
cttcaaagt	tcattcagat	gcgctcatct	gggagcaaga	gaaatgcctt	tgccacttgt	720
ggctcccacc	tcacgggtgt	ttctcttttg	tttgggtgct	gcattctctc	ctacatgaga	780
cccagggtccc	agtgcactct	attgcagaac	aaagtgggtt	ctgtgttcta	cagcatcatt	840
acgcccacat	tgaattctct	gatttatact	ctccggaata	aagatgtagc	taaggctctg	900
agaagagtgc	tgaggagaga	tgttatcacc	cagtgcattc	aacgactgca	attg	954

<210> 915

<211> 309

<212> DNA

<213> Unknown (H38g765 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(309)

<223> n = A,T,C or G

<400> 915

acgtgtgtgc	ccacagcctn	gctggncac	ttcatctgtg	agctgccggc	gttgtctcaag	60
ctggcccgcg	gagcatcgga	gacactaccg	agaaccagat	gttcgccgcc	cgcgtgggtca	120
tcctgtgtct	gccgtttgcc	gtcatcctgg	cctcctacgg	tgccgtggcc	gagctgtctg	180
ttgtatgcgg	ttcagcggag	gccggagagg	gcggtgggca	cgtgtgggtc	ccactgacag	240
ccgtctgcct	gttctacggc	tcggcatcta	cacctacctg	cagcccgcgc	agctaacaac	300
caggcacgg						309

<210> 916

<211> 313

<212> DNA

<213> Unknown (H38g766 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(313)

<223> n = A,T,C or G

<400> 916

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attggcatcg	tggctgtggt	ccgcggatcc	ctcttttttt	tcccactgcc	tctgtgtatc	180
aagcggctgg	ccttctgcca	ctccaatgtc	ctctcgcatc	cctattgtgt	ccaccaggat	240
gtaatgaagt	tggcctatgc	aagacanttt	gcccaatgtg	gtatatggtc	ttaactgncc	300

atTTTggttg gtc

313

<210> 917

<211> 960

<212> DNA

<213> Unknown (H38g767 nucleotide)

<220>

<223> Synthetic construct

<400> 917

atggaaacag	gaaatcaaac	acatgcccaa	gaatttctcc	tcctgggatt	ttcagcaacg	60
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gggaacctgc	tcatcatcct	ggccatatgc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctc	ccaacctgtc	ttttgctgac	ctctgtttta	cctccacgac	tgteccaaag	240
atgttactga	atatactgac	acagaacaaa	ttcataacat	atgcaggctg	tctcagtcag	300
atTTTTTTTT	tcacttcatt	tggatgcctg	gacaatttac	tcttgaccgt	gatggcctat	360
gaccgcttcg	tggccgtctg	tcacccctcg	cactatacgg	tcatcatgaa	ccccagctc	420
tgtggactgc	tggttctggg	gtcctgggtg	atcagtgtca	tgggttcctc	gctcgagacc	480
ttgactgttt	tgaggctgtc	cttctgcacc	aaaatggaaa	ttccacactt	tttttgtgat	540
ctacttgaag	tcctgaagct	cgcctgttct	gacaccttca	ttaataacgt	ggtgatatac	600
tttgcaactg	gcgtcctggg	tgtgatttcc	ttcactggaa	tatttttctc	ttactataaa	660
attgttttct	ctatactgag	gatttcctca	gctgggagaa	agcaciaaagc	gttttccacc	720
tgtggttccc	acctctcagt	ggtcaccttg	ttctatggca	cgggcttttg	ggtctatctc	780
agttctgcag	ccacaccatc	ttctaggaca	agtctgggtg	cctcagtgat	gtacaccatg	840
gtcaccccca	tgctgaacct	cttcatctac	agcctgagga	acacggacat	gaagagggcc	900
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<210> 918

<211> 937

<212> DNA

<213> Unknown (H38g768 nucleotide)

<220>

<223> Synthetic construct

<400> 918

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gagatggaag	tgctcctctt	ctggatcttc	tcctgttat	atctcttcag	cctgctggca	120
aatggcatga	tcttggggct	catctgtctg	gatcccagac	tgcgcacccc	catgtacttc	180
ttcctgtcac	acttggccgt	cattgacata	tactatgctt	ccagcaattt	gctcaacatg	240
ctggaaaacc	tagtgaaaca	caaaaaaaaa	tatctcgttc	atctcttgca	ttatgcagat	300
ggctttgtat	ttgacttttg	ctgctgcagt	gtgcatgatt	ttggtggtga	tgtcctatga	360
cagattttgtg	gcgatctgcc	atcccttgca	ttacactgtc	atcatgaact	ggagagtgtg	420
cacagtactg	gctattactt	cctgggcatg	tggattttcc	ctggccctca	taaatactaat	480
tctccttcta	aggctgccct	tctgtgggcc	ccaggagggtg	aaccacttct	tcggtgaaat	540
tctgtctgtc	ctcaaaactgg	cctgtgcaga	cacctggatt	aatgaaattt	ttgtctttgc	600
tgggtggtgtg	tttgtcttag	tcgggcccct	ttccttgatg	ctgatctcct	acatgcgcat	660
cctcttgggc	atcctgaaga	tccagtcaaa	ggaggggccgc	aaaaaagcct	tttccacctg	720
ctcctcccac	ctctgtgtgg	ttgggcttta	ctttggcatg	gccatggtgg	tttacctggt	780
cccagacaac	agtcaacgac	agaagcagca	gaaaattctc	accctgtttt	acagcctttt	840
caaccatttg	ctgaaccccc	tcactctacag	cctgcggaat	gctcaagtga	agggtgcctt	900
atacagagca	ctgcagaaaa	agaggaccat	gtgaatg			937

<210> 919

<211> 957

<212> DNA

<213> Unknown (H38g769 nucleotide)

<220>

<223> Synthetic construct

<400> 919

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cctggactgc	aacccttcct	ctttgggctg	ttcctgtcca	tgtacctgg	cactgtgctc	120
gggaacctgc	tcatactcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctc	ccaacctgtc	ctttgctgac	atttgtgtta	cttccaccac	cattccaaaa	240
atgctgatga	acatccagac	acagaacaaa	gtcatcacct	acatagcctg	cctcatgcag	300
atgtattttt	tcatactcct	tgctggattt	gaaaacttcc	tcctgtccgt	gatggcctat	360
gaccggtttg	tggccatctg	tcaccccttg	cactacatgg	tcattatgaa	ccctcacctc	420
tgtggactgc	tggttctagc	atcctggacc	atgagtgttc	tgtattcctt	gtacaaaatc	480
ttaatggtag	tacggctgtc	cttctgcaca	gccttagaaa	tccccactt	tttctgtgaa	540
cttaatcagg	tcatacact	tgcttgttct	gatagctttc	ttaatcacat	ggtgatatat	600
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ataatttctt	ccatacatgc	aatctcatca	gtcaggggga	agtacaaggc	attttccacc	720
tgtgcatctc	acctctcagt	tgtctcctta	ttttatgggtg	caatcctagg	ggtgtacctt	780
agttctgctg	ccaccgcaa	ctcacactca	agtgaacag	cctcagtgat	gtacactgtg	840
gtcaccccca	tgtgaaccc	ctttatctat	agtctgagga	ataaagacat	aaagagggtc	900
ctgggaatac	atttgttggtg	gggaacaatg	aaagggcaat	ttttcaagaa	gtgcccc	957

<210> 920

<211> 222

<212> DNA

<213> Unknown (H38g770 nucleotide)

<220>

<223> Synthetic construct

<400> 920

ggagacacta	cagagaacca	gatgttcgcc	gcccgcgtgg	tcatactgct	gctgccgtat	60
gacgtcatac	tggcctccta	aggtgccgtg	gcccagctg	tctgttgcac	gcgggttcagc	120
ggaggaccga	ggagggcgct	gggcacgtgt	gggtcccacc	cgacagccgt	ctggctgttc	180
taaggctcgg	gcaaataaac	ctatctgcaa	gccgcgcagc	ta		222

<210> 921

<211> 927

<212> DNA

<213> Unknown (H38g771 nucleotide)

<220>

<223> Synthetic construct

<400> 921

atgaaatcat	ggaacaatac	aataatttta	gaatttcttc	tcctgggaat	ttcagaggaa	60
ccagaattgc	aggccttcct	ctttgggctg	ttcctgtcca	tgtacctgg	cactgtgctc	120
gggaacctgc	tcatactcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctc	ccaacctgtc	cttcgtaggc	atctgttttg	tctctaccac	tgtcccgaag	240
atgctgggtga	acatccagac	acacaacaaa	gtcatcacct	atgcaggctg	catcacccag	300
atgtgctttt	tcttactcct	tgtaggattg	gataacttcc	ttctgaccgt	gatggcctat	360
gaccggtttg	tggccatctg	tcacccctctg	cactacatgg	tcattatgaa	ccctcaactc	420
tgtggactgc	tggttctggc	atcctggatc	atgagtgttc	tgaattccat	gttaciaaagc	480
ttaatgggtg	tgccactgcc	cttttgtaca	cacatggaaa	tccttcattt	tttctgtgaa	540
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atagtttctc	ccatactgac	aatctcatca	gtcaggggga	agtataaggc	attttccacc	720
tgtgcatctc	acctctcagt	tgtctcctta	ttttatggta	catgcttagg	ggtgtacctt	780
agttctgctg	ccaccacaaa	ttcacacaca	ggtgctgcag	cctcagtgat	gtacactgtg	840
gtcaccccca	tgtgaaccc	cttcatctac	agtctgagga	ataaacacat	aaagggtgct	900
atgaaaacat	tcttcagagg	aaagcaa				927

<210> 922

<211> 246

<212> DNA

<213> Unknown (H38g772 nucleotide)

<220>

<223> Synthetic construct

<400> 922

atgggtcacag agttcctccc actgggattt ctcctggggc caaggattca gatgctcctc	60
cttgggctct tctccctggt ctatgtcttc acccgcgtgg ggaatgggac catcccgggg	120
ctcatctcac tggactccag actccacacc cccatgtact tcttcctctc acacctgggc	180
gtcgtcaaca tcgcctatgc ctgcaacaca gtgccccaga tgctgggtgaa cctcctgcat	240
ccagcc	246

<210> 923

<211> 648

<212> DNA

<213> Unknown (H38g773 nucleotide)

<220>

<223> Synthetic construct

<400> 923

ctcatggacc tcaagctcat ctgcaccacc gtaccaaga tggccttcaa ctacctgtct	60
ggcagcaagt ccatttctat ggctgggtgt gtcacacaaa ttttcttcta tatatcactg	120
tctggctctg aatgttttct tttggctggt atggcttatg accgctatat tgctatttgc	180
cacctctaa gatataccaa tctcatgaat cctaaaattt gtggacttat ggctaccttc	240
tccctggatcc tgggctctac agatggaatc attgatgctg tagccacatt ttccttctcc	300
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tcatgcaatg acacatcaat atttgaagag gttattttca tctgctgtat agtaatgctt	420
gttttccctg ttgcaatcat cattgcttcc tatgctcgag ttattctggc tgtcattcac	480
atgggatctg gagagggtcg ttgcaaagct ttcacgacct gttectctca cctcatggtg	540
gtgggaatgt actatggagc agctttgttc atgtacatac ggcccacatc tgatcactcc	600
ccaacgcagg acaagatggt gtctgtattc tacaccatcc tcaactccc	648

<210> 924

<211> 916

<212> DNA

<213> Unknown (H38g774 nucleotide)

<220>

<223> Synthetic construct

<400> 924

atgaaaccag ggaatgatac acgaatttca gaatttcttc ttctaggact ttcagcagaa	60
ccagaattgc agcccttctt ctttgggctg ttcctgtcca tgtacctggt caccgtgctc	120
gggaacctgc tcatcatcct ggccacaatc tcagactccc acctccacac ccccatgtac	180
ttcttctctt ccaacctgtc ctttgcagat atcagttttg tgtctaccac tgtcccgaa	240
atgctggtga atatccagac gcagagcaga gtcacacct atgcaggctg catcaccag	300
atgtgctttt tctactatt tgcagtgttg gacagccttc tcttagctgt gatggcctat	360
gatcggtttg tggccatctg tcatcctctg tactacacaa tcatcatgaa ccctcagttc	420
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gcccttctat acagacatag caatccccca ctttttctgt gaacttaatc agataatctg	540
cattgcctgt tctgacacct ttcttaatga catcatgata tattgtgcaa ctgtgctgct	600
gggcgggtgt cccctcactg gaatccttta ctcttactct aagatagttt cctccatacg	660
tgcaatctca tcagctcagg ggaagtacaa ggcattttcc acctgtgcat ctcacctctc	720
agttgtctcc ttgttttatg gtacaagcct aggaatgtac cttagttctg ctgcaaccca	780
caactcacc ccaagtgcac cagcctcagt gatgtacact gtggtcaccc ccatgctgaa	840
cccctttatc tacagtctga ggaataaaga cctaaaggat gctctgaaac gcttcttcag	900
aaggaagcaa taaaag	916

<210> 925

<211> 360
 <212> DNA
 <213> Unknown (H38g775 nucleotide)

<220>
 <223> Synthetic construct

<400> 925
 ttttccctct cacacctggc ggttggtgac attgcctacg cctgcaacac ggtgccccgg 60
 atgctgggtga acctcctgca tccagccaag cccatctcct ttgcggggccg catgatgcag 120
 acctttctgt tttccacttt tgctgtcaca gaatgtttcc tcctggtggg gaagtccaat 180
 gatttgtaag tggccatctg ccacccctcc cgatatttgg ccatcatgac ctggagagtc 240
 tgcataccac tcgcggtgac ttcttgagac actggagtc ttttatcctt gattcatctt 300
 gtgttacttc tacctttacc cttctgtagg cccagaaaaa tttatcactt tttttgtgaa 360

<210> 926
 <211> 643
 <212> DNA
 <213> Unknown (H38g776 nucleotide)

<220>
 <223> Synthetic construct

<400> 926
 ttgcctgaca tcgggtttcac ctccaccacg gtccccaaga tgattgtgga atccaatctc 60
 acagcagagt catctcctat gcaggctgcc tgactcagat gtctctcttt gccatttttg 120
 gaggcatgga agagagacat gctcccgagt gtgatggcct atgaccgggt tgtagccatc 180
 tgtcacccctc tatatcattc agccatcatg aaccctgtgt tctgtggctt cctagttttg 240
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 ttcttgattt tatggaacag gcgttgagg gtacctcagt tcagatgtgt catcttcccc 600
 gagaaagact gcagtgacct cagtgtatgta cgcagtggtc acc 643

<210> 927
 <211> 498
 <212> DNA
 <213> Unknown (H38g777 nucleotide)

<220>
 <223> Synthetic construct

<400> 927
 gtgaaaaatc agacaatggt cacagagttc cttctatttg gatttttctt gagcccaagg 60
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 gggaccatcc tggggctcat ttactggac tccatactcc acaccccat gtactttctt 180
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 gtgaacctcc tgcattcagc caagcccatt tactttgctg gctgcatgac atatacttt 300
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 tacgtggcca tcttgacacc tctccgatat atcatcatta tgacctgtaa agtcttcac 420
 atctctgcca tcactttcat gtacatgtgg ttctttctg tcttggtcca tgtaagcctc 480
 atactaagac tgcctttt 498

<210> 928
 <211> 276
 <212> DNA
 <213> Unknown (H38g778 nucleotide)

<220>

<223> Synthetic construct

<400> 928

caaatgagct	tgtttgtaat	ctttgcctct	ggctgaatgc	aatttgttta	aactcgcaact	60
ggcctataga	ccctgtttac	tgccatctgt	gcacccaccc	gttctaccac	attgaccatg	120
tctaagaggc	cattatcttt	ttcttggtag	caggatgcta	ccttggtggg	ttagttaaga	180
tggtcactgt	gacaacttcc	atcacacaac	tatcgctttg	tcaaccatgt	gtccacctgc	240
cttctctgtg	acattccctc	atcttgtagc	tattcg			276

<210> 929

<211> 645

<212> DNA

<213> Unknown (H38g779 nucleotide)

<220>

<223> Synthetic construct

<400> 929

ttctctgac	tctgcttttc	ctctgtcaca	atacctaaat	tgcttcagaa	catgcagagc	60
caagtaccaa	cgatataccta	tcagattgc	ctgacacagc	tgtacttctt	tatgggtttt	120
ggagatatgg	agagcttcct	tcttggtggtc	atggcctatg	accgctatgt	ggccatctgc	180
tttcctttgc	attataccag	catcatgagc	accaaatttt	gtgctttact	agtgtacta	240
ctgtggatgc	tgacaatata	ccatgccctg	ctgcataccc	tactcatggc	tagattgtct	300
ttttgtgaga	agaatgtcat	tcttcacttt	ttctgtgata	tttctgctct	tctgaagttg	360
tctgtctcag	acacttatgt	taatgagttg	atgatattta	tcatgggagg	gatcatcagt	420
attattccat	ttctactcat	tgttatgtct	tatgtaagga	tttttttctc	cattctcaag	480
gttccatctt	ctcaggacat	ccacaaggtc	ttctctacct	gtggttccca	tctgtctgtg	540
gtgaccttgt	tttatgggac	aattattggt	ctctacttat	gtccatcagg	caataattct	600
actgtgaatg	agatttccat	ggccatgatg	tacacagtgg	tggt		645

<210> 930

<211> 657

<212> DNA

<213> Unknown (H38g780 nucleotide)

<220>

<223> Synthetic construct

<400> 930

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aacatgcaga	gccaagttcc	ttcaatcccc	tatgcaggct	gcctgacaca	aatgtacttc	120
cttttgtttt	ttggagatct	tgagagcttc	ctccttgtgg	ccatggccta	tgaccgctat	180
gtagccatct	gttccctct	tcattacacc	agcatcatga	gccccaggct	ctgtgtgagt	240
cttgtgctgc	tgtcctgggt	gctgaccatg	tccattccca	tgctgcacac	tttgccttta	300
actagggtgt	ctttctgtga	aaacaatgtg	atccccatt	ttttctgtga	tctgtctgcc	360
ctgctgaagc	tgccctgctc	tgatattcac	attaatgaat	tggtgatatt	gatcatagga	420
gggcttggtg	ttatacttcc	atttctactc	atcacagtgt	cttatgcacg	catcatctcc	480
tccattctca	agggtccctc	aactcaaggc	atccacaagg	tcttctccac	ttgtggttct	540
cacctgtctg	tggtgtcact	gttctatggg	acaattattg	gcctctactt	atgtccatct	600
gctaataact	ctactctaaa	ggacactgtc	atgtctatga	tgtacaccgt	ggtaact	657

<210> 931

<211> 942

<212> DNA

<213> Unknown (H38g781 nucleotide)

<220>

<223> Synthetic construct

<400> 931

atggagaaca	acacagaggt	gactgaattc	atccttgtgg	ggttaactga	tgaccagaa	60
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ctgcagatcc cactcttcat agtcttcctt ttcattctacc tcatcactct gggtgggaac 120
ctggggatga ttgaattgat tctactggac tctgtctcc acaccccat gtacttcttc 180
ctcagtaacc tctccctggt ggactttggt tattcctcag ctgtcactcc caaggtgatg 240
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aactccagcc atttcatggg cacagacaaa atggcatctg tgttctatgc catagtcatt 840
cccatgttga atccactggt ctacagcctg aggaacaaag aggttaagag tgcctttaa 900
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<210> 932

<211> 562

<212> DNA

<213> Unknown (H38g782 nucleotide)

<220>

<223> Synthetic construct

<400> 932

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acctggcctt gattgctcta attggctgaa attcatacct tcccaccccc aagctctggt 180
ttctttcacc cagtccttcc ctgatctcta ttgtcctggt tgcaccccca gaatgctcat 240
gacttttcta tcaaagaaaa acatcttcta tgtcaggtgc atgactcagc tgtcgcagct 300
tttctttctc ttattgttcc tactctatta aataccacgt gttgatgttc atagcctgtg 360
gttgcttagt ggccatctac aatccatcat tgcagaggt caccatgtct cctcaggtga 420
gagagagaga ggcagtggtt ttgttgggaa cactcccaca cagggcacat acttaggccg 480
aacttgtgta atattgatgt catcaatcat catcttatga cagcctcttg gtcctctaag 540
tttctgttac cagcacctgt gc 562

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<210> 933

<211> 933

<212> DNA

<213> Unknown (H38g783 nucleotide)

<220>

<223> Synthetic construct

<400> 933

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gcctggaacc tctccctcat tgttttaata aggatggatt cccacctcca tacacccatg 180
tatttcttcc tcagtaacct gtcctcata gatgtctgct atatcagctc cacagtcccc 240
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cagtacttta tcttttcaac gatgggactg agtgagtctt gtctcatgac agccatggct 360
tatgatcggt atgctgccat ttgtaacccc ctgctctatt catccatcat gtcaccacc 420
ctctgtgttt ggatgggtact gggagcctac atgactggcc tactgcttc tttattccaa 480
attgggtgct tgcctcaact ccacttctgt ggggtctaag tcatcagaca tttcttctgt 540
gacatgcccc aactgttaat cttgtcctgt actgacactt tctttgtaca ggtcatgact 600
gctatattaa ccatgttctt tgggtagca agtgccctag ttatcatgat atcctatggc 660
tatattggca tctccatcat gaagatcact tcagctaaag gcaggccaaa ggcattcaac 720
acctgtgctt ctcatctaac agctgtttcc ctcttctata catcaggaat ctttgtctat 780
ttgaggtcca gctctggagg ttctcaagc tttagcagat ttgcatctgt tttctacact 840
gtggtcattc ccatgttaaa tcccttgatt tacagtttga ggaacaaaga aattaaagat 900
gccttaaaga ggttgcaaaa gagaaagtgc tgc 933

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<210> 934
 <211> 935
 <212> DNA
 <213> Unknown (H38g784 nucleotide)

<220>
 <223> Synthetic construct

<400> 934
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 tcctggaaca taaacctcat cacccttatac aggacgactc ccatctgcat acacctatgt 180
 acttttttct tagtaatctg tcgtttcttg acatctgcta tgtttccact atagcccca 240
 agatgctctc agacttcttc aagaagcata aattcatctc ctttatgggg tgcagtatgc 300
 agtacttttt cttctctagc ctagggtctaa ctgagtgtctg tcttctggca gccatggctt 360
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 tctgctgca gatggtggca ggatcttgta taactggatt cttagggtca tttatccaac 480
 tctgtgccctt gcttcagctc catttctgtg ggccaaatgt catcaacct tttctctgtg 540
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 ctgtttcac agtgatcttt ggactcacgt ctgtcttagt tatcatgata tcttatgggt 660
 atatcattgc caccattctg aagatcacct cagctgaagg cagagccaaa tctttcaaca 720
 cttgtgcttc tcaccttaca gcagtgatcc ttttctttgg ctcaggtatc tttgtttata 780
 tgtatcctaa tgctggtgat tccctgagcc aaaacaagtt ggcatcagtc ttatacacag 840
 ttacaatccc catgttaaat ccagtgtatc acagcctgag gaacaaggaa atcaaagatg 900
 ctctaaccag atggaagaag agaattctt cctgg 935

<210> 935
 <211> 1330
 <212> DNA
 <213> Unknown (H38g785 nucleotide)

<220>
 <223> Synthetic construct

<400> 935
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 tattcaaaga ccactatttt tctcttttca gtattcctag ggatataacct cctgaccatg 120
 tcctgaaacg tgagtctcat cgcccttatac aggacggact cccatctaca tgcacctgtg 180
 tactttttcc ttagtaatcc gtcttttctg gacatctgct gtgtttccac tatagccccc 240
 aagatgccct cagacttttt caagaagcat aaattcattt ctttatgggg gtgcaccatg 300
 cagtacttct ctagcctgaa tgtgactgag tgctgtcttc ttacagccat ggcttatgat 360
 taatatgctg ccatttgtga tctctgtctc tacacagcca tcatgtcacc tgctctctgt 420
 atgccaatgg tggcaggatc ttgtacaact ggatactttg tctcatttat ccaactctgt 480
 gccttgcttc tgctccattt ctgtgagtca aatagcagcc atttcttttg tgacctgccc 540
 caactgctga ttctatcctg ttctcatact gttttttttt tctcaagtca tgaccactat 600
 gctcacagta acctttatac tcacctctat cttggttatc atgataactt atgggtatat 660
 cattgccaac attcatctct tttatgggat gcaccatgta atacttcttc tctagcctgg 720
 gtctgactga gtgctgtctt ctggaagcta tggcttataa ttgatatgct gccatttgtg 780
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 gctatgacac ctttttctgt caagtcatga catccatgct tacagtggta tttggactca 1020
 catctgtctt agttatcatg atattttatg gctatgtcat tgctaccatt ctgaagatca 1080
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 tagaaacaag gtggattcta ttgtatacac tgtggtgatc cccaggttga atccattgat 1260
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<210> 936

<211> 930
 <212> DNA
 <213> Unknown (H38g786 nucleotide)

<220>

<223> Synthetic construct

<400> 936

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aggattcaga	tgetcctctt	tgggctcttc	tccctgttct	atatcttcac	cctgctgggg	120
aacgggggcca	tcctgggggt	catctcactg	gactccagac	tccacacccc	catgtacttc	180
ttectctcac	acctggctgt	cgtcgacatc	gcctacaccc	gcaacacggt	gccccagatg	240
ctggcgaaac	tcctgcaccc	agccaagccc	atctcctttg	ctggctgcat	gacgcagacc	300
tttctctggt	tgagttttgg	acacagcgaa	tgtctcctgc	tgggtgctgat	gtcctacgat	360
cgttacgtgg	ccatctgcca	ccctctccga	tactccgtca	tcatgacctg	gagagtctgc	420
atcacccctgg	cgtcacttcc	ctggacgtgt	ggctccctcc	tggctctggc	ccatgtgggt	480
ctcatcctaa	gactgccctt	ctctgggccc	catgaaatca	accacttctt	ctgtgaaatc	540
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gcctgcgtgt	tcttctgggt	ggggccaccc	agcctgggtg	ttgtctccta	ctcgcacatc	660
ctggcgggcca	tcctgaggat	ccagtctggg	gaggggccga	gaaaggcctt	ctccacctgc	720
tcctcccacc	tctgcgtggg	gggactcttc	tttggcagtg	ccatcatcat	gtacatggcc	780
cccaagtccc	gccatcctga	ggagcagcaa	aaggctcttt	ttctatttta	cagttttttc	840
aaccacaacac	ttaacccctt	gatttacagc	ctgaggaacg	gagagggtcaa	gggtgccctg	900
aggagagcac	tgggcaagga	aagtcattcc				930

<210> 937

<211> 942

<212> DNA

<213> Unknown (H38g787 nucleotide)

<220>

<223> Synthetic construct

<400> 937

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cctgagctcc	aggggcagct	ctttgtgggt	ttcctgggta	tttatctggt	gacctgata	120
ggaaatgcca	ttattatagt	catcgtctcc	ctagaccaga	gcctccacgt	tcccatgtac	180
ctgtttctcc	tgaacttata	tgtgggtggc	ctgagtttca	gtgcagttat	tatgcctgaa	240
atgctgggtg	tcctctctac	tgaaaaaact	acaatttctt	ttgggggctg	ttttgcacag	300
atgtatttca	tccttctttt	tgggtggggc	gaatgttttc	ttctggggagc	aatggccttat	360
gaccgatttg	ctgcaatttg	ccatcctctc	aactacaaaa	tgattatgaa	taaaggagtt	420
tttatgaaat	taattatatt	ttcatggggc	ttaggtttta	tgttaggtac	tgttcaaaca	480
tcatgggtat	ctagttttcc	cttttgtggc	cttaatgaaa	ttaaccatat	atcttgtgaa	540
accccagcag	tgtagaact	tgcattgtgc	gacacgtttt	tgtttgaaat	ctatgcattc	600
acaggcacct	ttttgattat	tttggttcct	ttcttgttga	tactcttgtc	ttacattcga	660
gttctgtttg	ccatcctgaa	gatgccatca	accactggga	gacaaaaggc	cttttccacc	720
tgtgccgctc	acctcacatc	tgtgacccta	ttctatggca	cagccagtat	gacttattta	780
caacccaaat	ctggctactc	accggaaaac	aagaaagtga	tgctcattgtc	ttactcactt	840
ctgacaccac	tgtggaatct	gcttatctac	agtttgcgaa	atagtggat	gaagagggct	900
ttgatgaaat	tatggcgag	gcgagtgggt	ttacacacaa	tc		942

<210> 938

<211> 993

<212> DNA

<213> Unknown (H38g788 nucleotide)

<220>

<223> Synthetic construct

<400> 938

atgggtcacag	agttcctcct	actgggattt	ctcctgggcc	caaggattca	gatgctcctc	60
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t t t g g g c t c t	t c t c c c t g t t	c t a t g t c t t c	a c c c t g c t g g	g g a a t g g g a c	c a t c c t g g g g	120
c t c a t c t c a c	t g g a c t c c a g	a c t c c a c a c c	c c c a t g t a c t	t c t t c c t c t c	a c a c c t g g g c	180
g t c g t c a a c a	t c g c c t a t g c	c t g c a a c a c a	g t g c c c c a g a	t g c t g g t g a a	c c t c c t g c a t	240
c c a g c c a a g c	c c a t c t c c t t	t g c t g g c t g c	a t g a c a t a g a	c c t t t c t c t t	t t t g a g t t t t	300
g c a c a t a c t g	a a t g c c t c c t	g t t g g t g c t g	a t g t c c t a c g	a t c g g t a c g t	g g c c a t c t g c	360
c a c c c t c t c c	g a t a t t t c a t	c a t c a t g a c c	t g g a a a g t c t	g c a t c a c t c t	g g c c a t c a c t	420
t c c t g g a c a t	g t g g c t c c c t	c c t g g c t a t g	g t c c a t g t g a	g c c t c a t c c t	a a g a c t g c c c	480
t t t t g t g g g c	c t c g t g a a a t	c a a c c a c t t c	t t c t g t g a a a	t c c t g t c t g t	c c t c a g g c t g	540
g c c t g t g c t g	a t a c c t g g g t	c a a c c a g g t g	g t c a t c t t t t g	c a g c c t g c a t	g t t c a t c c t g	600
g t g g g a c c a c	t c t g c c t g g t	g c t g g t c t c c	t a c t c a c a c a	t c c t g g c g g c	c a t c c t g a g g	660
a t c c a g t c t g	g g g a g g g c c g	c a g a a a g g c c	t t c t c c a c c t	g t c c t c c c a	c c t c t g c g t a	720
g t g g g a c t c t	t c t t t g g c a g	c g c a t c c g t c	a t g t a c a t g g	c c c c t a a g t c	c c g c c a t c c t	780
g a g g a g c a g c	a g a a g g t c c t	t t t t c t a t t t	t a c a g t t c t t	t c a a c c c g a t	g c t a a a c c c c	840
c t g a t t t a c a	a c c t g a g g a a	t g t a g a g g t c	a a g g g t g c c c	t g a g g a g a g c	a c t g t g c a a g	900
g a a a g t c a t t	c c t a a g a g g t	g t g a c a t t t g	a a c t g c c a g c	c t c a g t t g t c	a c g t g g a c t c	960
t t g a t g c c c a	a t t a t t g c c t	c a a t c c a g a a	a a g			993

<210> 939

<211> 930

<212> DNA

<213> Unknown (H38g789 nucleotide)

<220>

<223> Synthetic construct

<400> 939

a t g g g g g a c a	a t a t a a c a t c	c a t c a c a g a g	t t c c t c t a c	t g g g a t t t c c	c g t t g g c c c a	60
a g g a t t c a g a	t g c t c c t c t t	t g g g c t c t t c	t c c c t g t t c t	a c g t c t t c a c	c c t g c t g g g g	120
a a c g g g a c c a	t a c t g g g g c t	c a t c t c a c t g	g a c t c c a g a c	t g c a c g c c c c	c a t g t a c t t c	180
t t c c t c t c a c	a c c t g g c g g t	c g t c g a c a t c	g c c t a c g c c t	g c a a c a c g g t	g c c c c g g a t g	240
c t g g t g a a c c	t c c t g c a t c c	a g c c a a g c c c	a t c t c c t t t g	c g g g c c g c a t	g a t g c a g a c c	300
t t t c t g t t t t	c c a c t t t t t g	t g t c a c a g a a	t g t c t c c t c c	t g g t g g t g a t	g t c c t a t g a t	360
c t g t a c g t g g	c c a t c t g c c a	c c c c c t c c g a	t a t t t g g c c a	t c a t g a c c t g	g a g a g t c t g c	420
a t c a c c c t c g	c g g t g a c t t c	c t g g a c c a c t	g g a g t c c t t t	t a t c c t t g a t	t c a t c t t g t g	480
t t a c t t c t a c	c t t t a c c c t t	c t g t a g g c c c	c a g a a a a t t t	a t c a c t t t t t	t t g t g a a a t c	540
t t g g c t g t t c	t c a a a c t t g c	c t g t g c a g a t	a c c c a c a t c a	a t g a g a a c a t	g g t c t t g g c c	600
g g a g c a a t t t	c t g g g c t g g t	g g g a c c c t t g	t c c a c a a t t g	t a g t t t c a t a	t a t g t g c a t c	660
c t c t g t g c t a	t c c t t c a g a t	c c a a t c a a g g	g a a g t t c a g a	g g a a a g c c t t	c t g c a c c t g c	720
t t c t c c c a c c	t c t g t g t g a t	t g g a c t c t t t	t a t g g c a c a g	c c a t t a t c a t	g t a t g t t g g a	780
c c c a g a t a t g	g g a a c c c c a a	g g a g c a g a a g	a a a t a t c t c c	c g c t g t t t c a	c a g c c t c t t t	840
a a t c c c a t g c	t c a a t c c c c t	t a t c t g t a g t	c t t a g g a a c t	c a g a a g t g a a	g a a t a c t t t g	900
a a g a g a g t g c	t g g g a g t a g a	a a g g g c t t t a				930

<210> 940

<211> 942

<212> DNA

<213> Unknown (H38g790 nucleotide)

<220>

<223> Synthetic construct

<400> 940

a t g a a a a g a c	a a a a t c a a a g	c t g t g t g g t t	g a a t t c a t c c	t c c t g g g c t t	t t c t a a c t t t	60
c c t g a g c t c c	a g g t g c a g c t	c t t t g g g g t t	t t c c t a g t t a	t t t a t g t g g t	g a c c c t g a t g	120
g g a a a t g c c a	t c a t t a c a g t	c a t c a t c t c c	t t a a a c c a g a	g c c t c c a c g t	t c c c a t g t a c	180
c t g t t c c t c c	t g a a c c t a t c	t g t g g t g g a g	g t g a g t t t c a	g t g c a g t c a t	t a c g c c t g a a	240
a t g c t g g t g g	t g c t c t c t a c	t g a g a a a a c t	a t g a t t t c t t	t t g t g g g c t g	t t t t g c a c a g	300
a t g t a t t t c a	t c c t t c t t t t	t g g t g g g a c t	g a a t g t t t t c	t c c t g g g a g c	g a t g g c t t a t	360
g a c c g a t t t g	c t g c a a t t t g	c c a t c c t c t g	a a c t a c c c a g	t g a t t a t g a a	c a g a g g g g t t	420
t t t a t g a a a t	t a g t a a t a t t	c t c a t g g a t c	t c a g g g a t c a	t g g t g g c t a c	t g t g c a g a c c	480
a c t t g g g t a t	t t a g t t t t c c	a t t t t g t g g c	c c c a a t g a a a	t t a a t c a t c t	c t t c t g t g a g	540

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actccccgg tactagagct tgtgtgtgca gacaccttct tatttgaaat ctatgccttc 600
acaggcacca ttttgattgt tatgggttct ttcttgttga tctcttgtc ttacattcga 660
gttctgtttg ccatacctgaa gatgccatca actactggga gacaaaaggc cttttccacc 720
tgtgcctctc acctcacatc tgtgacctg ttctatggca cagccaatat gacttattta 780
caacccaaat ctgggtactc acccgaaacc aagaaactga tctcattggc ttacacggtg 840
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ttgataaaac tatggcgaag aaaagtgatt ttacacacat tc 942

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<210> 941

<211> 936

<212> DNA

<213> Unknown (H38g791 nucleotide)

<220>

<223> Synthetic construct

<400> 941

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aatttctca ttgtggtgct ggtctccact gatgctgccc tcagtcctcc tatgtacttc 180
ttcttgcgca cctctcggc cttggagatt ggctatacgt ctgtcacggt ccccttgcta 240
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gcaacagccc tctcatcct ctgccccttt ggcctcatcc tgggctccta cgggcgtatc 660
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cctaaggcca gctacgatcc ggccactgac cctctggtgt cctcttcta tgctgtggtc 840
accccatcc tcaaccccat catctacagc ctgcggaaca cagaggtaa agctgcctta 900
aagagaacca tccagaaaac ggtgcctatg gagatt 936

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<210> 942

<211> 828

<212> DNA

<213> Unknown (H38g792 nucleotide)

<220>

<223> Synthetic construct

<400> 942

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gcctccacca tgggtccaaa gatgttggtg aacatccaga cacagagcaa agtcattacc 180
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aagtacaagg cactttccac ctgtgcatct cactctcag ttgtctccat attttatggt 660
acggggctag ggggtgacct tagctctact atgacccaaa acttacactc aactgtgtc 720
gcctcgggtg tgtacactgt ggtcaccccc atgtcaacc ccttcattta cagtctgagg 780
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<210> 943

<211> 950

<212> DNA

<213> Unknown (H38g793 nucleotide)

<220>

<223> Synthetic construct

<400> 943

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actgggaaca	ttctcattgt	ggtgtccatt	cacacagaaa	cctgtctatg	cacatccatg	180
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agatggcttt	cttcattgca	ctgggcagtg	ctgattgctt	cctcttggct	gccatggcct	360
atgaccgcta	tgtggccatt	tgccaccctg	tgcagtaccc	tctcctcatg	acattgactc	420
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tggaacccc	actgtcaaac	ccacttatct	atgccctgag	gaacagttag	atgaaagggg	900
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<210> 944

<211> 927

<212> DNA

<213> Unknown (H38g794 nucleotide)

<220>

<223> Synthetic construct

<400> 944

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gggaatctgc	tcatactcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
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atgtctatta	acatccagac	acagagcaga	gtcatcacct	atgcaggctg	catcaccacg	300
atgtgctttt	ttgtactttt	tggagggtta	gacagcttac	tcctggctgt	gatggcctat	360
gatcggtttg	tggccatctg	tcatactctg	cactacacag	tcatacatgaa	ccctcggctc	420
tgtggactcc	tggttctggc	atcctggatg	attgctgccc	tgaattcctt	gtcacaaagc	480
ttaatggtat	tgtggctgtc	cttctgcaca	gacttggaaa	tcctccactt	tttctgtgaa	540
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tttgcagcag	ggctgtggc	tggtggtccc	cttgtgggga	tcctttgtct	ttactctaag	660
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<210> 945

<211> 942

<212> DNA

<213> Unknown (H38g795 nucleotide)

<220>

<223> Synthetic construct

<400> 945

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ctggggatga	tcataattaat	cctgctggac	tctcatctcc	acactcccat	gtactttttt	180

ctcagtaacc	tgtctcttgc	aggcattggt	tactcctcag	ctgtcactcc	aaaggtttta	240
actgggttgc	ttatagaaga	caaagccatc	tcctacagtg	cctgtgctgc	tcagatgttc	300
ttttgtgcag	tctttgccac	tgtggaaaat	tacctcttgt	cctcaatggc	ctatgaccgc	360
tacgcagcag	tgtgtaaccc	cctacattat	accaccacca	tgacaacacg	tgtgtgtgct	420
tgtctggcta	taggctgtta	tgtcattggt	tttctgaatg	cttctatcca	aattggagat	480
acatttcgcc	tctctttctg	catgtccaat	gtgattcatc	actttttctg	tgacaaaacca	540
gcagtcatta	ctctgacctg	ctctgagaaa	cacattagtg	agttgattct	tgttcttata	600
tcaagtttta	atgtcttttt	tgcacttctt	gttaccttga	tttccctatc	gttcatattg	660
atcaccattc	ttaagaggca	cacaggtaag	ggataccaga	agcctttatc	tacctgtggt	720
tctcacctca	ttgccatfff	cttattttat	ataactgtca	tcatcatgta	catacgacca	780
agttccagtc	attccatgga	cacagacaaa	attgcatctg	tgttctacac	tatgatcatc	840
cccagtctca	gtcctatagt	ctataccctg	aggaacaaag	acgtgaagaa	tgcattcatg	900
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<210> 946

<211> 946

<212> DNA

<213> Unknown (H38g796 nucleotide)

<220>

<223> Synthetic construct

<400> 946

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ctggagatca	tactgttgat	cctgctggac	tcttgctccc	aattcccattg	tactttttcc	180
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ctaggttact	tagagggtag	gaggctaagt	tcctcgtaca	atgcttggtc	tgctcagatg	300
ttcttttttg	tagccttggc	cacagtggaa	aatatcgctg	ttgacatcaa	tggcctatga	360
ccactatata	gcagtgtgca	aacccttaca	ctacactacc	accacgatag	ccagtgtatg	420
tgctcatctg	gtcataggct	cctatgtctg	tggctttcta	aatgcctccc	tccgcattgg	480
ggacatattc	agtctctctt	tctgtaagtc	caatcttgct	catcaccttt	tctgtgatgt	540
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tgcctctcac	ctcattgcag	tctccatctt	ctatggaact	actatcttta	tgcacttaca	780
gcctagctcc	agccattcca	tggacacaga	tgaatgggca	tccttggtct	atgctgtggt	840
catctccatg	ctgaaccttg	tgttctacag	cctgaggagc	aaagaagtca	agaatgcatt	900
caaaaaggcg	gttgagaagg	caaaattttt	cttagaactg	tgattt		946

<210> 947

<211> 942

<212> DNA

<213> Unknown (H38g797 nucleotide)

<220>

<223> Synthetic construct

<400> 947

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ggcaacttgg	ccatcatcac	actgattctc	tctgtctccac	gcctccacat	ccccatgtac	180
atcttctctca	gtaacttggc	cttgacagac	atctgtcttca	cctccaccac	ggtccccaag	240
atgctgcaga	ttattttctc	ccctacaaag	gtaatttctc	acacaggctg	tttagcccaa	300
acttatttct	tcatttgctt	cgccgtcatg	gaaaacttca	tcctggctgt	gatggcctat	360
gacaggtaca	ttgccatctg	ccaccctttc	cactacacta	tgatcctgac	tagaatgctg	420
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tttctcatgg	gccaaactaat	cttctgtgca	gataacagaa	tccccactt	cttctgtgac	540
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<210> 948

<211> 948

<212> DNA

<213> Unknown (H38g798 nucleotide)

<220>

<223> Synthetic construct

<400> 948

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aaaaatccgt	atgcccaagg	gaggggcaag	ttctttggtc	tcttctatgc	agtgggcaact	840
ccttcactta	accctctcgt	atacaccctg	aggaacaagg	agataaagcg	agcactcagg	900
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<210> 949

<211> 971

<212> DNA

<213> Unknown (H38g799 nucleotide)

<220>

<223> Synthetic construct

<400> 949

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gatccagaac	tgcagccggt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatatggtc	120
acgggtgctga	ggaacctgct	cagcatcctg	gctgtcagct	ctgactcccc	gctccacacc	180
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<210> 950

<211> 474

<212> DNA

<213> Unknown (H38g800 nucleotide)

<220>

<223> Synthetic construct

<400> 950

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acactgtcaa	acatccggac	acagagtaaa	gtcatcacct	atgcaggttg	catcacccag	300
atgtactttt	ttgtactctt	tatagtgttg	gacagcttac	tcttgaccgt	gatggcctat	360
gaccagtttg	tggccatctg	tcacccctcg	cactacacgg	tcatcgtgaa	ccctcggtc	420
tgtggactgc	tggttctggc	gtcctggatc	atgagtgcc	tgaattcctt	gata	474

<210> 951

<211> 954

<212> DNA

<213> Unknown (H38g801 nucleotide)

<220>

<223> Synthetic construct

<400> 951

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atactgggga	atgtgacact	ggtgctgtc	atctcctggg	actccagact	gcactcacc	180
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aatgagctgg	ccatattctt	tgaggggtgg	ttccttatgc	tgggcccctg	tgccctcatt	660
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tcagtaatgt	atactgccat	tacacctttg	gccaacccat	ttgtgtatag	cctccacaat	900
aaggatgtca	aggggtgcact	ctgcaggctg	cttgaatggg	tgaaggtaga	cccc	954

<210> 952

<211> 921

<212> DNA

<213> Unknown (H38g802 nucleotide)

<220>

<223> Synthetic construct

<400> 952

atgctgaata	caacctcagt	caccgaattt	ctcctcttgg	gagtgcaga	cattcaagaa	60
ctgcagcctt	ttctcttcgt	ggttttcttc	accatctact	tcatcagtgt	gactgggaat	120
ggagccgttc	tgatgattgt	catctccgat	cctagactcc	attcccttat	gtatttcttc	180
ctgggaaacc	tgtcctacct	ggatatctgt	tactctacgg	tgacactgcc	aaaaatgctg	240
cagaactttc	tctctacaca	caaagcaatt	tctttcttgg	gatgcataag	ccagcttcac	300
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acttatctct	tcttcaagac	ccgttcttgt	agcatgctct	gtaaagcact	gtccacttgt	720
gcctcccact	tcatggtagt	tattcttttc	tatgcacctg	ttcttttcac	ctatatccat	780
cctgcgttag	agagcttcat	ggaccaggac	cggattgttg	ccatcatgta	cactgtggtc	840
actcctgtac	taaaccact	gatctatact	ttgaggaaaca	aggaagtga	gggggccttg	900
ggtagagtga	tcagaaggct	t				921

<210> 953

<211> 959

<212> DNA

<213> Unknown (H38g803 nucleotide)

<220>

<223> Synthetic construct

<400> 953

cagccacgga	atctcacaga	tgtctgagaa	ttcctcctca	tgggactctc	agaggatcca	60
gaactgcagc	ccgtcctcgc	tgggctgtcc	ctgtccatgt	atctggtcac	ggtgctgagg	120
aacctgctca	gcatacctggc	tgtcagctct	gactcccacc	tccacacccc	catgtacttc	180
ttcctctcca	acctgtgctg	ggctgacatc	ggtttcacct	cggccacggg	tcccaagata	240
attgtggaca	tgcatcgca	tagcagagtc	atctcttatg	tgggctgcct	gacacggatg	300
tcttttttgg	tcctttttgc	atgtatagaa	gacatgcttc	tgactgtgat	ggcctatgac	360
tgctttgtag	ccatctgtcg	ccctctacac	tacccagtca	tcgtgaatgc	tcacctccgt	420
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tctcaacttc	tcaagcttgc	ctgttctgac	agcatcatca	atagcatatt	catatatattc	600
gatagtacta	tgtttggttt	tcttccatt	tcagggatcc	ttttgtctta	ctgtaaaatt	660
gttccctcca	ttctaaggat	ttcaacatca	gatgggaaat	ataaagcctt	ctccacctgt	720
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acccccatgc	tgaacccttt	catctacagc	ctgagaaaca	gggacattca	aagcaccctg	900
cggaggctgc	tcagcagaac	agtcgaatct	catgatctgt	tccatccttt	ttcttgtgt	959

<210> 954

<211> 984

<212> DNA

<213> Unknown (H38g804 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(984)

<223> n = A,T,C or G

<400> 954

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ggaaacttgg	gcttggtaac	tctaattggg	ctgaactcac	accttcatac	ccccatgtac	180
ttcttctctt	ttaaacttgc	cttcatagat	ctctgttatt	cttctgtgtt	tatacccaaa	240
atgctaata	actttatttc	agagaagaat	attatgtcct	tcaaggggtg	catgacccaa	300
ctttctcttt	nctgattttt	ttggtcattt	ctgaagggtta	tgtgctgacg	tcaatggcgt	360
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tgtccagcc	ttatgttttg	ttcctatttg	atgccttttt	ctggtgccat	ggccccacact	480
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actgtgggtg	gcataacat	cattgtgccc	actgttacca	tctttatctc	ttatgggttc	660
atcctctcca	gcatacctcca	tatcagttcc	aaggagggca	ggtccaaagc	tttcagcact	720
tgcagttccc	atataattgc	tgtttctctg	ttctttggat	cagggtgcatt	tatgtatctc	780
aaacctctct	ctgctgggtc	catggataag	agaaaattat	cttctgtctt	ttatacaaat	840
gtggttccca	tgttgaacct	cttaatctac	agcctgagga	acaaagatgt	taaatttgcc	900
ctaagaaaag	ccctgagtag	taggaaactt	tgataagtaa	tagtatgtgt	ctgtgtgtat	960

agtcacaaga cagggatatt ctgt

984

<210> 955

<211> 930

<212> DNA

<213> Unknown (H38g805 nucleotide)

<220>

<223> Synthetic construct

<400> 955

atgggaagaa	ataacctaac	aagaccctct	gaattcatcc	tccttggact	ctcctctcga	60
cctgaggatc	agaagccgct	ctttgctgtg	ttcctcccca	tctaccttat	cacagtgata	120
ggaaacctgc	ttatcatcct	ggccatccgc	tcagacactc	gtctccagac	gcccatgtac	180
ttcttttctaa	gcatcctgtc	ttttgttgac	atttgctatg	tgacagtcac	tatccctaag	240
atgctggtga	acttcttata	agagacaaag	accatctctt	acagtgaagt	tctgaccag	300
atgtactttt	tcttagcctt	tggaacaca	gacagttacc	tgctagcagc	catggccatt	360
gaccgctatg	tggccatatg	taatcccttc	cactacatca	ccattatgag	tcacagatgc	420
tgtgtcctgc	tcttggttct	ctccttctgc	attccacatt	ttcactccct	cctgcacatt	480
cttctgacta	atcagctcat	cttctgtgcc	tcaaatgtca	tccatcactt	tttctgcat	540
gatcaaccag	tgtataaatt	gtcctgttcc	tccatttttg	tcaaagaaat	cacagtaatg	600
acagaaggct	tggctgtcat	aatgaccccg	ttttcatgca	tcatcatctc	ttattttaaga	660
atcctcatca	ctgttctgaa	gattccttca	gctgctggaa	agcgtaaagc	attttctacc	720
tgtggctctc	atctcacagt	ggtgaccctg	ttttatggaa	gcattagcta	tctctatttt	780
cagccctctg	ccaactatac	tgtcaaggat	caaatagcaa	caattatcta	caccgtactg	840
actcctatgc	taaatccatt	tatctatagt	ctgaggaaca	aagacatgaa	gcagggtttg	900
gcaaagttga	tgcacaggat	gaaatgtcag				930

<210> 956

<211> 945

<212> DNA

<213> Unknown (H38g806 nucleotide)

<220>

<223> Synthetic construct

<400> 956

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gacatccctg	aactgcattt	cttgtttttt	attgtattca	ctgctgtcta	tgtcttcac	120
atcatagggg	atatgtgat	tattgtagca	gtgggttagct	cccagaggct	ccacaaacct	180
atgtatattt	tcttggcgaa	tctgtccttc	ctggatatcc	tctacacctc	cgcagtgatg	240
caaaaaatgc	tggagggcct	cctgcaagaa	gcaactatct	ctgtggctgg	ttgcttgctc	300
cagttcttta	tcttcggctc	tctagccaca	gctgaatgct	tactgctggc	tgtcatggca	360
tatgaccgct	acctggcaat	ttgctaccca	ctccactacc	cactcctgat	ggggcccaga	420
cggtagatgg	ggctgggtgt	cacaacctgg	ctctctggat	ttgtggtaga	tggactgggt	480
gtggccctgg	tggcccagct	gaggttctgt	ggccccaacc	acattgacca	gttttactgt	540
gactttatgc	ttttcgtggg	cctggcttgc	tcggatccca	gagtggctca	ggtgacaact	600
ctcattctgt	ctgtgttctg	cctcactatt	ccttttggac	tgattctgac	atcttatgcc	660
agaattgtgg	tggcagtgtc	gagagttcct	gctggggcaa	gcaggagaag	ggctttctcc	720
acatgtcctc	cccacctagc	tgtagtgaac	acattctatg	gaacgctcat	gatcttttat	780
gttgaccctc	gtctgtcca	ttcccagctc	ctctccaagg	tcttctccct	gctctacact	840
gtggtcaccc	ctctcttcaa	tcctgtgatc	tataccatga	ggaacaagga	ggtgcatcag	900
gcacttcgga	agattctctg	tatcaaacaa	actgaaacac	ttgat		945

<210> 957

<211> 565

<212> DNA

<213> Unknown (H38g807 nucleotide)

<220>

<223> Synthetic construct

<400> 957

cactggaaaa	ttttaagaag	aaacagcaag	atgatacatg	aaattatata	gaccttatgc	60
caaatacctt	actcagagga	caaaacttgt	tacatacaga	tacaaagctt	gttttgtact	120
gacttggaag	tcccaaactt	tttctgtgaa	cttaattagg	tggtccacct	tgccgtgtct	180
gacaccttct	tcaaagacat	agtgaggat	tgtacaacta	tgctgctgag	tggtgggtccc	240
attgctggta	tttttttact	ctttctctaa	gatcatttca	tccatatgtg	caatccccatc	300
agctcagggg	aagcataaag	catttcccac	ctgcgtgtct	cacctctcaa	atatgtcctt	360
attttattgt	aggagcacag	gattgtacct	tagttttgct	gctaccacac	actcatgctc	420
taatgcaact	gcctcagtg	ggcacactgt	ggttaaacc	ttactaaacg	ttttcatctt	480
aaagtcaagt	aataaagaca	taaaatgagc	tctgaaagta	ttcttcagag	gaaagcaatg	540
gaagcatcat	ttttcaaaaa	gtgca				565

<210> 958

<211> 939

<212> DNA

<213> Unknown (H38g808 nucleotide)

<220>

<223> Synthetic construct

<400> 958

atggaaaaaa	gaaatctaac	agttgtcagg	gaattcgtcc	ttctgggact	tcctagctca	60
gcagagcagc	agcacctcct	gtctgtgtct	tttctctgta	tgtatttagc	caccaccttg	120
gggaacatgc	tcatcattgc	gacgattggc	tttgactctc	acctccattc	ccctatgtac	180
ttcttcctta	gtaacttggc	ctttgttgac	atctgcttta	cgctcgactac	agtcccccaa	240
atggtagtga	atatcttgac	tggcaccaag	actatctctt	ttgcaggctg	cctcaccag	300
ctcttcttct	tcgtttcttt	tgtgaatatg	gacagcctcc	ttctgtgtgt	gatggcgtat	360
gatagatatg	tggcgatttg	ccacccttta	cattacaccg	ccagaatgaa	cctgtgcctt	420
tgtgtccagc	tagtggtctg	actgtggctt	gttacttacc	tccacgcctt	cctgcatact	480
gtcctaatag	cacagctgtc	cttctgtgcc	tccaatatca	tccatcattt	cctctgtgat	540
ctcaatcttc	tcctgcagct	ctcttgcctt	gacgtctcct	tcaatgtaat	gatcattttt	600
gcagtagggc	atctattggc	tctcacgccc	cttgtctgta	tcctcgatc	ttatggactt	660
atctttctcca	ctgtttctgaa	gatcacctct	actcagggca	agcagagagc	tgtttccacc	720
tgcagctgcc	acctgtcagt	ggtgggtgtg	ttttacggca	cagccatcgc	cgtctatttc	780
agcccttcat	cccccatat	gcctgagagc	gacactctgt	caaccatcat	gtattcaatg	840
gtggctccga	tgctgaatcc	tttcatctat	accctaagga	acagggatat	gaagagggga	900
cttcagaaaa	tgctttctcaa	gtgcacagtc	tttcagcag			939

<210> 959

<211> 936

<212> DNA

<213> Unknown (H38g809 nucleotide)

<220>

<223> Synthetic construct

<400> 959

atggatggag	gcaaccagag	tgaaggttca	gagttccttc	tcctggggat	gtcagagagt	60
cctgagcagc	agcagatcct	gttttggatg	ttcctgtcca	tgtacctggt	cacggtgggtg	120
ggaaatgtgc	tcatcactct	ggccatcagc	tctgattccc	gcctgcacac	ccccgtgtac	180
ttcttctctg	ccaacctctc	cttcaactgac	ctcttctttg	tcaccaacac	aatccccaag	240
atgctgggtga	acctccagtc	ccataacaaa	gccatctcct	atgcagggtg	tctgacgcag	300
ctctacttcc	tggtctcctt	ggtggccctg	gacaacctca	tcctggctgt	gatggcatat	360
gaccgctatg	tggccatctg	ctgccccctc	cactacacca	cagccatgag	ccctaagctc	420
tgtatcttac	tcctttcctt	gtgttgggtc	ctatccgtcc	tctatggcct	catacacacc	480
ctcctcatga	ccagagtgc	cttctgtggg	tcacgaaaaa	tccactacat	cttctgtgag	540
atgtatgtat	tgctgaggat	ggcatgttcc	aacattcaga	ttaatcacac	agtgtgtgatt	600
gccacaggct	gcttcatctt	cctcattccc	tttggattcg	tgatcatttc	ctatgtgctg	660
attatcagag	ccatcctcag	aataccctca	gtctctaaga	aatacaaaagc	cttctccacc	720
tgtgcctccc	atttgggtgc	agtctccctc	ttctatggga	cactttgtat	ggtataccta	780

aagccccctcc	atacctactc	tgtgaaggac	tcagtagcca	cagtgatgta	tgctgtgggtg	840
acacccatga	tgaatccctt	catctacagc	ctgaggaaca	aggacatgca	tggggctctg	900
ggaagactcc	tagataaaca	ctttaagagg	ctgaca			936

<210> 960

<211> 951

<212> DNA

<213> Unknown (H38g810 nucleotide)

<220>

<223> Synthetic construct

<400> 960

atgggaatgt	ccaacctgac	aagactctct	gaattttatc	tcttgggact	ctcctctcgg	60
tctgaagacc	agaggccact	ctttgccctc	tttcttatca	tatacctggg	cactttgatg	120
ggaaatctgc	tcacatctct	ggctatccac	tctgatccct	gacttcaaaa	ccctatgtat	180
tttttcctaa	gcatcttgct	ctttgctgat	atttgctaca	caacagtcac	agtcccaaag	240
atgctcgtga	acttcttctc	agagaaaaag	accatttccct	atgctgaatg	tctggcacag	300
atgtatttct	tcctgggttt	tggaaacata	gatagttatc	tcctggcggc	tatggccatc	360
aaccgctgtg	tagccatttg	taacccattc	cattatgtca	ctgttatgaa	ccgcagatgc	420
tgtgtgttgc	tactagcatt	ccccatcact	ttctcctatt	tccactctct	cctacatgtc	480
ctcctgggtga	atcggtctac	cttttgtaca	tcaaatgtta	tccatcattt	tttttgtgat	540
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acagaagggc	tggcctctgt	gatggctcca	tttgtctgta	tcatcatctc	ttatctaaga	660
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tgcagctccc	atctcactgt	ggtgattctg	ttttatggga	gtattagcta	tgtctatttg	780
cagcctttgt	ccagctatac	tgtcaaggac	cgaatagcaa	caatcaacta	cactgtgttg	840
acatcagtgt	tgaacccatt	tatctacagt	ttaagaaaca	aagacatgaa	acggggctta	900
cagaaattga	taaacaagat	taagtctcaa	atgagtaggt	tctctacaaa	g	951

<210> 961

<211> 926

<212> DNA

<213> Unknown (H38g811 nucleotide)

<220>

<223> Synthetic construct

<400> 961

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ctgcagcctt	ttctcttcgt	tgttttcctt	accatctact	tcatcagtgt	ggctgggaat	120
ggagccattc	tgatgattgt	catctctgat	cctagactcc	attcccctat	gtattttctt	180
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cagaacttcc	tctctgcaca	caaagcaatt	tctttcttgg	gatgcataag	ccaactccat	300
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tttgtggcta	tttgcaagcc	acttcgctac	actgtcatta	tgaacctca	gctctgtacc	420
cagatggcca	tcacaatctg	gatgattggt	tttttccatg	ccctgctgca	ctccctaattg	480
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ccattgctaa	agctgagctt	aatcagtggc	tgtcagtagc	tgtcacaggg	acaatcgcca	600
tgggcccctt	ctttctcaca	ttactctcct	atttctacat	tatcacccat	ctcttcttca	660
agactcattc	tttttagcatg	ctccgcaaag	cactgtccac	ttgtgcctcc	cacttcatgg	720
tagttattct	tttgtatgca	cctgttctct	tcacctatat	tcatcatgce	tcagggaacct	780
ccatggacca	ggaccggatc	actgccatca	tgtatactgt	ggtcactcca	gtactaaacc	840
cactgatcta	cactttgagg	aacaagggaag	tgaagggggc	ctttaataga	gcaatgaaaa	900
ggtggccttg	gcctaaagaa	atcttg				926

<210> 962

<211> 983

<212> DNA

<213> Unknown (H38g812 nucleotide)

<220>

<223> Synthetic construct

<400> 962

tcagtggacc	aagtaaata	ctctctggta	acagaatttg	tattacttgg	acttgcacaa	60
tccttggaaa	tgcagttttt	cctttttctc	ttcttctctt	tattctatgt	gggaattatc	120
ctgggaaacc	tcttcattgt	gttcacagtg	atctttgatc	ctcacttaca	ctccccatg	180
tatattctgc	tggccaacct	atcgctcatt	gacttgagcc	tttcatctac	cacagttcct	240
agggttgatct	acgatctttt	tactgattgt	aaagttat	ccttccataa	ttgtatgata	300
caaaagttct	ttatccatgt	tacgggagga	gttgaaatgg	tgctgctgat	agtcattgaa	360
tatgataggt	acactgcat	ctgcaagcct	ctccactatc	caactattat	gaatcccaaa	420
atgtgcatgt	ttttggtagc	agcagcttgg	gtcattgggg	tgattcatgc	tatgtctcag	480
tttgtttttg	tcataaatta	accttctgtg	gccctaataa	tggtgggagc	ttttattgtg	540
attttctctg	ggttattaaa	cttgcattga	tggacactta	cgggctagaa	tttgtggtca	600
ctgccaacag	tggattcata	tcgatgggca	ccttcttttt	cttaattgta	tcatacat	660
ttattctggt	cactgtccaa	cgacattcct	caaagtattt	atccaaagca	ttcttcactt	720
cgtaggctca	catcacgcta	gtggttttgt	tttttgctcc	atgcatgttt	ctctacgtgt	780
ggcctttccc	tactaagtca	ttggataaat	tttttgccat	catgaacttt	gttgtcacc	840
ctgtcttaaa	tcctgccatc	tatactttta	ggaacaaaga	tatgaagttt	gcaatgagaa	900
ggctgaatca	acatatattt	aattctatgg	agacgacata	acacatttgg	ttgatgagag	960
cacaggataa	atgccatgga	cca				983

<210> 963

<211> 817

<212> DNA

<213> Unknown (H38g813 nucleotide)

<220>

<223> Synthetic construct

<400> 963

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ccctggctag	agacacccct	ctgtaatcct	tctgggtggc	tacatctttt	ccctatttgg	120
aaatatctcc	attatcctag	tttcccatct	ggatccccag	cttgacagtc	ccatgtactt	180
ttttgtctct	aatctatcct	ttctggacct	ctgctatacc	accagcactg	tcccacagat	240
gctggtcaac	ctccggggac	cagaaaagac	cattagctat	gggggttggt	ttgcccact	300
ctatatattt	ttggccctgg	gttctactga	atgcatactt	ctagccatca	tggcctttga	360
ccgttacgct	gccatatgca	agccccttca	ctaccagtc	atcatgaacc	atagacgctg	420
tatccacatg	gctgctggca	cttggatcag	tggttttgct	aactcccttg	tccagtccac	480
tctcacagtg	gtggccccaa	gatgtggaca	gagggtgttg	gaccatttct	tctgtgaagt	540
tccagccctt	ttgaaactag	cctgtattga	tattcgtgtg	aatgaaatgg	agctcaatgt	600
actaggcgct	ttgcttctcc	tgatgccact	cacctcatc	ctgggcactt	atgtgttcat	660
tgctcaggca	gtaatgagaa	tctgctctgc	tgaaagtcgc	tgggaaggct	tcaatacctg	720
tgccctcat	ttgctggtgg	tctccctctt	ctacttcaca	gccatcagta	tgtatgtcca	780
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<210> 964

<211> 945

<212> DNA

<213> Unknown (H38g814 nucleotide)

<220>

<223> Synthetic construct

<400> 964

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ttctcttgtg	agtggaaca	tcagatcttc	ctcttctcac	tctttactac	aacatatgca	120
ctgactataa	caggaatgg	agccattgct	tttgcctgt	ggtgtgaccg	gcgacttcac	180
actcccatgt	acatgttctt	gggaaatttc	tcctttttag	agatatggta	tgtctcttct	240
acagttccca	agatgttgg	caacttcctt	tcagagaaaa	aaaacatctc	ctttgctgga	300
tgttttctcc	agttttat	cttcttctct	ttgggtacat	cagaatgctt	gcttttgact	360

gtgatggcct	ttgatcagta	ccttgetatc	tgccgtccct	tgtcttatcc	taatatcatg	420
actgggcac	tctatgccaa	actggtcata	ctgtgctggg	tttgtggatt	tctgtgggtc	480
ctgatcccca	ttgttctcat	ctctcagatg	cccttctgtg	gccccaaacat	tattgaccat	540
gttgtgtgtg	acccagggcc	acgatttgca	ttggattgtg	tttctgcccc	aagaatccaa	600
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gtcatgtatg	tgagcccagg	actcggacat	tctacaggga	tgcagaaaat	tgaaactttg	840
ttctatgcta	tggtgacccc	actcttcaat	ccccttatct	atagcctcca	gaataaggag	900
ataaaggcag	ccctgaggaa	agttctgggg	agttccaaca	taatc		945

<210> 965

<211> 915

<212> DNA

<213> Unknown (H38g815 nucleotide)

<220>

<223> Synthetic construct

<400> 965

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tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggtat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
ctcattgac	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaaag	tcattctctt	caagggctgc	cttgttcaga	tatttctcct	tcacttcttt	300
ggtgggagt	agatgggtat	cctcatagcc	atgggctatg	acagatatat	agcaatatgc	360
aaaccactaa	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcgggt	agccagttgg	cctttgccgt	gcacttaccc	480
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gcctgtacag	atacctacag	gctagatatt	atggctcattg	ctaacagtgg	tgtgctcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaattgac	catccagcat	660
cgccctttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagtatgt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccc	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcacccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 966

<211> 953

<212> DNA

<213> Unknown (H38g816 nucleotide)

<220>

<223> Synthetic construct

<400> 966

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cccaactttc	agagttggca	gcacttgctg	tccttgcccc	tcagcctcat	ttcctcctgg	120
ccatggggac	caacacccac	ccccccatc	accatccacc	tgagggcctc	tctgcacctg	180
cccctgtact	acctgcccag	cctcctctcc	ctgtgggaca	tcgtgctctg	cctcaccgtc	240
atccccaaag	tcctggccat	cttctggttt	gatcttaggt	cgatcggtt	ccctgcctgc	300
ttccttcaga	tgttcatcat	gaacagtctc	ctccccatgg	agtcctgcac	attcatggtc	360
aaggactatg	atcattatgt	ggccatctgc	caccactgtc	agtacctgtc	catcatcact	420
catcaatttg	tgcccaaagc	tagtgtcttc	attgtgggtc	agaatgcttt	gctgctttca	480
cctgttccta	ttctctctgc	ccagctccat	tactgtagga	aaaatgtgat	tgagaactgc	540
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taccaatttg	tggtggttg	gaccttctctg	ggctcggatt	tcactctcat	cttctctctc	660
tacaccttca	ttctaagagc	tgtgcttaga	ttcaaggtgg	agggggtggc	agtgaaggcc	720
ctgagcacat	gtggctccca	ctttatctct	atcctcttct	tcagcacctg	ctgggtgtgg	780
tgttgacaaa	tgtggccaga	aagaaggtcc	ccatggacat	cctgatcctg	tttaatgtcc	840
ttcatccctt	tagtctctct	gcattaaacc	ctatcatatg	tggatttcaa	actaaagagt	900

taaagaagga attttagaag ttgctgcaga ggggcctttg aaaacacgga agg 953

<210> 967

<211> 954

<212> DNA

<213> Unknown (H38g817 nucleotide)

<220>

<223> Synthetic construct

<400> 967

aaacacaatc	acacggcagt	gaccaaggtg	actgaattta	ttctcatggg	gattacagac	60
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ataggcaatc	tgggcattgt	tatctttgac	ctactttgga	ctccaagcta	cacaccccca	180
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ggtatgcaa	tcacagagca	cgctttgaga	ggaacatcat	ctctcaccgc	ggcattctat	360
cagcaacgaa	caatgagccc	tacaaacca	tcactaaaca	acttctgaac	ccgatcatca	420
tgccagagaa	aatacgggag	gagcaaataa	ccgttcccga	gctcgataaa	acgtgtgcgc	480
cactatttct	caaaagggaag	tgagtcaaaa	cagtctccac	caaccagac	acaaccaaca	540
attgtcacgg	tgaagggacc	gctaaaatgt	gaatactccg	ttctgaaaaa	aagaaaataa	600
caataataaa	ggcgatgacc	gcaggaaccg	aacatgctca	tctccctctc	aattgttctc	660
atatactaca	tgttttattct	agtggccaat	ctcagaatga	actcaaggaa	agggaggtac	720
aaagccttct	ccacctgtag	ctctcatctg	acagtgggtg	tcatgttcta	tgggacattg	780
ttattttatt	acttgcaacc	caagtccagt	catactttgg	ctattgataa	aatggcctca	840
gtgtttttata	ccctgttgat	tcctatgctg	aatccgttga	tctacagcct	aaggaacaaa	900
gaagtaaaag	atgctctaaa	gagaacttta	accaatcgat	tcaaaattcc	catt	954

<210> 968

<211> 660

<212> DNA

<213> Unknown (H38g818 nucleotide)

<220>

<223> Synthetic construct

<400> 968

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ttggctcctt	ttgcatgtat	agaagacatg	ctcctgactg	tgatggccta	tgactgcttt	180
gtagccatct	gtcgccctct	gcactacca	gtcatcatga	atcctcacct	ctgtgtcttc	240
ttcgttttgg	tgctcctttt	ccttagcctg	ttggattccc	agctgcacag	ttagattgtg	300
ttacaattca	ctttcttcag	taatgtggaa	attgctaatt	ttgtctatga	gccatctcaa	360
cttctcaacc	ttgactgttc	tgacaccgtc	atcaatagca	tatttatata	tttcgatagt	420
actgtttggg	tttcttccca	tttcagggat	cctttgtctt	agtataaaat	tgtcccctcc	480
attctaagga	tgatcatgct	agatgggaag	tataaagcct	tcgccacctg	tggtctctac	540
ctagcagttg	tttgctgatt	tgatggaaca	ggcattggca	tgtacctgac	ttcagctgtg	600
tcaccacccc	ccaggaatgg	tgtggcggcg	tcagtgatgt	acgtgtgggt	caccccatg	660

<210> 969

<211> 933

<212> DNA

<213> Unknown (H38g819 nucleotide)

<220>

<223> Synthetic construct

<400> 969

attgaaaaaa	gcaataatag	cactttgttt	attctcttgg	ggttttccca	aaataagaac	60
attgaagtcc	tctgctttgt	attatttttg	ttttgctaca	ttgctatttg	gatgggaac	120
ttactcataa	tgatttctat	cacgtgcacc	cagctcattc	accaacccat	gtatttcttc	180

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ctcaattacc tctcactctc cgacctttgc tacacatcca cagtgacccc caaattaatg 240
gttgacttac tggcagaaaag aaagaccatt tcctataata actgtatgat acaactcttt 300
accaccattt tttttggagg catagagatc ttcattctca cagggatggc ctatgaccgc 360
tatgtggcca tttgcaagcc cctgcactac accattatta tgagcaggca aaagtgtaac 420
acaatcatca tagtttggtg tactggggga tttatacatt ctgccagtca gtttcttctc 480
accatctttg taccattttg tggcccaaat gagatagatc actacttctg tgatgtgtat 540
cctttgctga aattggcctg ttctaataa cecatgatag gtctcttagt cattgctaata 600
tcaggcttaa ttgctttggt gacatttgtt gtcttggtgt tgtcttatgt ttttatattg 660
tataccatca gagcatactc tgcagagaga cgcagcaaag ctcttgccac ttgtagtctt 720
catgtaattg ttgtggctct gttttttgct cctgcattgt tcatttacat tagaccggtc 780
acaacattct cagaagataa agtgtttgcc cttttttata ccatcattgc tcccattgtc 840
aaccctctca tatacacgct gagaaacaca gagatgaaga acgccatgag gaaagtgtgg 900
tgttgtcaaa tactcctgaa aagaaatcaa ctt 933

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<210> 970

<211> 666

<212> DNA

<213> Unknown (H38g820 nucleotide)

<220>

<223> Synthetic construct

<400> 970

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gcaattatca ccaggaataa gactatttcc tataacaact gtgcagccca actcttttct 120
tttatcttca tgggggtgac tgaattttac attttaactg ccatgtccta tgaccgctat 180
gttgccatct cgaagccctc tcattacaca tccatcatga acaggaaact ctgcactcta 240
cttgtgctgt gtgcctggct aagtgggttt cgcaccattt tcccaccctt tatgcttctc 300
ctccagctgg actactgtgc ttccaacgtc attgatcact ttgcatgtga ctattttccc 360
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ttggttactt tgctgttcac tttggcatta gtgattttat cttacatgta cattatcagg 480
accattttga gaatcccgtc tgccagtcaa agaaaaaagg ctttctccac ttgttcttct 540
cacatgattg tcatttccat ttcttatgga agctgtatat tcatgtatgc taatccatct 600
gcaaaaagaa aggcattcatt gacaaaagga atagctattc tcaatacatc tgttgcccc 660
atgctg 666

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<210> 971

<211> 799

<212> DNA

<213> Unknown (H38g821 nucleotide)

<220>

<223> Synthetic construct

<400> 971

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ataattttgt gttttttcat cataggtaac tctcaggata attcccaaact gactttgatg 60
gataacattt cagaagtgaac agaattcggt ctctgtgggt taacagatgt cctagagctt 120
caggtccctt tatttatcat ctttactgtc atttatctca ccactctggt tgggaacttt 180
gggatgatca tggtgattct gttggactcc cggtccaca ttcccattgta ctttttcctt 240
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ttacgcacat gagattgtgc tcttcatatt ggcagcattt aatatctttt tcaactctctt 480
gattatcttg aactcttatg tttttatttt tattgctatc ctgaggatgc attcagctga 540
gggacaaaag aaggtctttt ccacctgtgc ctatcacctc actactgttt ccatcttcta 600
tgggacaatc acctttatgt acttacagcc aagttctggt cattccatgg acacagacaa 660
aatctcatct gtgttctaca ccatggtcat ccccatgctt aaccctctag tctatagcct 720
gaggaacaaa gaagtccaga gtgcattcaa ggtggttatt ggaaaagcaa agtcttcatt 780
gggcttagcc tactattta 799

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<210> 972

<211> 946
 <212> DNA
 <213> Unknown (H38g822 nucleotide)

<220>
 <223> Synthetic construct

<400> 972
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 gtggcaacac agccatcatc tgggttgtgt gcacatacag cgttctccga accccaatgt 180
 atttcttctt gtccaacctg tcctttgtag agatctgcta caccaccgtt gtggtgccct 240
 tgatgctttc caacatTTTT ggggcccaga agccatttcc attggctgga tgtggggccc 300
 aaatgttctt ctttctcaca cttggttgtg ctgactgttt cctcttggcg atcgtggcct 360
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 gtgcgtgcag atgctgggag gcgctgtggg cctggccctc ttcctctccc tgcagctcac 480
 cgccttaatc ttcaccttgc ccttctgcgg ctaccgccag gaaattaacc acttctctctg 540
 cgatgtaccc cccgtcctgc gcctggcctg cgttgccatc cgtgttcacc aggtgtcctt 600
 ctatgtcgtg agcatcctcg tgcctgacct ccccttcttg ctcatctgag tctctacgt 660
 gttcatcacc tgtgccatcc tgagcatccg ttctgctgag ggccgccacc aggccttctc 720
 cacctgctcc tcccacctca ccgtggctct gctgcagtat ggctgctgtg ccttggcata 780
 cttgcatccc cagtcagct cctctgcaga tgaggatcgc cagtttgccc ttgtttacac 840
 ctttatcaca ccattactca accctttgat ttacaccctt aggaacaagg atgtcaaagg 900
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<210> 973
 <211> 936
 <212> DNA
 <213> Unknown (H38g823 nucleotide)

<220>
 <223> Synthetic construct

<400> 973
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 ctgcaggctc ccttctttat catgttttgt ctcatctatc tcatcaatgt agttggaaac 120
 ttggggatga tcattttgat tctctgttac tctcagctcc acaatccaat gtacttcttc 180
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 actgggctcc tttagaaga caaaatcatt tcctatactg tgtgggctac tcagacattc 300
 ttttctgatt cctttgccag tgtggtaaat ttattattgg ccttaatggc ctctggccac 360
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 acattcagtc tctttctgta tgteccagtga agtccatcac tttttctgtg aggttccagc 540
 agtcatggct ctgtcttgct ctgatagaca tgtgaatgta gtggttcttg tttatgtaac 600
 cagctcaata tcctctttgc ccttctagtt atcttgatat cctacttatt gatgtttatc 660
 accatcctaa agatgcactc aactgcagga taccagaagg ctttggccat ttgtgcctct 720
 cacctcactg cagttgccat cttctatggg actattatct tcatgcatat acagcccagc 780
 tccagtcatt ccattgacac agacaaaatt gcagctgtgt tttatactat tgtcttcccc 840
 atggtgaacc atgtgtgcta aagattgaag aacaagggtga agagtacatt caagaaaatt 900
 gttgagaagg taaaattgtc cctaggattg tgagtt 936

<210> 974
 <211> 954
 <212> DNA
 <213> Unknown (H38g824 nucleotide)

<220>
 <223> Synthetic construct

<221> misc_feature
 <222> (1)...(954)

<223> n = A,T,C or G

<400> 974

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ggtaactccc	tgatcatcct	cctcacacag	gtcagccctg	ccctgcactc	ccccatgtac	180
ttcttctctg	gccaaactctc	agtgggtggag	ctcttctaca	ccactgacat	cgtgcccagg	240
accctggcca	atctgggctc	cccgcatccc	caggccatct	ctttccaggg	ctgtgcagcc	300
cagatgtacg	tcttcatgtg	cctgggcata	tcggagtgt	gcctgctcac	ggccatggcc	360
tatgaccgat	atgttgccat	ctgccagccc	ctacgtatt	ccaccctctt	gagcccacgg	420
gcctgcatgg	ccatgggtggg	tacctcctgg	ctcacaggca	tcatacaggg	ccaccacca	480
tgcctccctc	atcttctctc	tacctttctg	cagccaccgg	atcatcccg	actttctctg	540
tgacatcctg	ccagtactga	ggctggcaag	tgtctgggaag	cacaggagcg	agatctccgt	600
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gtcatcacac	ccatgtctaa	ccccatcata	aacacccacg	ggaacaagga	cgtgaggagg	900
gccttgcggg	acttggtgaa	gaggcgccgc	ccctcgccgg	gaagggggctc	gggt	954

<210> 975

<211> 933

<212> DNA

<213> Unknown (H38g825 nucleotide)

<220>

<223> Synthetic construct

<400> 975

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aaccctaagc	tgcaaaaacc	tctcttttgc	atcttcttca	tcattgtacct	actcactgcg	120
gtggggaatg	tgctcatcat	cctggccatc	tactctgacc	ccaggctcca	cacccttatg	180
tacttttttc	tcagcaactt	gtctttcatg	gatatctgct	tcacaacagt	catagtgcct	240
aagatgctgg	tgaattttct	atcagagaca	aagattatct	cttatgtggg	ctgcctgac	300
cagatgtact	tcttcatggc	atttgggaac	actgacagct	acctgctggc	ctctatggcc	360
atcgaccggc	tggtggccat	ctgcaacccc	ttacactatg	atgtgggttat	gaaaccatgg	420
cattgcctac	tcattgctatt	gggttcttgc	agcatctccc	acctacattc	cctgttccgc	480
gtgctactta	tgtctcgctt	gtctttctgt	gcctctcaca	tcattaagca	ctttttctgt	540
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tttaggcctc	tgtccatgta	ctcagtgatg	aagggccggg	tagccacagt	tatgtacaca	840
gtagtacac	ccatgtctga	ccctttcatc	tacagcctga	ggaacaaaga	tatgaaaagg	900
ggtttgaaga	aattaagaca	cagaatttac	tca			933

<210> 976

<211> 390

<212> DNA

<213> Unknown (H38g826 nucleotide)

<220>

<223> Synthetic construct

<400> 976

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ctgactatcc	tcacccctac	cttgctggac	tcccaccttc	agactcccat	gtatttcttt	180
ctccggaact	tctccttctt	ggaaatttcc	ttcacaaca	tcttcattcc	aagggctcctg	240
attagcatca	caacagggaa	caagagtatc	agctttgtg	gctgcttcac	tcagtatttc	300
tttgccatgt	tccttggggc	tacagagttt	taccttctgc	tgccattcct	atgaccgcta	360

tgtgccatct gcaaactgat gactatgcac

390

<210> 977

<211> 933

<212> DNA

<213> Unknown (H38g827 nucleotide)

<220>

<223> Synthetic construct

<400> 977

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aaccctcagc	tgcagaaacc	tctcttttgc	atcttctcca	tcattgtacct	gctegctgcg	120
gtggggaatg	tgtcatcat	cccggccatc	tactctgacc	ccaggctcca	caccctatg	180
tacttttttc	tcagcaactt	gtctttcatg	gatatctgct	tcacaacagt	catagtgcct	240
aagatgctgg	tgaattttct	atcagagaca	aagggttatct	cctatgtggg	ctgcctggcc	300
cagatgtact	tctttatggc	atgtgggaac	actgacagct	acctgctggc	ctctatggcc	360
atcgaccggc	tggtggccat	ctgcaacccc	ttacactatg	atgtggttat	gaaaccacgg	420
cattgcctgc	tcattgctatt	gggttcttgc	agcatctccc	acctacattc	cctgttccgc	480
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atgactgaga	ccttagctgt	cattgtgacc	cccttctctg	gtatcatctt	ctcctacctg	660
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gtagtgcac	ccatgctgaa	ccctttcatc	tacagcctga	ggaacaaaga	tatgaagagg	900
ggtttgaaga	aattacagga	cagaattttac	cgg			933

<210> 978

<211> 939

<212> DNA

<213> Unknown (H38g828 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(939)

<223> n = A,T,C or G

<400> 978

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ggaacctgaa	tcattcatcag	ccatgacctt	gctggacacc	cgcatgcaga	catctatgta	180
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gactttttcc	acatcttctg	ggggccacag	agttcttctc	cctgacagcc	atggcctatg	360
accagtatat	tgccatctgc	aagccctccc	actaccccat	gctcataagt	agtagagtct	420
gcacacagct	catcctcacc	tgtgtgttac	taggtttctc	cttcatcatc	atgcctgtca	480
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cctctccagg	aaagtgggtt	gatgtcaaca	angggagtgt	ctctaataca	tacaattatt	840
gccccactgt	taaatccctt	catctgtact	ctgaggaacc	aacaagttaa	gcaggtaatg	900
aaagacctag	tcagaaaaat	gactttgtcc	gaaaataaa			939

<210> 979

<211> 951

<212> DNA

<213> Unknown (H38g829 nucleotide)

<220>

<223> Synthetic construct

<400> 979

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atcacaaatc	gctgggacct	gcgtgtggcc	ctcttctga	cctgcctgcc	tgtctacctg	120
gtgagcctgc	tgggaaacat	gggcatggcg	ctgctgatcc	gcatggatgc	ccggctccac	180
acacctatgt	acttcttcct	ggccaacctc	tccctgctgg	atgcctgcta	ttcctccgcc	240
atcggcccca	agatgctagt	ggacctgctg	ctgccccgag	ccaccatccc	ttacacagcc	300
tgtgcccctc	agatgtttgt	ctttgcaggt	ctggctgata	ctgagtgttg	cttgctggca	360
gccatggcct	atgaccgcta	cgtggccatc	agaaaccac	ttctctatac	aacagctatg	420
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ttctataccc	tggtcatccc	gtctctcaac	ccactcatct	acagcctccg	caataaggag	900
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<210> 980

<211> 948

<212> DNA

<213> Unknown (H38g830 nucleotide)

<220>

<223> Synthetic construct

<400> 980

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actgtttctg	gaaacatcct	cattgtcctt	ctagttttag	tcagacatca	tctccacacc	180
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atccccaaaa	tggtgctgat	tatcatagct	gaatagaaga	ctatctctgt	ggctggctgg	300
ctggcacaa	tctacttctt	cggatccctg	gctgccacgg	agtgcctctt	gctcactgtg	360
atgtcctatg	atcgctacct	agccatctgc	cagcctcttt	gctaccgtgt	cctcatgact	420
ggcccccttt	gcacaggctt	agctgctggc	tcttggttct	gctgcttctt	ccttacagca	480
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ttttgtgact	tcacccctct	ggttcatctc	tcttgcatgg	atacctcagt	gactgagacc	600
attgcctttg	ccacctcttc	tgacagtaact	ctgatcccat	ttctcctcat	tgtagcctcc	660
tactcctgcg	tcctttctgc	tatcctaaga	atcccatctt	gcacaggcca	gaaaaaggcc	720
ttctccacct	gctcttccca	cctcactgtg	gtcatagtgt	tttatgggac	actgattgcc	780
acataccttg	tgccttcagc	caactcatcc	caactcttgt	gcaaagggtc	ctctctgctc	840
tacatcatcc	tgacacccat	gtttaacccc	atcatttata	gcctgagaaa	tagagacatc	900
catgaagctc	tgaagaagtg	cttgaggaag	aagtcagggtg	tttgcctt		948

<210> 981

<211> 925

<212> DNA

<213> Unknown (H38g831 nucleotide)

<220>

<223> Synthetic construct

<400> 981

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ggcaaccttc	tcattgtggg	gaccattatt	gccatgcctc	ccttggtgactc	cccagtgtcc	180

ttcttctctg	catgcctgtc	atattattgat	gctgtatatt	ccacttcctt	ttcccctaag	240
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gctattttata	aactacccat	ttgggtggtat	tgagggtctt	cttttggtgg	gtatggcctg	360
tgatcactat	gtggacatct	gtaagctact	gcactatttg	accatcatga	actggcaggt	420
ttgcatcctc	ctgtttatgg	tggtgtgtac	tgagggtttt	tgacattctat	gtttcaaatt	480
gttggtgtgt	acagtctccc	ttctgtggc	cccaatgtca	ttgaccattt	tgtgacatgt	540
acccattatt	ggaaatgggtg	tgactgaca	cttactttat	aggcctcact	gtgattgcca	600
atgggtggagc	agtctgtatg	gtcatcttca	tccttctact	aatctcctat	ggagtcaccc	660
taaactccct	taaaacttat	agtcagggaag	gcgggcataa	agccctgtct	acctgcagct	720
ccaacattac	tggtgtgtcc	ccttttttga	tcctgtatt	ttcatctatg	ttagacctga	780
ttcaaacttt	cctattgata	aattcatgac	tgtgttttat	acaattatca	cacctatgtt	840
gaatccatta	atatacacac	tgagaaattt	agagggtgaga	attgctgtga	aaaatctctg	900
gtgtaaaaac	taaactatag	taaga				925

<210> 982

<211> 958

<212> DNA

<213> Unknown (H38g832 nucleotide)

<220>

<223> Synthetic construct

<400> 982

atggatagag	taaataattc	tgcggtatct	aaattttgat	tgattggact	ttcaagctct	60
tgaggagatgc	atccttttct	tttttggttc	ttctctgtgt	tctacatggg	aattatcctg	120
gaaaatctct	tcattgtgtt	cacagtaatt	attgactctc	atttaaattc	cccaggctact	180
gcctactggc	caacatttat	cttcttgatc	tggtctctct	cctacagtcc	tgactttttc	240
actaactgca	gcattcattc	ttttccaaga	tgcatgatac	agatattttt	catttggtgc	300
atgctgtaaaa	attgagatgg	tgctgctcat	aaccatggca	tagagcaggt	acactgcca	360
tctgtaagcc	tccccattac	ctgaccacaa	tgaaccccaa	aatgtgtgtt	tactttgttg	420
gaggcatcct	ggatagtcag	gataatccat	gctgtatctc	agtttgtttt	tgccataaac	480
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tagggatttt	gttttttatg	ccatgtatat	ttctctatgt	gtagcctttg	cctaaaacaa	780
cacatgatta	atatttggtc	attgttcctt	ttgctatcac	ccctgtctag	gatctacaca	840
ttaagaaaca	aagacatgaa	cgtctccatg	gaaagactgg	gaaaatggat	tgacaggttct	900
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<210> 983

<211> 927

<212> DNA

<213> Unknown (H38g833 nucleotide)

<220>

<223> Synthetic construct

<400> 983

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ggaaatgcta	caattgcagt	cattgttcag	atcaatcatt	ccctccacac	ccccatgtac	180
tttttcttgg	ctaactctggc	agttctagaa	atcttctata	catcttccat	cacccatttg	240
gccttgccaa	acctccttcc	aatgggcaaa	actcctgttt	ccatcacggg	atgtggcacc	300
cagatgtttt	tctttgtctt	cttgggtggg	gctgattgtg	tcctgtgggt	agtcattggct	360
tatgaccggt	ttatagcgat	ctgtcaccct	ctgcgataca	ggctcatcat	gagctgggtcc	420
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gacatgcctg	cagtcacgcg	cctggcttgt	gcagacacac	gcgttcacaa	gactgctctg	600
tatatcatca	gcttcacgt	ccttagcatc	cccctctcat	tgatctccat	ctcctatgtc	660
ttcatcgtgg	tagccatttt	acggatccgg	tcagcagaag	ggcgccagca	agcctactct	720

acctgctctt	ctcacatctt	agtggctctc	ctgcagtatg	gctgcaccag	ctttatatac	780
ttgtccccc	gttccagcta	ctctcctgag	atggggccgg	tggtatctgt	ggcctacaca	840
tttatcactc	ccattttaaa	ccccttgatc	tatagtttga	ggaacaagga	actgaaagat	900
gccctaagga	aagcattgag	aaaattc				927

<210> 984

<211> 987

<212> DNA

<213> Unknown (H38g834 nucleotide)

<220>

<223> Synthetic construct

<400> 984

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caatccttg	aaatgcagtt	tttccttttt	ctcttcttct	ctttattcta	tgtgggaatt	120
atcctggga	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactccccc	180
atgtatattc	tgtggccaa	cctatcgctc	attgacttga	gcctttcatc	taccacagtt	240
cctaggttga	tctacgatct	ttttactgat	tgtaaagtta	tttccttcca	taattgtatg	300
atacaaaagt	tctttatcca	tgttacggga	ggagttgaaa	tggtgctgct	gatagtcacg	360
gcatatgata	ggtacactgc	gatctgcaaa	cctctccact	atccaactat	tatgaatccc	420
aaaatgtgca	tgtttttggg	agcagcagct	tgggtcattg	gggtgattca	tgctatgtct	480
cagtttgttt	ttgtcataaa	tttacccttc	tgtggcccta	ataatgtggg	gagcttttat	540
tgtgattttc	ctcgggttat	taaacttgca	tgcatggaca	cttatgggct	agaattttgtg	600
gtcactggca	acagtggtat	catatcgatg	ggcaccttct	ttttcttaat	tgtatcatatc	660
atttttattc	tggtcactgt	ccaacgacat	tcctcaaatg	atztatccaa	agcattcttc	720
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agaaggctga	atcaacatat	tttaaattct	atggagatga	cataacacat	ttggttgatg	960
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<210> 985

<211> 770

<212> DNA

<213> Unknown (H38g835 nucleotide)

<220>

<223> Synthetic construct

<400> 985

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gcccctctga	ctctggccaa	tgctctaccc	atggggagaa	acctcatttc	cctgcccggc	120
tgtggaggcc	agatgttctt	cttcactctc	ctgggaaggg	ctgactgcat	cctgctggcc	180
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ttctactgtg	atgtcctccc	tgctatgaga	ctggcctgtg	cagatacctg	ggtccatgag	420
gccactatgt	ctatggtcag	caccaccttt	ctcacctgct	ccttctgct	catcactctt	480
tcctatgtct	ccatcatggc	cgccatcttg	aagatttgct	ctgcagaggg	gaggcacaag	540
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tcgccttctt	gtgtcccagc	tctagctact	atcctgagag	gggccaggca	gtgtctgtgg	660
tttacacctt	cattaccctt	gtgtgaacc	ctttgatcta	cagcatgagg	aacacagaac	720
ttaaggatgc	tttgaagaga	gcaatgacga	gggtcccgt	gctctaaaca		770

<210> 986

<211> 915

<212> DNA

<213> Unknown (H38g836 nucleotide)

<220>

<223> Synthetic construct

<400> 986

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acagtgggat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
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gataaattcc	ttgctgtatt	ttattctgtg	atcaccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacggc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 987

<211> 958

<212> DNA

<213> Unknown (H38g837 nucleotide)

<220>

<223> Synthetic construct

<400> 987

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gaaaatctct	tcatttgtgt	cacagtaatt	attgactctc	atttaaattc	cccagggtact	180
gcctactggc	caacattttat	cttcttgatc	tgggtcttct	cctacagttc	tgactttttc	240
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tctgtaagcc	tccccattac	ctgaccacaa	tgaaccccaa	aatgtgtgtt	tcctttgttg	420
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cacatgatta	atatttgttc	attgttcctt	ttgctatcac	ccctgtctag	gatctacaca	840
ttaagaaaca	aagacatgaa	cgtctccatg	gaaagactgg	gaaaatggat	tgcaagggtct	900
agcaggatgt	cataataaat	ggtgcataac	cagagtgcac	gatgattcag	tctcacca	958

<210> 988

<211> 982

<212> DNA

<213> Unknown (H38g838 nucleotide)

<220>

<223> Synthetic construct

<400> 988

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aagtcttggc	atatcctctc	catagcattt	ctagcaatct	atgtgggttac	cccagtaggt	180
aatattggaa	tgatcctact	tatcaaaatt	gatgcttctc	ttcatatccc	catgtaaatt	240
ttctccaac	acttggcatt	tgttgatctc	tgttacacct	ctgctatcac	tccaagatg	300
ttgaaaaact	ttgtagaaac	aaaaaaatct	atctcatgta	taggatgtat	ggtgcaatta	360

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actaacagaa aaaaagtatt tc 982

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<210> 989

<211> 1006

<212> DNA

<213> Unknown (H38g839 nucleotide)

<220>

<223> Synthetic construct

<400> 989

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ccttctcca tattccaatg tatttatttt tatttttttg gcattgacta tgttggaat 240
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gcgtatggaa ccaagacgta actgatgcag tagagagact tgtggcaaga atgtccttgt 960
tctaacagcc agaaatattc cttcttaaaa aatatttccc taacta 1006

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<210> 990

<211> 987

<212> DNA

<213> Unknown (H38g840 nucleotide)

<220>

<223> Synthetic construct

<400> 990

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atcctgggaa acctcttcat tgtgttcaca gtgatctttg atcctcactt aactcccc 180
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gtgtggcctt tccctactaa gtcattggat aaattttttg ccatcatgaa ctttgttgtc	840
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<210> 991

<211> 736

<212> DNA

<213> Unknown (H38g841 nucleotide)

<220>

<223> Synthetic construct

<400> 991

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ccagaactgc agccccctct tgggctgttt ctgtccatga acctgggtcac agtgcttgga	120
aacctgctca ttatcctggc catcagttct gactcccacc tccacaagcc tatgtacttc	180
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aacaaccttt attctatcat cttatgcttc tggttatgca acagttgact ctcaatgctt	600
tatttatttt ttaaacatga tgattactat taacctcttt gtaagattta aaaatatctt	660
tatgcacagt agtatctcaa taaattacaa ctattatttt aaaaaataaa ataaagggtgg	720
tatctatgag atatat	736

<210> 992

<211> 915

<212> DNA

<213> Unknown (H38g842 nucleotide)

<220>

<223> Synthetic construct

<400> 992

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tttatgttgt tttttgtatt ctatggagga atcgtgtttg gaaaccttct tattgtcata	120
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gcatggggaa ttggctttct ccattcgggt agccagttgg cctttgccgt gcacttacc	480
ttctgtggtc ccaatgaggt cgatagtttt tatttgacc ttcctagggt aatcaaaactt	540
gcctgtacag atacctacag gctagatatt atggtcattg ctaacagtgg tgtgtctact	600
gtgtgttctt ttgttcttct aatcatctca tacactatca tcctaataac catccagcat	660
cgcccttttag ataagtcgtc caaagctctg tccactttga ctgctcacat tacagtagtt	720
cttttgttct ttggaccatg tgtctttatt tatgcctggc cattcccat caagtcatta	780
gataaattcc ttgctgtatt ttattctgtg atcacccctc tcttgaacct aattatatac	840
acactgagga acaaagacat gaagacggc ataagacggc tgagaaaatg ggatgcacat	900
tctagtgtaa agttt	915

<210> 993

<211> 927

<212> DNA

<213> Unknown (H38g843 nucleotide)

<220>

<223> Synthetic construct

<400> 993

atggctgcag	gaaatcactc	tacagtgaca	gagttcattc	tcaagggttt	aacgaagaga	60
gcagacctcc	agctccccct	ctttctcttc	ttcctcggga	tctacttggg	caccatcgtg	120
gggaacctgg	gcatgatcac	tctaatttgt	ctgaactctc	agctgcacac	ccccatgtac	180
tactttctca	gcaatctgtc	actcatggat	ctctgctact	cctccgtcat	tacccttaag	240
atgctgggtga	actttgtgtc	agagaaaaac	atcatctcct	acgcaggggtg	catgtcacag	300
ctctacttct	tccttggttt	tgtcattgct	gagtgttaca	tgctgacagt	gatggcctac	360
gaccgctatg	ttgccatctg	ccaccctttg	ctttacaaca	tcattatgtc	tcatacacacc	420
tgcttgcgtc	tggtggctgt	ggtctacgcc	atcggactca	ttggctccac	aatagaaact	480
ggcctcatgt	taaaactgcc	ctattgtgag	cacctcatca	gtcactactt	ctgtgacatc	540
ctccctctca	tgaagctgtc	ctgctctagc	acctatgatg	ttgagatgac	agtcttcttt	600
tcggctggat	tcaacatcat	agtcacgagc	ttaacagttc	ttgtttctta	caccttcatt	660
ctctccagca	tcctcggcat	cagcaccaca	gaggggagat	ccaaagcctt	cagcacctgc	720
agctcccacc	ttgcagccgt	gggaatgttc	tatggatcaa	ctgcattcat	gtacttaaaa	780
ccctccacaa	tcagttcctt	gacccaggag	aatgtggcct	ctgtgttcta	caccacggta	840
atccccatgt	tgaatcccct	aatctacagc	ctgaggaaca	aggaagtaaa	ggctgccgtg	900
cagaaaacgc	tgaggggtaa	actgttt				927

<210> 994

<211> 930

<212> DNA

<213> Unknown (H38g844 nucleotide)

<220>

<223> Synthetic construct

<400> 994

atggcagcca	aaaactcttc	tgtgacagag	tttatcctcg	aaggcttaac	ccaccagccg	60
ggactgcgga	tccccctctt	cttcctggtt	ctgggtttct	acacggtcac	cgtgggtggg	120
aacctgggct	tgataaccct	gattgggctg	aactctcacc	tgcaactcc	catgtacttc	180
ttccttttta	acctctcttt	aatagatttc	tgtttctcca	ctaccatcac	tcccaaaatg	240
ctgatcagtt	ttgtctcaag	gaagaacatc	atttccttca	cagggtgtat	gactcagctc	300
ttcttcttct	gcttctttgt	cgtctctgag	tccttcatcc	tgtcagcgat	ggcgtatgac	360
cgctacgtgg	ccatctgtaa	cccactgttg	tacacagtca	ccatgtcttg	ccagggtgtg	420
ttgctccttt	tggtgggtgc	ctatgggatg	gggtttgctg	gggccatggc	ccacacagga	480
agcataatga	acctgacctt	ctgtgctgac	aaccttgtca	atcatttcat	gtgtgacatc	540
cttcctctcc	ttgagctctc	ctgcaacagc	tcttacatga	atgagctggg	ggtctttatt	600
gtggtggctg	ttgacgttgg	aatgcccatt	gtcactgtct	ttatttctta	tgccctcatc	660
ctctccagca	ttctacacaa	cagttctaca	gaaggcagg	ccaaagcctt	tagtacttgc	720
agttccacaa	taattgtagt	ttctcttttc	tttgggtctg	gtgctttcat	gtatctcaaa	780
cccccttcca	tcctgcccct	cgagcaaggg	aaagtgtcct	ccctgttcta	taccataata	840
gtccccgtgt	taaacccatt	aatctatagc	ttgaggaaca	aggatgtcaa	agttgccctg	900
aggagaactt	tgggcagaaa	aatcttttct				930

<210> 995

<211> 473

<212> DNA

<213> Unknown (H38g845 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(473)

<223> n = A,T,C or G

<400> 995

atgggagaag	caaggaacag	gacagtagtc	caggaattta	tcctggaggg	atttctctgt	60
gtccagcatc	tggggaatgt	ccttttctctg	gtgcacctgc	tggcatacct	ggcctccatc	120
atggcaaaaca	tgctcataat	caccatcacc	tgggctgacc	atcacctcca	gacacctatg	180

tattttcttc	tcagcagttt	ttccttctgt	gaatgctgtt	ttatcaccac	agttattcct	240
aaacttcttg	tcattccttc	tttcaggcag	ggcaaataat	ccccctttct	actaccttgt	300
ctcatgcagt	ccccctttca	tttttatntt	cttgggtcaa	cagtttttct	tcccttaatg	360
gctgtgatgt	ccccttggat	tgatactgg	ccatttgcaa	gcctctgcat	tactccacca	420
tcatgagcct	gaggactagc	ttccacaagg	tcactgctg	gctttgtcct	ggg	473

<210> 996

<211> 998

<212> DNA

<213> Unknown (H38g846 nucleotide)

<220>

<223> Synthetic construct

<400> 996

acagaccac	agaatctaac	aacagatgct	tcaatatcc	tcgtcctaga	actctcagag	60
gatccagaac	tacagccggt	cctcgctggg	ctgttcctgt	ccatgtgcct	ggcatgggtg	120
ctggggaacc	tgctcatcat	cctggccgtc	agccctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgctt	gacatggttt	cacctccacc	atgggtcccca	240
agatgattgt	ggacatccaa	tctcacagca	gtcatctcct	atgcgggctg	cctgactcag	300
atgtctcttt	ttgccatttt	tggaggcatg	gaagaaagac	atgctcctga	gtgtgatggc	360
cctatgaccg	gtttgtagcc	atctgtcacc	ctctatatta	ttcagccatc	atgaacccat	420
gtttctgtgg	ctttctagtt	ctgttgtctt	gttgtctcag	tcttttagac	tcccagctgc	480
acaatttgat	tgccttgcaa	attacctgct	tcaaggatgt	ggaaattcct	aatttcttct	540
gtgacccttc	tcaactcccc	caccatgcgt	gttgtgacac	cttcaccaat	aacatagtca	600
tgtatttccc	tgctgccata	tttggttttc	ttcccacctc	ggggatcctt	ttctcttact	660
ataaaattgt	ttcctccatt	ctgagggttt	catcatcagg	tgggaactat	aaagccctct	720
ctgcctgtgg	gtctcacctg	tcagttgttt	gcttatttta	tggaaacaggc	gttggagggt	780
acctcagttc	agatgtgtca	tcttccccca	gaaagggtgc	agtggcctca	gtgatgtaca	840
cgggtgtcac	ccccatgctg	aaccccttca	tctacagcct	gagaaacagg	gatattaaaa	900
gtgtcctgcg	gcgcctgcac	ggcagaacag	tctaacttca	atatcttatt	atctgttcca	960
ttccttttgt	agtgtgggtt	taaaaaggca	gcaaggtc			998

<210> 997

<211> 666

<212> DNA

<213> Unknown (H38g847 nucleotide)

<220>

<223> Synthetic construct

<400> 997

agtcaactgt	cccttatgga	cctcatgctc	atctgcacca	ctctacccaa	gatgatcttc	60
agctacttgt	ctgggaagaa	atctatctct	ctggcaggtt	gtggaaactca	gatattcttc	120
tatgtgtccc	tgccttgagc	tgaatgtttc	ttgttggctg	tcattggctta	tgaccgctat	180
gtggctatat	gtcaccctct	tcagtacacc	atcctcatga	atccggaact	ctgtgtcttc	240
atgactgttg	cttcctggac	cttggggctc	cttgatggga	tcattagtgt	tgacagctgc	300
ctgtcatttt	cttactgcag	ctctctggaa	attcatcatt	ttttctgtga	tgttgctgcc	360
cttttacctc	tatcctgcac	agaaacatct	gcatttgaaa	gactacttgt	catttgttgt	420
gtggtaatgc	taatctttcc	agtttcagtt	atcatacttt	cctattccca	tgctcctcga	480
gccgtcatcc	acatgggctc	tggggaaagt	cgctgcaagg	ccttcactac	ctgctcctcc	540
cacccgtctg	tggtcggact	ctactacggt	gctgctatgt	tcattgtacat	gagaccagct	600
tctaaacata	cgccagacca	ggacaagatg	gtgtcggcct	tctacactaa	tctcaccctc	660
atgctg						666

<210> 998

<211> 342

<212> DNA

<213> Unknown (H38g848 nucleotide)

<220>

<223> Synthetic construct

<400> 998

cttgccctgca	tagttggata	gaagtttgca	tttattattt	ctccaaacca	tcacttcatg	60
ataatgggtca	cattcattttt	agttaacatt	taaaaacatt	cttcaggaaa	cttatccagt	120
gctcttatca	ttttgttcat	tttcatccct	gttggtttctc	tatttttcac	tccatgcgta	180
gttctctatg	tttggcctac	tttgccacca	tcacttgata	aaaatatgtt	cattgttgac	240
tttggttgca	accctgtctt	gaagcctgcc	acctacatat	tacagaacaa	agacataaag	300
gtagcacttt	gaaatttgca	tgaaaagaga	acttattcca	gc		342

<210> 999

<211> 915

<212> DNA

<213> Unknown (H38g849 nucleotide)

<220>

<223> Synthetic construct

<400> 999

atgggtgactg	aattcatttt	tctgggtctc	tctgattctc	agggactcca	gaccttccta	60
tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggtat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
ctcattgatc	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaag	tcattctctt	caagggctgc	cttggtcaga	tatttctcct	tcacttcttt	300
gggtgggagtg	agatgggtgat	cctcatagcc	atgggctttg	acagatatat	agcaatatgc	360
aaacccctac	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcggtg	agccagttgg	cctttgccgt	gcacttaccc	480
ttctgtggtc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggt	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atggtcattg	ctaacagtgg	tgtgctcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaattgac	catccagcat	660
cgcccttttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagtagtt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattcccat	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcaccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 1000

<211> 669

<212> DNA

<213> Unknown (H38g850 nucleotide)

<220>

<223> Synthetic construct

<400> 1000

tccaacctgt	ccttgctga	catcggtttc	ccctcccca	cggccccaa	gatggttggtg	60
gacatccaat	ctcacagcag	tcattctcct	atgcaggtcg	cctgactcag	atgtctctct	120
ttgccatttt	tggaggcatg	gaagagacac	atgctcctga	atgtgatggc	ctatgtccgg	180
tttgtagcca	tctgtcaccc	tctatatcat	tcagccatca	tgaaccctg	tttctgtggc	240
ttcttacttt	tgttgtcttt	tttttttctc	agtcttttag	acgcccagct	gcacaacttg	300
attgccttac	aaatgacctg	cttcaaggat	gtggaaattc	ctaatttctc	ctgtgacctt	360
tctccactcc	cccatcttgc	atgttggtgac	accttcacca	ataacataat	catgtatttc	420
cctgctgcc	tatttggttt	tcttccatc	tcggggaccc	ttttctctta	ctataaaatt	480
gtttctctca	ttctgagggt	ttcatcatca	ggtgggaagt	ataaggcctt	ctccacctgt	540
gggtctcacc	tgctcggtgt	ttgctgattt	tatggaacag	gcgttgagg	gtacctcggt	600
tcagatgtgt	catcttcccc	gagaaagagt	gcagtggcct	cagtgatgta	cacggtgggtc	660
accccatg						669

<210> 1001

<211> 986

<212> DNA

<213> Unknown (H38g851 nucleotide)

<220>

<223> Synthetic construct

<400> 1001

gattcagtg	accaagtaaa	tgactctctg	gtaacagaat	ttgtattact	tggaacttgca	60
caatccttgg	aaatgcagtt	tttccttttt	ctcttcttct	ctttattcta	tgtgggaatt	120
atcctgggaa	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactccccc	180
atgtatattc	tgctggccaa	cctatcgctc	attgacttga	gcctttcatc	taccacagtt	240
cctaggttga	tctacgatct	ttttactgat	tgtaaagtta	tttccttcca	taattgtatg	300
atacaaaaagt	tctttatcca	tgttacggga	ggagtggaaa	tggtgctgct	gatagtcag	360
gaatatgata	ggtacactgc	gatctgcaag	cctctccact	atccaactat	tatgaatccc	420
aaaatgtgca	tgtttttggg	agcagcagct	tggttcattg	gggtgattca	tgctatgtct	480
cagtttgttt	ttgtcataaa	ttaaccttct	gtggccctaa	taatgtgggg	agcttttatt	540
gtgattttcc	tgggtttatt	aaacttgcat	gcattggacac	ttacgggcta	gaatttgtgg	600
tcactgccaa	cagtggtatt	atatcgatgg	gcaccttctt	tttcttaatt	gtatcataca	660
tttttattct	ggtcactgtc	caacgcacatt	cctcaaatga	tttatccaaa	gcattcttca	720
cttcgtaggc	tcacatcacc	gtagtgggtt	tggtttttgc	tccatgcatg	tttctctacg	780
tgtggccctt	ccctactaag	tcattggata	aattttttgc	catcatgaac	tttgtgtgca	840
cccctgtctt	aaatcctgcc	atctatactt	taaggaacaa	agatatgaag	tttgcaatga	900
gaaggctgaa	tcaacatatt	ttaaattcta	tgagagcgac	ataacacatt	tggttgatga	960
gagcacagga	taaatgccat	ggacca				986

<210> 1002

<211> 659

<212> DNA

<213> Unknown (H38g852 nucleotide)

<220>

<223> Synthetic construct

<400> 1002

agtgtgctgt	ctattttctga	gacctattat	accgtggcca	tcaacccccca	aatgctgtcc	60
ggtctcctca	gtcctcaaca	aaccatctcc	atcccaggct	gtgccgctca	gctctttttc	120
tatctcactt	ttggtgtcaa	taaatgcttc	ctgctcacag	ccatggggta	tgaccactat	180
gtggccatct	gcaaccctct	acagtattca	gtcatcatgg	gcaaaaaggc	ttgtatacaa	240
ctggtcagtg	gacccctgaa	cattggcctg	agcacagcta	tcattcagg	gtcttctgta	300
ttcagccttc	ccttctgtga	tgctaatttc	atctccact	tcttttgtga	tatccggccc	360
ataatgaagc	ttgcctgtgc	agacactact	atcaaggagt	ttattacttt	gctcatcagt	420
ctctgtgtcc	ttgttctgcc	catggtattg	atcttcatct	cctatgtcct	aattgtcacc	480
accatcctca	agattgcac	agctgagggc	ggagaaaggc	ctttgtact	tgtgcctcac	540
acctcacagt	ggtcattgtc	cactatggcc	gtacttcttt	catctaccta	aaacccaaat	600
cccaaaattc	cctgcaggac	agacttatct	ctgtgacata	cactgttatt	actcctctg	659

<210> 1003

<211> 939

<212> DNA

<213> Unknown (H38g853 nucleotide)

<220>

<223> Synthetic construct

<400> 1003

atgtctacgt	ctaatacacac	ccagttccat	ccttcttcat	tcctactgct	gggtatccca	60
gggctagaag	atgtgcacat	ttggattgga	gtcccttttt	tctttgtgta	tcttgttgca	120
ctcctgggaa	acactgctct	cttgtttgtg	atccagactg	agcagagtct	ccatgagcct	180
atgtactact	tcctggccat	gttggtattc	attgacctgg	gcttgtctac	agccaccatc	240
cccaaaatgt	tggtcatctt	ctggttcaat	accaaagaaa	tatcttttgg	aggctgcctt	300
tctcacatgt	tttcttccat	gctatggaga	gcattgtgtt	gggtggcatg		360
gcctttgacc	gctacattgc	catttgcaaa	cctcttcggg	acaccatgat	cctcaccagc	420

aaaatcatca	gcctcattgc	aggcattgct	gtcctgagga	gcctgtacat	ggttgttcca	480
ctgggtgtttc	tccttctgag	gtcgcccttc	tgtgggcatc	gtatcatccc	tcatacttat	540
tgtgagcaca	tgggcattgc	ccgtctggcc	tgtgccagca	tcaaagtcaa	cattagggtt	600
ggccttggca	acatatctct	cttgttactg	gatgttatcc	ttattattct	ctcctatgct	660
aggatcctgt	atgctgtctt	ctgcctgccc	tcctgggaag	ctcgactcaa	agctctcaac	720
acctgtgggt	ctcatattgg	tgttatctta	gcctttttta	caccagcatt	tttttcatte	780
ttgacacatc	gttttggcca	taatatccca	cagtatatac	atattatatt	agccaacctg	840
tatgtgggtg	ccccaccagc	cctcaatcct	gtaatctatg	gagtcaggac	aaagcagatt	900
cgagagagag	tgctgaggat	ttttctcaag	accaatcac			939

<210> 1004

<211> 877

<212> DNA

<213> Unknown (H38g854 nucleotide)

<220>

<223> Synthetic construct

<400> 1004

tacatgataa	ccatcttatg	ggaaatatct	aagccagtaa	ataatatatt	tctaacactt	60
tctgtaagat	atcaaagtct	aatcactact	gtgtcataat	tgtaaatgaa	attataatat	120
aaattttactg	agtttttctg	agtaccta	gagttaaaaa	atatgggagc	atatgtagta	180
ctgtgcttgt	atcaatatgg	ataaggtatc	tggaagtctt	ttctgaacat	ctttcggtgc	240
tgctgagatt	attccactga	tggggatgg	ccatggctgc	tatgtgacca	tctgcactgc	300
atgaaaatca	tgactcaata	taggtgtggc	catcttgctg	gaatggcatg	cactggaaga	360
tttatccagg	cacagtttag	atcctctccc	cagctgact	tcctttctat	aattccaatg	420
tcacaatatg	aatagcccat	tcatatgtga	cttaaacact	ttgttgaagc	tcctctgcat	480
aggtagtatg	atacacttgg	tctctttgtt	gctgccaatg	atgggttcaa	ctgcctgtta	540
aacatcatct	tcttgatgg	ttcttaagtg	gccatcctat	atactttgaa	atcccacagc	600
ttggaggaaa	gatacaaagc	tctctctacc	tggtgtctct	acaccaccgt	ggccatctaa	660
ttctttgtgt	tctgtatact	tgtttatctg	tgcccagtg	cccttcccca	gtcagtaaag	720
cagtggctgt	gctttacacc	atgataacgc	ctacattaaa	cccttagtc	taaccctcag	780
aatgacagag	gtgaaaagtg	ttgagaaact	tctgggtcaa	aagatgactt	gaagagagaa	840
ataatccaaa	cataagatga	ttttactctt	tcaatgg			877

<210> 1005

<211> 927

<212> DNA

<213> Unknown (H38g855 nucleotide)

<220>

<223> Synthetic construct

<400> 1005

atggagaaga	aaaagaatgt	gactgaattc	atttttaata	gtcttacaca	gaaccccata	60
atggagaaaag	tcacgtttgt	agtatttttg	gttcttttaca	tgataaacact	ttcaggcaac	120
ctgctcattg	tgggttaccat	taccaccagc	caggctctga	gtcccccat	gtacttcttc	180
ctgacccacc	tttctttgat	agacacagtt	tattcttctt	cttcagctcc	taagttgatt	240
gtggattcct	ttcaagagaa	gaaaatcatc	tcctttaatg	ggtgtatggc	tcaagcctat	300
gcagaacaca	tttttggtgc	tactgagatc	atcctgctga	cagtgtatggc	ctgtgactgc	360
tatgtggcca	tctgcaaacc	tctgaactac	acaaccatta	tgagccacag	cctgtgcatt	420
ctcctgggtg	cagtggcctg	ggtgggagga	tttcttcatg	caactattca	gattctcttt	480
acagtattggc	tgcccttctg	tggccccaat	gtcataggcc	acttcatgtg	tgacttgtac	540
ccattgttaa	aacttgtttg	catagacact	catacccttg	gtctctttgt	tgctgtgaac	600
agtgggttta	tctgcttatt	aaacttcctt	atcttggtgg	tatcctatgt	gatcatcttg	660
agatcttttaa	agaacaatag	cttgaggggg	agggtgaaag	ccctctccac	ctgtatttct	720
cacatcatag	tagttgtctt	attctttgtg	ccctgtatat	ttgtgtatct	gcgtcagtg	780
accactctgc	ccattgataa	agctgttgct	gtattttata	ctatgggtgg	cccaatgtta	840
aatcccgtgg	tctacacact	cagaaatgct	gaggtaaaaa	gtgcaataag	gaagctttgg	900
agaaaaaaag	tgacttcaga	taatgat				927

<210> 1006
 <211> 738
 <212> DNA
 <213> Unknown (H38g856 nucleotide)

<220>
 <223> Synthetic construct

<400> 1006
 tgtattcaac aacattgac tccactttgt ctctgcatgt tctcctttta ttttaatttg 60
 taccattttt ttcccaaata aaagtacttg cactcactta gagatgctga aataaattga 120
 ttggtataaa gtaaggatc tgattaacca aatttacact aaagccaatt ggccttttca 180
 tggattataa cactatgcac aaccactcca tactcaaaca tgcatttctt tctccaatgt 240
 tatatgatgc agcacctagc tctttacagg acattttttt cttgggtgggt cacagatttt 300
 ccttctgttg gtgatggcct aggccactat agggccatct gcaagtcctt gcagtatttg 360
 gttgtcatga agcaatggct gtgtgttggt ctgctgggtg tgctctgggc tggaggattt 420
 ttgcacatag taattcaact tggacttatt tatgggctcc catcttatga cccaatgctc 480
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 gctcagactg gactgtttcc ttttgggtgat tgcacctcat tattcttttg tcattttttc 660
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 agagatacgg agcctacc 738

<210> 1007
 <211> 786
 <212> DNA
 <213> Unknown (H38g857 nucleotide)

<220>
 <223> Synthetic construct

<400> 1007
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 gacttggtct ttgggaataa ttccatatcc tcccatctt gcttggccca gctctttaca 180
 gagcaccttt ttggtgggtc agaggctctt cttctgttgg tgatggccta tgaccttgca 240
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 taccatgtt attggcctct tagtgggtgc caatggagga ctaggttgca ctatttgtgt 480
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 gttccctgta tttttatgta tgctagacct gctaggacct tccccattga caaatcagtg 660
 agtgtgtttt atacagtcac aactccaatg ctgaaccctt taatctacac tctgagaaat 720
 tctgagatga caagtgtat gaagaagctc tggagaagag acttcatatc aagtagtaca 780
 taagtg 786

<210> 1008
 <211> 930
 <212> DNA
 <213> Unknown (H38g858 nucleotide)

<220>
 <223> Synthetic construct

<400> 1008
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 ctgctcattg tgggtgactat tattgccagc ccttcttgg gctcctcaat gtacttcttc 180
 cttgcctgcc tgtcatttat agatgctgca tattccacta caatttctcc caaattgatt 240
 gtagacttac tctgtgataa aaagactatt tctttcccag cttgcatggg ccagttattt 300

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tgcggctgct	cgtggctgtc	gtcgactcg	aggtgttctg	cattcgctgt	ctcatattgt	480
gagtgtgtat	acagtctcgc	ctactgtggc	cccaatgtca	ttgactactt	tgtctgtgac	540
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tgtcaatggt	ggaacaatct	gtatagtcgt	cttcaccctt	ctactaatct	cctatggagt	660
catcctaaac	tcccttaaaa	cttacagtca	agaagggagg	cataaagtcc	tgtttacctg	720
cagctccac	attatcgtct	ttgccctctt	ttttgttccc	tgtattttca	tgtatgttag	780
acctgtttca	aacatccctt	tgataaatc	ctgacagtgt	tttatacagt	tatcacaccc	840
atgttgaatc	ctttaatata	cacattgaga	aattcagaga	tgagaaatc	tgtagaaaca	900
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<210> 1009

<211> 915

<212> DNA

<213> Unknown (H38g859 nucleotide)

<220>

<223> Synthetic construct

<400> 1009

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aatagcacc	tcacgtgtt	gatctgtaat	gactcccacc	tccacacacc	catgtatttt	180
gtcgttgaa	atctgtcgtt	tctggatctc	tggtattctt	ctgtctacac	cccaaagatc	240
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ttcttctctg	cagggctggc	ctatagttag	tgctgcttac	tggctgccat	ggcttatgac	360
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gcattgctgg	tagcagtctc	atattgtggt	ggctttatta	actcttcaat	catcaccaag	480
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atcacagtg	tcttgaggat	ctcctcctcc	aagggtacc	tcaaagcctt	ctccacatgc	720
tctcccacc	tgacctctgt	cactttatac	tatggctcca	ttctctacat	ctacgctctc	780
cccagatcta	gctattcttt	tgatatggac	aaaatagttt	ctacatttta	cactgtggta	840
ttcccctatg	tgaatctcat	gatctacagc	ctaaggaata	aggatgtgaa	agaggctctg	900
aaaaaacttc	tccca					915

<210> 1010

<211> 948

<212> DNA

<213> Unknown (H38g860 nucleotide)

<220>

<223> Synthetic construct

<400> 1010

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ggcaactttc	ttattgtcac	agttaccagt	gtggatctcg	cacttcaaac	acccatgtac	180
ttctttcttc	aaaatctgtc	acttcttgaa	gatgttttca	ccttggttat	ggtgccaaaa	240
atgctttag	atctagtgtc	cccaaggaaa	attatctctt	ttgtgggctg	tggtaaccag	300
atgtacttct	tcttcttctt	tggcagttct	gaatgtttcc	ttctctccat	gatggcttat	360
gatcgctttg	tggccatctg	taacctctc	cattattcag	tcataatgaa	caggtcccta	420
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gcctccacac	tectgtttat	catgtttccc	tttgtctca	tttgggttcc	ctacaccgcg	660
attatcataa	caattctgag	gatgtctct	gccactggcc	gccagaaggc	attttctact	720
tgttctctac	acctcattgt	ggtgtccctc	ttctacggaa	cagccagtct	gacctacctg	780
cggcccaaat	caaaccagtc	ccctgagagc	aagaagctag	tgctattgtc	ctacactgtc	840

atcacaccta tgctaaaccc catcatctac ggcctgagga acaatgaagt gaaaggggct 900
gtcaagagga caatcactca aaaagtctta cagaagttag atgtgttt 948

<210> 1011

<211> 927

<212> DNA

<213> Unknown (H38g861 nucleotide)

<220>

<223> Synthetic construct

<400> 1011

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gtgctcattg tggtcacat cactgccagc ccatcactga gatcccccatt gacttttttc 180
ctggcctatc tctcctttat tgatgcctgc tattectctg tcaatacccc taagctgac 240
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ggagaacatt ttttcagagg tgttgaggtc atcctactta ctgtaatggc ctatgaccac 360
tatgtggcca tctgcaagcc cttgactat accaccatca tgaagcagca tgtttgtagc 420
ctgctagtgg gagtgtcatg ggtaggaggc tttcttcacg caaccataca gatcctcttc 480
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actttgatca atcttgctg cactaatacc cacactctag gactcttcat tgctgccaac 600
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gctactttac ccattgataa agcagttgct gtattctaca ctatgataac ttctatgtta 840
aacccttaa tctacacctt gaggaatgct caaatgaaaa atgccattag gaaatttgtg 900
agtaggaaag ctatttcaag tgtcaaa 927

<210> 1012

<211> 488

<212> DNA

<213> Unknown (H38g862 nucleotide)

<220>

<223> Synthetic construct

<400> 1012

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ccatagccca agatactaag tattatagga ttgaaatgaa atataaatga aactttgtaa 120
atgttaaatt ataacacaaa tcatatggtc agtgtcgatg tcctaattgt tcctaactcc 180
tcatcacact ctctacttcc ttcatgtgg ctgccatcct gatatccgct ctgcagaggg 240
gaggcacaa gcttttccca cctgctcctt ccacctggtt taattctcct ccagcacaa 300
gaacaagcct cacctatttg tgccccagct ccactctctc ttatgagagg ggcaaggtag 360
tgtctacggt ttacacatgc atcactcctg tgccaaaccc cttgatctgc agcatgagga 420
agaaggaaat caagcatgct cttaaaaaaa aagaagaaat tgcaagggtc ttgctgctca 480
gaacacat 488

<210> 1013

<211> 953

<212> DNA

<213> Unknown (H38g863 nucleotide)

<220>

<223> Synthetic construct

<400> 1013

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gtggcttttt cttctataga agaattacag cttgtactct tcattgtgtt cttaatcatc 120
acttatgcac tataggagga aatatcatca tcatctccct gatctggatc acccctgccc 180
tgcacactcc aatgtatttc ttcctggtga acctctcatt tctggagatg tgctatacca 240

ccagtgtggt	gcctcatgct	ggtgcacctg	ctggtggaga	ccaaaaccat	aagtgtgggt	300
ggctgtgcaa	cccagatgta	catatttgcc	atcttgggac	tgacagaatg	ctgcttgcta	360
gcagctatgg	cttacgateg	ctttgtagct	atttgttacc	cactgcatta	cactctcttc	420
atggggccctc	gtgtttggtt	gaaattggct	gcagcatctt	ggttcactgg	agtgggtggtg	480
gagtcagccc	agatcacccct	gatcttcact	ttgcctttct	gtggaacagg	aaagattcaa	540
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gctcccacat	gcacatccct	gtgaccatct	tgagaatccc	ttcagcagct	ggaagacaca	720
aagctttctc	cacttgttct	tctcatatct	tggttgtttc	tctgttctat	ggcactgcct	780
tgttcactta	tctgcaacct	aagactgcac	acactccaga	aacagacaaa	gcaactgcac	840
tcattgtacac	aatgggtcac	cctgctttga	atcctgttat	ctataccttg	aggaacaagg	900
aagtaaagga	agcctttcaa	aggataaacc	aaaggaactc	tcttagacaa	acg	953

<210> 1014

<211> 873

<212> DNA

<213> Unknown (H38g864 nucleotide)

<220>

<223> Synthetic construct

<400> 1014

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ttcacctcgg	ccacagttcc	caagatgatt	gtggacatgc	agtcgcatag	cagagtcac	180
tcttatgcgg	gctgcctgac	acagatgtct	ttctttgtcc	tttttgcatt	tatagaagac	240
atgctcctga	ctctgatggc	ctatgaccga	tttgtggcca	tctgcccac	tgacaccccc	300
tgactacacg	agtcacatg	aatcctcacc	tctgtgtctt	cttagttttg	gtgtcctttt	360
tccttagcct	gttggattcc	cagctgcaca	gctggattgt	gttacacaa	tcaccttctt	420
caagaatgtg	gaaatctata	atcttttttc	tgtagcccat	ctcaacttct	caaccttgcc	480
tgttctgaca	gcacatcaa	taacatatta	tgtattttag	atatccctat	atttggtttt	540
cttcccattt	cagggatcct	tttgtcttac	tataaaattg	tctcctccat	tccaagaatt	600
ccatcgtcag	atgggaagta	taaagccttc	tccacctgtg	gctctcacct	ggcagttggt	660
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aggaatggag	tggtggcatc	agtgatgtac	gctgtgtgtc	tcccatgct	gaaccctttc	780
atctacagcc	tgagaaacag	ggacattcat	agtgcctgt	ggaggctgcg	cagcagaaca	840
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<210> 1015

<211> 981

<212> DNA

<213> Unknown (H38g865 nucleotide)

<220>

<223> Synthetic construct

<400> 1015

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tggtcctcag	ccctgactcc	caacctccca	cccacatgta	cttcttcttc	tccaacctgt	180
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cccccatctt	gcatgtttgt	acaccttcac	caataacatc	atcgtgtatt	tcctgtctgt	600
catatttggt	ttccttccca	tctcggggac	ccttttctct	ttaaaactgt	ttcctccatt	660
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aacccttca tctacagcct gagaaacagg gatatgaaaa gtgtcctgcg gcggccgcac 900
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aaaaaggca gcaaggtaaa a 981

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<210> 1016

<211> 762

<212> DNA

<213> Unknown (H38g866 nucleotide)

<220>

<223> Synthetic construct

<400> 1016

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gttcttttgg ggaacattag tgtgatgaca atcattgtaa ctgattccca gctgaacaca 180
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tacctgtata ttgtatctc agtcttgaag atccctcca gtgaaggagg aaagaaagac 720
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<210> 1017

<211> 1008

<212> DNA

<213> Unknown (H38g867 nucleotide)

<220>

<223> Synthetic construct

<400> 1017

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atcaaaaggg tcctgtgggt gttgcatggc agaacagttt aatctcatta ttttattatc 960
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<210> 1018

<211> 949

<212> DNA

<213> Unknown (H38g868 nucleotide)

<220>

<223> Synthetic construct

<400> 1018

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agcatcctgg	ctgtcagctc	tgactgcccc	ctccacaccc	ccatgtactt	cttcctctcc	180
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ctccttggtg	catgtataga	aggcatgtc	ctgactgtga	tggcctatga	ctgctttgta	360
gccatctgtc	gccctctgca	ctaccagtc	atcgtgaatc	ctcacctctg	tgtcttcttc	420
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<210> 1019

<211> 939

<212> DNA

<213> Unknown (H38g869 nucleotide)

<220>

<223> Synthetic construct

<400> 1019

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atccttctag	ggaatgttgg	gatgatgacc	attattatga	ctgatcctcg	gctgaacaca	180
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gaacccaagg	ctatgatcaa	cttctgggtc	gaaaacaagt	ctatctcctt	tgcaggctgt	300
gtggcccagc	tctttctctt	tgccctcctc	attgtgactg	agggatttct	cctggcggcc	360
atggcttatg	accgctttat	tgccatctgc	aaccctctgc	tctactctgt	tcaaagtctc	420
acacgtctgt	gtactcagtt	ggtggctggg	tcctattttt	gtggctgcat	tagctcagtt	480
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tacatgtata	ttgtgtccac	agttctaaag	atacattcta	ctgagggaca	taagaaggcc	720
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atgtatctca	ctcctgacag	atttctctgag	ctgagtaaag	tggcatcctt	atgttactcc	840
ctagtcactc	ccatgttgaa	tcctttgatt	tactctctga	ggaacaaaga	tgtccaagag	900
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<210> 1020

<211> 828

<212> DNA

<213> Unknown (H38g870 nucleotide)

<220>

<223> Synthetic construct

<400> 1020

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ctgccacacc	tccatgtacc	tttatatctt	tagcttttcc	ttcatagggtt	tcttctatcc	180
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tgtgacatca	aacactcagc	cttttcctct	ggcttctttg	tcattagtga	ttactccata	300
tttatcccac	tggccttgga	tcactatgag	gccatgaccc	tgccggctct	tttcataagt	360
ttcatttctg	tagatgggtc	ataagttata	gaatttgctg	atgctgtggg	ccatcaaggg	420


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acatggacca attcctgttt tgtgatcaca gttgcatgag ccttaacttg tgtaacatag      480
gcccgcctca ggctgcctga atcagtacct atgtcagaag caggtggatt tgattcatg      540
agaaccagca gtgtaccatg ctgtgttatc attttcatat ttgttttca ttcttttcaa      600
catttttcat taaccagtg gtccaaatct tcagccagat tccataaatc tgtttatttc      660
tttttttggg ttagggacat tcatgtacct cagatctcca gaagctatgg gttagtgtaa      720
attacagtgt ccttcaccaa gatggggcca gtgatgaacg gtctgttcaa caccttgagg      780
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<210> 1021

<211> 1001

<212> DNA

<213> Unknown (H38g871 nucleotide)

<220>

<223> Synthetic construct

<400> 1021

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ctggagaacc tgctcatcat cctggccgct agccctgact cccacctcca caccctcatgt      180
acttcttctc ctccaacctg tccttgccctg acatcggttt cacctccaca cgggtcccaa      240
gatgattgtg gacatccagt ctacacagcag agtcatctcc tatgcaggct gcctgactca      300
gatgtctctc tttgccattt ttggaggcag ggaagagaga catgctcctg agtgtgatgg      360
cctacgacca gtttgtagcc atctgtcacc ctccatctcg ttcagccatc ttgaaccctg      420
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gtgtctctcg gcggccgcac agcagcgcag tctaattctca atatcttctt atctgttcca      960
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<210> 1022

<211> 1025

<212> DNA

<213> Unknown (H38g872 nucleotide)

<220>

<223> Synthetic construct

<400> 1022

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gatacagacc cacagagtct aacagatgtc tctatatctc tcctcctcga actctcagag      60
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ctggggaacc tgctcatcat cctggccgct agccctgact cccacctccc caccctcatg      180
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aagatgagcg tggacatcca gtctcacagc agagtcatct cctatgcagg ctgcctgact      300
caaatgtctc tctttgccat ttttgagggc atggaaaaaa gacatgctcc tgagggtgatg      360
gcctatgacc tgttgttacc catctgtcac cttctatata gttcaaccat cttgaaccctg      420
tttgtccgtg gcttctctaaa tttgttgctt ttgttggttg tttttttttt ttttctctca      480
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gcctgagaaa cggggatatt aaaagtgtcc tacggcggcc gcatggcagc acagtctaatt      960
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tcaaa

1025

<210> 1023

<211> 1044

<212> DNA

<213> Unknown (H38g873 nucleotide)

<220>

<223> Synthetic construct

<400> 1023

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accattggag	gcaccctcag	catactggcg	gccataccta	tggaaaccaa	actccacagc	180
cccatgtact	tcttctggg	gaacttgtcc	ctgccagatg	tggggtgtgt	cagtgtcact	240
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ctctccgagc	tcttcttctt	ccacctctg	gctggggcag	actgcttctt	gctgaccatc	360
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aacactgtca	tcagcccat	gctgaacca	ctcatctact	ggacatctct	gctggacgtc	900
gggtgcatca	gtcactgttc	ctccgatgct	ggcgtgtctc	caggcccacc	agtgcagagt	960
tccctatgct	gctgcagtt	cacagctctt	ctttccccac	ctcctggctg	gggtggactg	1020
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<210> 1024

<211> 688

<212> DNA

<213> Unknown (H38g874 nucleotide)

<220>

<223> Synthetic construct

<400> 1024

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aaaaccgtag	tgggggccct	catcttgatc	actctagttt	tccttaattc	tcagcttcac	180
cctcccatgt	actacgtcat	cagaaattta	tcattttatg	atcactgcaa	ttgctctatt	240
agtaccctca	aaatactggt	gaagttttgt	ttagagaaga	ccatcatctc	ctatgaggac	300
ggcatgtcac	agctttgtag	tgcttcgtgt	ttatatgttc	atggccaagc	gtaacatgcy	360
gaccagcaac	tgctgtcatc	acatttcac	aagtcagctc	cctgctggta	gttgtagtat	420
ttatatggag	ttgactggta	caacaataga	tattttgcct	tgtattaaaa	tagtactagt	480
gtgagttatt	catcagtcac	acttctctca	tgcactagca	tctatgatat	tgataggaca	540
attttctttt	ttacttgatg	caatattgta	gtcactagat	taacagttgt	ttctactcc	600
ttttctctcc	agcatcctcc	acatcagctt	tacaaagggc	aagctctggg	tttttcccgt	660
aggtctgacg	cattcatgct	gttgccct				688

<210> 1025

<211> 993

<212> DNA

<213> Unknown (H38g875 nucleotide)

<220>

<223> Synthetic construct

<400> 1025

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atgggtgctga	ggaacctgct	caacatcctg	gctgtcagct	ctgactcccc	cctccacacc	180
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gttcccaata	tgattgtgga	catgcagtcg	catagcagag	tcattctctca	tcgggactgc	300
ctgacacaga	tttctcttct	gtctcttttt	gcattgtatag	aaggcatgct	cctgactgtg	360
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cctcacctct	gtgtcttctt	cgttttgggt	tcctttttcc	ttagcctgtt	ggattcccag	480
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ttcatgcatt	tccataatac	tatgtttggt	tttcttccca	tttcagggat	ccttgtgtct	660
tactataaaa	tcgtcccttc	cattcttagg	atttcatcgt	cagatgggaa	gtataaagcc	720
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caaagtgcc	tgtggaggct	gctcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
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<210> 1026

<211> 965

<212> DNA

<213> Unknown (H38g876 nucleotide)

<220>

<223> Synthetic construct

<400> 1026

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cgggtgctgag	gaacctgtct	agcatcctgg	ctgtccgctc	tgactcccc	ctccacaccc	180
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ttcccaaat	gattgtggac	atgcagtcg	atagcagagt	catctctcat	gcaggctgcc	300
tgacgcagat	gtctttcttg	gtcctttttg	catgtataga	aggcatgctc	ctgactgtga	360
tggcctatga	ctgctttgta	gccatctgtc	accctctgca	ctaccagtc	atcgtgaatc	420
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aaagtgcct	gtgggggctg	cacagcagaa	cagtcgaatc	tcattgatctg	ttccatcctt	960
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<210> 1027

<211> 945

<212> DNA

<213> Unknown (H38g877 nucleotide)

<220>

<223> Synthetic construct

<400> 1027

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acggtcaggg	gcaacctcag	catcctggca	gctgtcttgg	tggagcccaa	actccacacc	180
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cttaccacgc	tcttcttctt	ccatctgttc	gttggagtgg	actgcttctt	gctgaccgcc	360
atggcctatg	accaattcct	ggccatctgc	cggccctcca	cctacagcac	ccgcatgagt	420

cagacagtc	agaggatgtt	ggtggctg	tcctgggctt	gtgctttcac	caacgcactg	480
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aactatatgc	gactgggttc	aaccaagctt	tcagacaagg	ataaagctgt	tggaattttc	840
aacactgtca	tcaatcccat	gctgaaccca	atcatctaca	gcttcagaaa	ccctgatgtg	900
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<210> 1028

<211> 969

<212> DNA

<213> Unknown (H38g878 nucleotide)

<220>

<223> Synthetic construct

<400> 1028

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tttctctttg	tttatcttat	caccctggga	ggtaacttgg	ggatgatcac	tctcatatgg	180
attgatccca	gactccacac	tcctatgtac	ttttttctta	ggcacttgct	ctttgtagat	240
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gacatcactt	ttctgggttg	tgctgcacag	atgtggttct	ttggtctctt	tgaggcagct	360
gagtgttttc	tcctggctgc	catggcatat	gaccggtagt	tggccatctg	caagcccttg	420
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tcaaatatta	tcaatcactt	tttctgtgat	atttttccac	tgctttccct	agcatgtgca	600
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agcttgagga	ataaggaggt	gaaagatgca	ttcagaagaa	aaattgagag	gaaaaaattt	960
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<210> 1029

<211> 687

<212> DNA

<213> Unknown (H38g879 nucleotide)

<220>

<223> Synthetic construct

<400> 1029

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atccaagaga	aaaaccattt	tcttcattgg	ttgtgttaagt	gttttataat	tctacttttt	360
cattgtctcg	ataatcagag	attatcatat	gcttacagtg	atggctaagt	actgctacat	420
ggccatttgc	aagcccttgt	tatatggtag	taaaatgtcc	agatttgtct	gcctctctct	480
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gttagtcctc	ccttgccgag	gtacctgtgt	caaataaatc	atcatgttga	tgagaccaca	660
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<210> 1030

<211> 859

<212> DNA

<213> Unknown (H38g880 nucleotide)

<220>

<223> Synthetic construct

<400> 1030

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aagtacaaag	ccttctcagc	ctgtggctgt	cacctggcag	ttgtttgctt	attttatgga	660
acaggcattg	gctgtgtacc	tgacttcagc	tgtggcacca	cccctcagga	atgggtatgg	720
ggcgtcagtg	atgtacgctg	tggtcacccc	catgctgaac	cctttcatct	acagcctgag	780
aaacagggac	attcaaagtg	ccctgtggag	ggtgtgcaac	aaaacagtcg	aatctcatga	840
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<210> 1031

<211> 975

<212> DNA

<213> Unknown (H38g881 nucleotide)

<220>

<223> Synthetic construct

<400> 1031

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actggaaact	tgggaatgat	tgctcctc	cgaattgatt	cccgccttca	cacacccatg	180
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gatattgtcc	ccttactttc	ccttgatagt	gctgatacca	ggctcaataa	gttggcagtt	600
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gcagtgatcc	ctatgttgaa	cccacttatc	tacagcttga	gaaacaagga	agtcaaagat	900
gccatccaca	ggactgtcac	tcagaggaag	ttttgcaagg	cctaaattct	tatccagaag	960
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<210> 1032

<211> 941

<212> DNA

<213> Unknown (H38g882 nucleotide)

<220>

<223> Synthetic construct

<400> 1032

atggagactg	aaaacaatac	aacagtgaca	gagttcatta	ttttgggatt	aacagacaat	60
cctatgctat	gtgccatttt	cttcgtgttt	tttctagcag	tttatatagt	tactataccg	120

ggaaatatta	gcataatcct	cttaatccaa	agcagcccac	agcttcacac	gctaattgtac	180
ctttttctca	gccatttggc	ttctgtggac	attgggtatt	ccatatcagt	tacgccaatc	240
attctcatca	atttcttaag	agagaaaacg	actattcctg	tcacaggctg	tatagcacag	300
cttggctctg	atgtcatggt	tggaaccaca	gagtgtctcc	tgtgtgtcac	tatgtggcta	360
tctgtctctc	cctgctttac	tccatccaaa	tgccccagc	cgtctgtctc	ctcctactgg	420
gagcctccta	cctgggtgga	tgccctgaacg	cttctgtctt	tacaggctgt	ttgatgaacc	480
tgctcttctg	cggtcctaat	aaaatcaacc	actttttctg	tgacctcttc	ccactcttga	540
agctttcttg	tggccatggt	tacattgctg	aaatatcccc	tgccatctcc	tctgcatctg	600
tccttatcag	cacgctgttt	accataatcg	tgtctacat	ctacatcctt	cactccatcc	660
tgaagggtgtg	ctctactgag	ggaaggaaga	aggctttctc	cacctgcgct	tcccacctca	720
ctgcagtcac	tttgttctat	gggaccattt	tgtttgttta	tgtgatgccc	aagtcaagct	780
attcagcgga	tcagggtcaag	gtggcatttg	tgatctacac	ggtggtgatt	cccattgctga	840
acccctcat	ctacagtctc	aggaataagg	agggtgaaaga	ggccatgaga	aaattgatgg	900
caagaacaca	ttggttttcc	tgaattaaat	cagtataatc	c		941

<210> 1033

<211> 606

<212> DNA

<213> Unknown (H38g883 nucleotide)

<220>

<223> Synthetic construct

<400> 1033

atctttgcca	tcttgaccac	cattgactgc	tgtgtatttg	tctgggaatt	cctggagtgc	60
acagtctttg	tgaataagag	ggcatgtgac	cagctggcgt	gtggtgcctt	ttgcattggc	120
ctgatcatga	cagtgggtcta	aataaccaca	gtgtcacaga	ggtacaaaag	gagcacatat	180
gctattttaga	ctgcttcttg	tttgacaccc	ttcttgtcat	gaaactctcc	tgcattgaca	240
atactatcta	tgaataaac	agtattttat	tcaccacaca	tgtgtgcagg	tgtccatggg	300
tttggtttgc	atttcttata	ttgacatccc	tggtacctcc	atcgtgctta	gaatttccta	360
atctgaggtc	tttgccacct	gtgtccccca	acccccacct	catcatggtc	attgtctata	420
tgtctgtgct	tgtactgctt	acctcaagca	caagccaatg	aattcaatag	aaaacaggtc	480
ttctataaga	gacctacatt	atcatcattc	attctgcctc	tggacactgt	tgtttacact	540
ctgaggtaca	tggaggccaa	ggataccatg	tacagagctg	tggacagaaa	tatttcttaa	600
cagatt						606

<210> 1034

<211> 945

<212> DNA

<213> Unknown (H38g884 nucleotide)

<220>

<223> Synthetic construct

<400> 1034

atggagccag	aagctgggac	caataggacc	gctgttgctg	agttcattct	actgggccta	60
gtgcaaacag	aagagatgca	gccagttgtc	tttgtgtctc	tcctctttgc	ctatctggtc	120
acaactgggg	gcaacctcag	catectggca	gccgtcttgg	tggagcccaa	actccacgcc	180
cccattgtact	tcttctctgg	gaacctgtca	gtgctggatg	tcggatgtat	cactgtcact	240
gttctctgaa	tgttgggtcg	tctcttgtcc	cacaagtcca	caatttccta	tgacgcctgc	300
ctctcccagc	tcttcttctt	ccaccttctg	gctgggatgg	actgcttcct	gctgaccgcc	360
atggcctatg	accgactcct	ggccatctgc	cagccccctc	cctacagcac	ccgcatgagt	420
cagacagtcc	agaggatggt	ggtggctgcg	tccttggctt	gtgccttcac	caacgcactg	480
accacactcg	tggccatgtc	cacgtcaaac	ttctgtggcc	ccaatgaggt	caatcacttc	540
tactgtgacc	tcccacagct	cttccagctc	tcctgtctca	gcacccaact	caatgagctg	600
ctgctctttg	ctgtgggttt	catcatggca	ggcacacctt	tggttctcat	catcactgcc	660
tacagccacg	tggcagctgc	agttctacga	atccgttcag	tggagggccg	aaagaaggcc	720
ttctccacgt	gtggctccca	cctcacctg	gtttgtcttt	tctttggaag	aggatcttcc	780
aactacatga	gactgggttc	agaggaggct	tcagacaagg	ataaaggggt	tggagttttc	840
aacactgtta	tcaaccctat	gctgaaccct	cttatctaca	gcctcagaaa	ccctgatggt	900
cagggtgctc	tgtggcaaat	atttttgggg	aggagatcac	tgacc		945

<210> 1035
 <211> 927
 <212> DNA
 <213> Unknown (H38g885 nucleotide)

<220>
 <223> Synthetic construct

<400> 1035
 atgaagagaa agaacttcac agaagtgtca gaattcattt tcttgggatt ttctagcttt 60
 ggaaagcatc agataaccct ctttgtggtt ttcctaactg tctacatttt aactctggtt 120
 gctaaccatca tcattgtgac tatcatctgc attgaccatc atctccacac tcccatgtat 180
 ttcttctctaa gcatgctggc tagttcagag acggtgtaca cactgggtcat tgtgccacga 240
 atgcttttga gcctcatttt tcataaccaa cctatctcct tggcaggctg tgctacacaa 300
 atgttctttt ttgttatctt ggccactaat aattgcttcc tgcttactgc aatgggggtat 360
 gaccgctatg tggccatctg cagacccctg agatacactg tcatcatgag caaggggacta 420
 tgtgcccagc tgggtgtgtg gtcctttggc attggtctga ctatggcagt tctccatgtg 480
 acagccatgt tcaatttgcc gttctgtggc acagtggtag accacttctt ttgtgacatt 540
 taccagtgca tgaactttc ttgcattgat accactatca atgagataat aaattatggt 600
 gtaagttcat ttgtgatttt tgtgcccata ggctgatata ttatctccta tgtccttgtc 660
 atctcttcca tccttcaaat tgcctcagct gagggccgga agaagacctt tgccacctgt 720
 gtctcccacc tcaactgtgt tattgtccac tgtggctgtg cctccattgc ctacctcaag 780
 ccgaagtcag aaagttcaat agaaaaagac cttgttctct cagtgcacgt caccatcatc 840
 actcccttgc tgaaccctgt tgtttacagt ctgagaaaca aggaggtaaa ggatgcccta 900
 tgcagagttg tgggcagaaa tatttct 927

<210> 1036
 <211> 958
 <212> DNA
 <213> Unknown (H38g886 nucleotide)

<220>
 <223> Synthetic construct

<400> 1036
 atgttgacaga gagttgggga aatggatgga ggcaaccaga gtgaaggttc agagttcctt 60
 ctcttgggga tctcagagag tcttgagcag cagcagatgc tgttttggat gttcctggtc 120
 aggtacctgg tcacgggtgct gggaaatgtg ctcacatcc tggccatcag ctctgattcc 180
 cgctgcaca ccccatgta cttcttctg gccaacctct ccttactga cctcttctt 240
 gtcaccaaca caatcccaa gatgctggtg aacctccagt cccagaacaa agccatctcc 300
 tacacagggt gtctgacaca gctctacttc ctggtctcct tgggtggcct ggacaacctc 360
 aacctggccg tgatggcgta tgatcgctat gtggccatct gccgtcccct ccactatgtc 420
 acagccatga tccctgggct ctgtatcttg ctctctctct tgtgttgggt gttctctgcc 480
 tctatggcc tcatccatat cctcctcatg accagtgac cttctgtggg tctcaaaaga 540
 tccactacct cttctgtgag atgtacttcc tgctaaggct ggcatgttcc aacatccacg 600
 tcaaccacac agtactggtt gccacgggct gcttcatctt cctcatcccc ttaggtttca 660
 tgatcacatc ctacgcccgc attgtcagag ccatectcca aataccctca gccactggga 720
 agtacaaaag cttctccacc tgtgcttccc atttggctgt ggtctccctc ttctatggga 780
 ctctgggtat ggtgtacctg cagccctcc aaacctactc catgaaggac tcagtagcca 840
 cagtgatgta tgcgggtggtg acgcatgat taacctttc atctacagcc tgaggaaaca 900
 ggacatgcat ggggctctgg gaagacttcg ccaaggaaaa gccttcaga agttgaca 958

<210> 1037
 <211> 828
 <212> DNA
 <213> Unknown (H38g887 nucleotide)

<220>
 <223> Synthetic construct

<400> 1037
 atgcgaagaa agaacctcac agaggtaaca gagtttgttt tcttgggatt ctccagattc 60
 cacaaacatc acatcactct ctttgtgggt tttctcatcc tgtacacatt aactgtgggt 120
 ggcaatgcc aatcatgac catcatctgc attgaccgtc acctccacac tcccatgtac 180
 ttcttctga gcatgctggc tagctcaaag acagtgtaca cactgttcat cattccacag 240
 atgctctcca gcttcgtaac ccagaccag ccaatctccc tagccggttg taccacccaa 300
 acgttcttct ttgttacctt ggccatcaac aattgcttct tgctcacagt gatgggctat 360
 gaccactata tggccatctg caatcccttg agatacaggg tcattacgag caagaagggtg 420
 tgtgtccagc tgggtgtgtg agccttttagc attggcctgg ccatggcagc tgtccaggta 480
 acatccatct ttaccttacc tttttgtcac acgggtggtg gtcatttctt ctgtgacatc 540
 ctccctgtca tgaaactctc ctgtattaat accactatca atgagataat caattttgtt 600
 gtcaggttat ttgtcactct ggtccccatg ggtctggtct tcatctccta tgtctctc 660
 atctccactg tectcaagat tgcctcagct gaggggtgga agaagacctt tgccacctgt 720
 gccttccacc tcaactgtgt cattgtccat tatggctgtg cttccattgc ctacctcatg 780
 cccaagtcag aaaactctat agaacaagac ctcttctctc cagtgcac 828

<210> 1038

<211> 936

<212> DNA

<213> Unknown (H38g888 nucleotide)

<220>

<223> Synthetic construct

<400> 1038
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 cctgagcagc agcagatcct gttttggatg ttctgttcca tgtacctggg caggtgtgctg 120
 ggaaatgtgc tcatcatcct ggccatcagc tctgattccc acctgcacac ccccatgtac 180
 ttcttctctg ccaacctctc ctccactgac ctcttctttg tcaccaaacac aatccccaag 240
 atgctggtga acttccagtc ccagaacaaa gccatctcct atgcagggtg tctgacacag 300
 ctctacttcc tgggtctcctt ggtgacctg gacaacctca tcttggccgt gatggcgtat 360
 gatgctatg tggccatctg ctgccccctc cactatgtca cagccatgag ccttgggctc 420
 tgtgtcttgc tctctcctt gtgttggggg ctgtctgttc tctatggcct cctcctcacc 480
 ttcttctga ccagggtgac ctctgtggg cctcgagaga tccactacct ctctgtgac 540
 atgtacatcc tgggtgtggt ggcattgtcc aacaccacac tcattcacac agcattgatt 600
 gccactggct gcttcatctt cctcaccctc ttaggggtca tgaccacatc ctatgtacgt 660
 attgtcagaa ccatccttca aatgccctcg gcctctaaga aatacaaaac tttctctacc 720
 tgtgctcgc atttgggtgt ggtctcctc ttttatggga cgcttgctat ggtgtacctg 780
 cagccctcct atacctact catgaaggac tcagtagcca cagtgtgta tggctgtctg 840
 acacctatga tgaaccctt catctacagc ctgaggaaca aagacatgca tggggctccg 900
 ggaagagtcc tatggagacc ctttcagagg cctaaa 936

<210> 1039

<211> 898

<212> DNA

<213> Unknown (H38g889 nucleotide)

<220>

<223> Synthetic construct

<400> 1039
 atggctgatg gaaatataaa aggatcacag aattcatttt tgtaggctta aggtatcatc 60
 ttcagctgca agtcttcctt ttcttaccat ttctaccttt tttacctcat tactatgaca 120
 gaaaacttgg gcatgatggg tgcacatctg ctctgattct gctttcacac acctatgtac 180
 tttgtcctca gctacctgtc ctttgtggac atctgcttct catccgttgt gggccacaag 240
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 gacaattatg tggccatctg taaccatttg ttgtactcag tggccatgta atagagactg 420
 tgcattcagc tgggtgttgt acgttatgca gctgatttct tcaacacctt aactcacaca 480
 acggctgctt ttcatcttcc cttttttcac tccaacatta tcaatcattt ctctgtgac 540
 atgtctctcc ttctttctct cgtgtgtgct gacgcccggg tcaataaatt gttagttttc 600

attgtggctg	gagctgtact	agttgtcagt	agcctgacca	ttataatctc	ctatTTTTac	660
atccttactg	acattctgag	gatctgctct	gctaattggg	aagaacaaaa	ctTTTTccac	720
ctgctcttca	cacttaacag	ctgtttccat	cttttatggg	tctctcttct	ttagctacgt	780
ttcgaccagg	tgcaactttt	taccgggaac	tcaataaaat	agtgttgggtg	ttctgtacat	840
ccccatgttg	aaacctctca	tctacagctt	gataaataaa	gaagtatcct	agccacta	898

<210> 1040

<211> 934

<212> DNA

<213> Unknown (H38g890 nucleotide)

<220>

<223> Synthetic construct

<400> 1040

atggaaaaaa	taaacaacgt	aactgaattc	atTTTctggg	gtctttctca	gagcccagag	60
attgagaaaag	tttgTTTTgt	gggtTTTTct	ttcttctaca	taatcattct	tctgggaaat	120
ctcctcatca	tgctgacagt	ttgcctgagc	aacctgttta	agtcacccat	gtatttcttt	180
ctcagcttct	tgtcttttgt	ggacatttgt	tactcttcag	tcacagctcc	caagatgatt	240
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aaaatgttat	tagggacgtg	ggtaggtggg	ttcttacct	ccattatcca	agtggctctg	480
gtagtccaac	tacccttttg	tggacccaat	gagatagatc	actacttttg	tgatgttcac	540
cctgtgttga	aacttgcttg	cacagaaaca	tacattgttg	gtgtgtgtgt	gacagccaac	600
agtggtagca	ttgctctggg	gagttttgtt	atcttgctaa	tctcctacag	catcatccta	660
gtttccctga	gaaagcagtc	agcagaaggc	aggcgcaaa	ccctctccac	ctgtggctcc	720
cacattgcca	tggtcgttat	ctttttcgag	ccctgtact	tttatgtaca	tgcgccctga	780
tacgaccttt	tcagaggata	agatgggtggc	tgtattttac	accattatca	ctcccatgtt	840
aaatcctctg	atttatacac	tgagaaatgc	agaagtaaag	aatgcaatga	agaaactgtg	900
gggcagaaat	gttttcttgg	aggctaaagg	gaaa			934

<210> 1041

<211> 951

<212> DNA

<213> Unknown (H38g891 nucleotide)

<220>

<223> Synthetic construct

<400> 1041

atggactata	gaaatcaaac	tttggttact	gaattttttt	ccgtgggatt	aacaaatctc	60
tttcagcaca	agattgctct	ctttctggta	tttctctttg	tttatcttgt	cactgttccg	120
ggaaacttgg	gaatgatcac	tcttatTTtg	atggattctc	gactccagac	ccccaagtac	180
ttttctctct	gccacttgtc	ctttgtggat	gtctgtctct	cttctgccat	cggTcccaag	240
atgttgactg	atatcttctg	ggagaaaaaa	gtaatctctt	tggttgtgtt	gccagttat	300
ggtttttttg	ccatttttga	gtaactgaat	gtttcttct	ggctgccatg	gcataTgacc	360
ggtataggct	atctataagc	ctttgttTga	tacactcatt	atgtcccaac	aggTctgtgt	420
gcagctgggtg	gtgggcctta	tgctgtgggc	cttataagca	ccatgaccca	tatgactttc	480
acctttcgcc	tactctactg	tggTccaaac	atcatcaatc	acttcttctg	tgaccttctc	540
cctgtcctct	ccctggcata	tgagataacc	catattaata	aatgtttact	ttttatcttg	600
gtgggtgccc	tgggagtact	cagtgggtgtg	atcatcttgg	tctcctacat	ttacattgtc	660
attgccatcc	tgagaattcg	ctctgtctgac	gcgagacgca	aagacttctc	cacttgctct	720
tcacacctga	tggctgtctc	catcctgtat	gggacactct	tctttatctg	tgtatgtcca	780
agctctagtt	tctctatcaa	catcaataaa	gtggtttccc	tgttctacac	agcagtgate	840
cccatgttga	atcccccttat	ctacagcctg	agaaacaagg	aggtaaaaga	ttcattcagc	900
aagaagtttg	aaagaaagaa	gtttcttata	ggtaggtgaa	ctagaatacc	a	951

<210> 1042

<211> 930

<212> DNA

<213> Unknown (H38g892 nucleotide)

<220>

<223> Synthetic construct

<400> 1042

atggtgaatt ttacacatgt ctcagaatth gttctacttg ggtccaagg ggggtcccggg	60
atgcaggcta tgctatttct gatttttctg atcctgtatg gcatagctgt ggtgggaaac	120
cttggcatga ttgtaattat ctgggtagat gcacacctcc acacccaat gtatgccttc	180
ctgcaaagcc ttctattgtt ggacatctgc tttctctcca caattgcacc cagggctctg	240
gcgaactcca tgcaagagga ccacacaatt tcctttggcg gatgtgctgc tcagttcttt	300
ttctttgtctc tctttgttat cacagaggct ttcctcctgg ctgccatggc ctatgaccgc	360
ttcatcgcca tctgcaaccc tcttctgtac tctgtgagca tgtctcacca ggtctgtgtg	420
ctgttaatat caggatccta cttgtgggtg gtagtcaatg ccattgctca aacaaccatg	480
accttcaggt tgcctttctg tgggtccaat gagatcaacg actttttctg tgatgttccc	540
ccactcttgt ccctctcatg ttcagatacc tttataaacc aactggttct tcttggttta	600
tgtggctcca ttattgtcag tacctttttg attgtcctgg tctcatatc ttacatcatc	660
tcaacaattc tgaggatccc gaccatgcag ggacgctaga aagccttctc cacgtgcgct	720
tccacaccaa caggagtgtg cttgtttttt ggtactgttt tcttcatgta tgcacaaccc	780
agtgccatct tcttcatgga gcaaagtata atagtgtcca tattctacac tatggtcac	840
cccatgtga atccctgat atacagcctg aggaacaaag aggtcaagca ggctctgaga	900
cggagcatgc agaagctgtc tttgtgatca	930

<210> 1043

<211> 927

<212> DNA

<213> Unknown (H38g893 nucleotide)

<220>

<223> Synthetic construct

<400> 1043

atgagggaaa ataaccagtc ctctacactg gaattcatcc tcctgggagt tactgggtcag	60
caggaaacagg aagattttct ctacatcctc ttcctgttca tttaccccat cacattgatt	120
ggaaacctgc tcattgtcct agccatttgc tctgatgttc gccttcacaa ccccatgtat	180
tttctccttg ccaacctctc cttggttgac atcttcttct catcggtaac catccctaag	240
atgctggcca accatctctt gggcagcaaa tccatctctt ttgggggatg cctaacgcag	300
atgtatttca tgatagcctt gggtaacaca gacagctata ttttggctgc aatggcatat	360
gatcgagctg tggccatcag ccaccactt cactacacaa caattatgag tccacggctc	420
tgtatctggc ttattgtctg gtcttgggtg attggaaatg ccaatgccct cccccact	480
ctgctcacag ctagtctgtc cttctgtggc aaccaggaag tggccaactt ctactgtgac	540
attacccctt tgctgaagtt atcctgttct gacatccact ttcatgtgaa gatgatgtac	600
ctagggggtg gcattttctc tgtgccatta ctatgcata ttgtctccta tattcgagtc	660
ttctccacag tcttccaggt tccttccacc aagggcgtgc tcaaggcctt ctccacctgt	720
ggttcccacc tcacggttgt ctctttgtat tatggtacag tcatgggcac gtatttccgc	780
cctttgacca attatagcct aaaagacgca gtgatcactg taatgtacac ggcagtgacc	840
ccaatgttaa atcctttcat ctacagtctg agaaatcggg acatgaaggc tgccctgcgg	900
aaactcttca acaagagaat ctcctcg	927

<210> 1044

<211> 927

<212> DNA

<213> Unknown (H38g894 nucleotide)

<220>

<223> Synthetic construct

<400> 1044

atgaagaaag aaaatcaatc ctttaacctg gattttattc tcctgggagt tactagtcag	60
caagaacaga ataattgtct ctttgtgatt tttttgtgca tttaccccat cacactgact	120
ggaaatctgc tcatcatctt ggccatctgt gctgacattc gccttcacaa ccccatgtat	180

tttctccttg	ccaacctctc	cttggttgac	atcatcttct	catccgtaac	catccctaag	240
gtgctggcca	accatctctt	gggcagcaag	ttcatctcct	ttgggggatg	cctaatagcag	300
atgtatttca	tgatagcctt	ggccaaggca	gacagctata	ccttggtgctgc	aatggcatac	360
gacgagctg	tggccatcag	ctgcccactt	cattacacaa	caattatgag	tccacgggtct	420
tgtatcctgc	ttattgctgg	gtcttgggtg	attggaaaca	ccagtgtctct	ccccacact	480
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attatgcctt	tgctgaagtt	gtcctgttct	gacgtccact	ttaatgtgaa	gatgatgtac	600
ctaggggtcg	gcgttttctc	tttgccatta	ctatgcatca	ttgtctccta	tggtcagggtc	660
ttttccacag	tcttccaagt	tccatctacc	aagagtctat	tcaaagcctt	ctgcacctgt	720
ggctcccacc	tcacagttgt	ttttttatat	tatggtacaa	cgatgggcat	gtatttccgc	780
cctctgacca	gttacagccc	caaagatgca	gtgataactg	tgatgtatgt	ggcagtgacc	840
ccagcattaa	atcctttcat	ctatagtctg	agaaattggg	atatgaaggc	agccctacag	900
aaactcttca	gcaagagaat	ctcctca				927

<210> 1045

<211> 990

<212> DNA

<213> Unknown (H38g895 nucleotide)

<220>

<223> Synthetic construct

<400> 1045

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tctatagtga	cagagttcag	tctcagggga	ttaacgaagc	agccagatct	ccagctcttt	120
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cccctaattg	acagcctgaa	aaacaaggat	gtaaaagctg	ccatgcagaa	aacactaagg	960
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<210> 1046

<211> 948

<212> DNA

<213> Unknown (H38g896 nucleotide)

<220>

<223> Synthetic construct

<400> 1046

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acagtgggtga	ctccccctgct	gaacccccctt	atttacagca	tgcggaacaa	ggacatgaag	900
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<210> 1047

<211> 1007

<212> DNA

<213> Unknown (H38g897 nucleotide)

<220>

<223> Synthetic construct

<400> 1047

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tacttggttcc	tctccaacct	gtcccttgcc	tgacatcggg	ttcacctcca	ccacgggtccc	240
caagatgatt	gtggacatcc	agtctcacag	cagagtcac	tcctatgcag	gctgcctgac	300
tcagatgtct	ctctttgcc	tttttgagg	tatggaagag	agacatgtc	ctgagtgtga	360
tgccctatga	ccggtttgta	gccatctgtc	accctctata	ttgttcagcc	atctttaacc	420
cgtgtttctg	tggcttccta	gatttggtgt	cttttttttt	ttttttctca	gtctttcaga	480
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taattttctt	tgggaacctt	ctcaactctc	ccatcttgca	tggttgtaga	ccttcaccag	600
gaacatcagt	atttccctgc	tgccatattt	ggttttcttc	ccatcttggg	gaccttttc	660
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tgaaaagtgt	cctgcggcgg	ccgcatggca	gcacagtcta	atctcaacat	cttcttatct	960
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<210> 1048

<211> 926

<212> DNA

<213> Unknown (H38g898 nucleotide)

<220>

<223> Synthetic construct

<400> 1048

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gtgcaaaaag	cattatttgt	catattttta	ctcacatact	tggtgacagt	gggtgggaac	120
ctgtctcattg	tggtgactat	tattaccagc	ccttcttggg	gctcccaat	gtacttcttc	180
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gtagacttac	tctgtgataa	aaagactatt	tctttccag	cttgcatggg	ccagttattt	300
atataccact	tggttggtgg	ttctgaggtc	ttccttcttg	tggtgatggc	ctgtgatcac	360
tatgtggcca	tctgtaagcc	actgcactat	ttgaccatca	tgaatcgaca	ggtttgaatc	420
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gtatacagtc	tcgctttctg	tgcccccaat	gtcattgact	actttgtctg	tgacatgtac	540
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gggtggaacaa	tctgtatagt	cgtcttcacc	cttctactaa	tctcctatgg	agtcaccta	660
aactccctta	aaacttacag	tcaagaaggg	aggcataaag	tctgttttac	ctgcagctcc	720
cacattatcg	tctttgccct	cttttttgtt	ccctgtatct	tcatgtatgt	tagacctgtt	780
tcaaacatcc	ttttgataaa	ttcctgacag	tgttttatac	agttatcaca	cccatgttga	840
atcctttaat	atacacattg	agaaattcag	agatgagaaa	ttctgtagaa	acactcttgt	900
gtaaaagtta	actgtattag	agtaag				926

<210> 1049

<211> 939

<212> DNA

<213> Unknown (H38g899 nucleotide)

<220>

<223> Synthetic construct

<400> 1049

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ctcaggctaa ggacactcct ttttgtgttc ttttttctaa tctacatcct gactcagctg	120
ggaaacctgc ttattttaat cactgtcttg gcagacccaa ggctccatgc ccgccccatg	180
tacatctttc ttgggtgttc ctcagtcatt gatatgagca tctcctccat cattgtccct	240
cgccctcatg tgaacttcac tttaggtgtc aaaccatcc catttggtgg ctgtgttgct	300
caactctatt tctatcactt cctgggcagc acccagtgtc tctctacac cctaattggcc	360
tatgacaggt acctggcaat atgtcagccc ctgcgctacc ctgtgtcat gactgctaag	420
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gccatccctaa ccttccgcct gccctactgt gggcccaatc aggtggatta cttcttctgt	540
gacatccctg cagtgttgag actggcctgt gctgacacaa cagtcaacga gctggtgacg	600
tttgtagaca ttgggggtgt ggttgccagt tgcttctccc tgatcctcct ctctacata	660
cagatcattc aggccatcct gagaatccac acagctgatg ggccggcgccg ggctttttca	720
acttgtggag cccatgtaac cgtggtcacc gtgtactatg tgccctgtgc cttcatctac	780
ctgaggcctg aaaccaacag cccctgggat ggggcagctg ccctagtccc cacggccatc	840
actcctttcc tcaacccct tatctacact ctgcggaacc aagaggtgaa gctggccctg	900
aaaagaatgc tcagaagccc aagaactccg agtgaggtt	939

<210> 1050

<211> 954

<212> DNA

<213> Unknown (H38g900 nucleotide)

<220>

<223> Synthetic construct

<400> 1050

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ctcactcagc tggggaacct gctcattctg ctaccctgtt gggctgaccc gaagctccgt	180
gctcgcccca tgtacattct tctgggagtg ctctcatctc tggacatgtg gctctcctca	240
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ggctgtgttg ctcaactgta tttctttcac ttcttgggca gcaccagtg cttctcttac	360
accttgatgg cctatgacag gtacctggca atatgtcagc ccctgcgcta cccagtgtct	420
atgaatggga ggttatgcac agtccttctg gctggagctt gggctcgccg ctccatgcat	480
gggtctatcc aggccaccct gaccttccgc ctgcccact gtgggcccac tcaggtagat	540
tactttatct gtgacatccc cgcagtattg agactggcct gtgctgacac aactgtcaat	600
gagcttgtga ctttgtgga catcggggta gtggccgcca gttgttctat gttaattctg	660
ctctcgtatg ccaacatagt aaatgccatc ctgaagatac gcaccactga tgggagggcg	720
cgggccttct ccacctgttg ctcccaccta atcgtggtca cagtctacta tgtcccctgt	780
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tacactgttg tcaactccatt actgaacccc ctcatctata cactgaggaa ccaggaagtg	900
aagtctgccc tgaagaggat aacagcaggt caagggactg aatgaaaata agta	954

<210> 1051

<211> 930

<212> DNA

<213> Unknown (H38g901 nucleotide)

<220>

<223> Synthetic construct

<400> 1051

atgggaaaga caaaaaacac atcgctggat gccgtggtga cagatttcat tcttctgggt	60
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ctcactcagc	tggggaacct	gctcattctg	ctcaccatgt	gggctgacct	gaagctctgt	180
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tacactgttg	tcaactccatt	actgaacccc	ctcatctata	cactgaggaa	ccaggaagtg	900
aagtctgccc	tgaagaggat	aacagcaggt				930

<210> 1052

<211> 900

<212> DNA

<213> Unknown (H38g902 nucleotide)

<220>

<223> Synthetic construct

<400> 1052

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gaggattcct	ggctccacaa	ccccatgtat	tattttctta	gtgttttata	attcttggat	180
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gctggcattt	tacatgtac	tatacatata	gtggctacat	ttagcctgtc	cttctgtgga	480
tccaatgaaa	ttaggcattg	cttttgtgat	atgcctcctc	tccttgctat	ttcttgttct	540
gacactcaca	caaaccagct	tctactcttc	tactttgtgg	gttctattga	gatagtcact	600
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gctaagggaa	ggcaaaaaggc	cttctctaca	tgtggctctc	acctaactgg	agtgacaatt	720
tatcatggaa	caattctcgt	cagttatatg	agaccaagtt	ccagctatgc	ttcagaccat	780
gacatcatag	tgtcaatatt	ttacacaatt	gtgattccca	agttgaatcc	catcatctat	840
agtttgagga	acaaagaagt	aaaaaaggca	gtgaagaaaa	tgttgaaatt	ggtttacaaa	900

<210> 1053

<211> 974

<212> DNA

<213> Unknown (H38g903 nucleotide)

<220>

<223> Synthetic construct

<400> 1053

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acgggtgctga	ggaacttgct	gagcatcctg	gctgtccgct	ctgagtcctc	gtccacaca	180
accatgtact	tcttctcttc	catectgtgc	tgggctgaca	tcggtttcac	ctcagccaca	240
gttcccaaga	tgattgtgga	catgcagtgg	tatagcaaag	tcattctctca	tgcgggctgc	300
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atggcctatg	actgctttgt	aggcatctgt	cgccctctgc	actacccagt	catcgtgaat	420
cctcatctct	gtgtcttctt	tgttttgggt	tcctttttcc	ttagcctgtt	ggattcccag	480
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atacaaagt	ccctgctggag	gctgcccac	aaaacagtcg	aatctcatga	tctgttccat	960
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<210> 1054

<211> 1006

<212> DNA

<213> Unknown (H38g904 nucleotide)

<220>

<223> Synthetic construct

<400> 1054

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atgtctctct	ttgccatttt	tggaggcatg	gaaaaaagac	atgtcctcga	gtgtgatggc	360
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tttctgtggc	ttcctaaatt	tgttgtcttt	tttttttttc	cctcagtctt	ttagactccc	480
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taaaagtgtc	ctgctggcgc	cgcaaggcag	cacagtctca	tctcaatacc	ttcttatctg	960
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<210> 1055

<211> 929

<212> DNA

<213> Unknown (H38g905 nucleotide)

<220>

<223> Synthetic construct

<400> 1055

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tccttatcat	ggtgaccatc	atggccagcc	agtccttggg	ttcccccatg	tacttttttc	180
tggttctttt	atcattttata	cataccgtct	attatactgc	cattgctccc	aaaatgattg	240
ttgacctgct	ctctgagaaa	aagaccattt	cttttcaggg	ttgtatggct	caacttttta	300
tggatcattt	atttgctggg	gctgaagtca	ttcttctggg	ggtaatggcc	tatgatcaat	360
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<210> 1056

<211> 925

<212> DNA

<213> Unknown (H38g906 nucleotide)

<220>

<223> Synthetic construct

<400> 1056

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<210> 1057

<211> 499

<212> DNA

<213> Unknown (H38g907 nucleotide)

<220>

<223> Synthetic construct

<400> 1057

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atgtacacga ctttactcat ggcccaggtt gtgtctctgt gcagacaatg gatccacac      60
tctttctgtg atatgtctgc tctgctgaag ctggccctct ctgacactcg agttaatgaa    120
tgagtgatat ttatcatggg agggctcatt cttgtcatcc catccatact catccttggg    180
tcctatgcaa gaattgtctc ctccatcctc aaggctccctt cttctaagtg tatctgcaag    240
gccttctcta cttgtggctc ccacctgtgc tgtggtgtca ctgttctatg gaaccgttat    300
tggctctctac ttatgctcat cagctaatag ttctactcta aaggacactg tcatggctat    360
gatgtacact gtggtgaccc ccatgctgaa ccccttcac tacagcctga ggaacagaga    420
catgaaggga gccctgagca gagtcatcca tcagaagaaa actttcttct ctctctgatg    480
ataacacttg gagctatta                                     499

```

<210> 1058

<211> 996

<212> DNA

<213> Unknown (H38g908 nucleotide)

<220>

<223> Synthetic construct

<400> 1058

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atgggaccaa agaatctaac tcgtgttttg gaattcttcc tcctccactt cttagatgac      60
ttggaactgc agcctttcct cttcaggctg tccctgaacc atgcacctag tcacagtgtc    120
tgcgaaactg ctcacatcct tctgactgtc agctttgccc tcacctccac aaccccatga    180
acttcaacct gtccttagct gacatttggt tcacctctgc cacaatttca aagataactg    240
tagacctcca aactcacagc agaatcattt tatacatgag ctgcctgaaa tagatgtctt    300
ttaaaattat ttttgatgt ttgcacaatc tactcatgac tgtgatggcc tatgacctat    360
ttgtggcgac ctgtcatctc ttgtactaca cagtgatcag gaatcccccac ctctgtggcc    420
tcctgtctct ggtctctctc tctctctctc tttttttttt ttgatcagtc ttttgaaac    480
ccagctgtac agtttgatgg tgtcacaagt tctctcatgc aaatgtagac attcctcatt    540

```


tcttctgtga	cccttctcag	tttctccacc	tttctgttc	tgacactgcc	accaataaca	600
cattaatgca	ttttattggt	gccatctctg	tggtccattc	tcagggatcc	tttactgtta	660
tactcaaatt	atgttctcca	tactcataac	cctataaaat	gtgggaagta	taaagcaaac	720
cttctccacc	catcgctctc	acctgtcagt	tgtttgctta	ttttatggaa	caggccttgg	780
agtatacctt	agtttggctg	gctcaccttc	cccaagaaca	ggtgtggtgg	cctcaatggt	840
atataccaca	gtcacctca	tgttgaaccc	tgcatccaca	gcctgaggaa	cagagacatc	900
aagaatacct	ggtggtggct	cctcagcata	actgcctggt	atcaatacct	gtgctatcct	960
ttatggagtg	tggttagaaa	aaacagcaaa	ctcaaa			996

<210> 1059

<211> 923

<212> DNA

<213> Unknown (H38g909 nucleotide)

<220>

<223> Synthetic construct

<400> 1059

atggggactt	caaataatga	gactgaattc	attcttttgg	gcattacaaa	aaatccagaa	60
ctaaggaaaa	tattctctgc	tttgtttcta	gccatgtatg	tgaccacagt	gttgggaaat	120
ctattcattg	tggtgactct	ggctgcaagt	tgaggtctga	gatcacctat	gtacttttcc	180
cttacttctt	tgtctctcat	gggtgccacc	tactcttcca	tcactgcccc	taagatgact	240
gtggactctt	tgagaacact	accattttcc	ttgaaggctg	catgaccag	ctctttgcag	300
agcattttct	tgatggtgta	gcgatcatcc	ttctcactgt	gatggtctgt	gactgctatg	360
aggccatcag	taagccccctg	catgacacaa	ccatcatgag	tcacgggtg	tgctgctgtt	420
ggtggttagaa	gcttgggtgg	ggggattaac	acatgccaca	atacagcttt	ttttttttca	480
tatatcaaat	acccttctgt	ggtcccaata	ttattgacca	ttttatatgt	gatttgtttc	540
cattgttaaa	acttgcttac	atggacaccc	acatgctggg	tctcttagtc	atcctcaaca	600
gtggggtgat	gtgtatggcc	atcttcttta	tctaattgc	atcctacatt	gtcacctgt	660
actctctgaa	gtcttgacg	tcggtaggtc	gacgcaacac	actttccacc	tggtgctccc	720
accacacagt	ggtcattctt	ttcttcgtgg	agtgtatttt	cttgtacata	agacctgtgg	780
tcacttacc	catagacaag	gatatggcta	tttcttttac	tattgttgca	cccattgttaa	840
atcctctgat	ctataccctg	aggggcatca	aggtaaaaaa	tgccataaga	aaaatgtgga	900
tgaacaggg	gacctaggt	ggt				923

<210> 1060

<211> 950

<212> DNA

<213> Unknown (H38g910 nucleotide)

<220>

<223> Synthetic construct

<400> 1060

atggctccga	ccaacctcac	atctgcccc	gctgttcctc	ctctcggcc	tggtggacgg	60
aacagacgcc	caccgcctgc	tgttcctgct	ctgccttggg	tctatctgct	caacgccctg	120
agcaacctga	gcatggtggc	gctggtgaga	tccgacgggg	ccctccgctc	ccccatgtat	180
tacttcttgg	gtcactgagc	ctcgtggacg	tctgctttac	caccgtcacg	gtccccaggc	240
tgctggccgg	cctgctccac	ccgggcccagg	ccatatcctt	ccaggcgtgt	ctgccgagat	300
gtactttctt	gtgactctgg	catcacccag	agctacctca	tgccggccat	gtcctagcga	360
gcccagacgc	gcgtgccggc	acctctgtac	ggcgcgctgg	tgacgccatc	ggcgtgcgcc	420
tgctggtgct	tgcgtcgtgg	gccgtgacgc	acctgcactc	gctgctgcac	acgctgctcc	480
tctccgcgct	ctcctacccc	taccccaccc	ccgtgcgccc	cttcttttgc	gacatgacgg	540
tgatgctgag	cttggcgacc	tcggacacgt	ccgcgcggga	gacggccatc	ttctccgagg	600
gcctggccgt	ggtgttggcc	ccgtgctccc	tcgtgttcct	tttctacgc	gcgcctcctg	660
gtcgcggtgc	tcggcttgcg	cggccgcgcc	gcgccttctc	cacctgcggg	gcccacctag	720
tgccggtggc	ggtggcgctt	ttctttggct	ctgtcctctc	cgtgtatttc	ccgcctcgt	780
ctgcctactc	agcccgtac	gaccgcctgg	ccagcgtggt	ctacgctgtc	atcacgcga	840
ccttgaaccc	tttcatcaac	agccttcgca	acaaagaggt	caagggcgcc	ctgaaaaggg	900
ggctcagcat	ggagggctgc	accccaagag	gcgtgagggc	aaatctggct		950

<210> 1061
 <211> 933
 <212> DNA
 <213> Unknown (H38g911 nucleotide)

<220>
 <223> Synthetic construct

<400> 1061
 atgaaagggg caaacctgag ccaagggatg gagtttgagc tcttgggcct caccactgac 60
 cccagctcc agaggctgct cttcgtgggtg ttcttgggca tgtacacagc cactctgctg 120
 gggaaacctg tcatgttcct cctgatccat gtgagtggca ccctgcacac acccatgtac 180
 tccctcctga agagcctctc cttcttggat ttctgctact cctccacggt tgtgccccag 240
 accctgggtga acttcttggc caagagggaaa gtgatctctt attttggctg catgactcag 300
 atgttcttct atgcgggttt tgccaccagt gagtgctatc tcatcgctgc catggcctat 360
 gaccgctatg ccgctatttg taacccccctg ctctactcaa ccatcatgtc tcctgaggtc 420
 tgtgcctcgc tgattgtggg ctccacagt gcaggattcc tcaattctct tatccacact 480
 ggcgttatct ttagtctgaa attctgcggt gctcatgtcg tcaactcatt cttctgtgat 540
 gggccacca tcctgtcctt gtcttgtgta gacacctcac tgtgtgagat cctgctcttc 600
 atttttgctg gtttcaacct tttgagctgc accctcacca tcttgatctc ctacttctta 660
 attctcaaca ccatcctgaa aatgagctcg gccaggggca ggtttaaggc attttccacc 720
 tgtgcatccc acctcactgc catctgcctc ttcttgggca caacactttt tatgtacctg 780
 cgccccaggt ccagctactc cttgacctcag gaccgcacag ttgctgtcat ctacacagtg 840
 gtgatccag tgctgaacct cctcatgtac tctttgagaa acaaggatgt gaagaaagct 900
 ttaataaagg tttggggtag gaaaacaatg gaa 933

<210> 1062
 <211> 948
 <212> DNA
 <213> Unknown (H38g912 nucleotide)

<220>
 <223> Synthetic construct

<400> 1062
 atgcaaaacc aaagctttgt aactgagttt gtcctcctgg gactttcaca gaatccaaat 60
 gttcaggaaa tagtatttgt tgtatttttg tttgtctaca ttgcaactgt tgggggcaac 120
 atgctaattg tagtaacct tctcagcagc cctgctcttc tgggtgtctcc tatgtacttc 180
 ttcttggggt tcctgtcctt cctggatgcg tgcttctcat ctgtcatcac cccaaagatg 240
 attgtagact ccctctatgt gacaaaaacc atctcttttg aaggctgcat gatgcagctc 300
 tttgctgaac acttctttgc tgggggtggag gtgattgtcc tcacagccat ggcctatgat 360
 cgttatgtgg ccatttgcaa gcccttgcat tactcttcta tcatgaacag gaggctctgt 420
 ggcattctga tgggggtgag ctggacaggg ggcctcttgc attccatgat acaaattctt 480
 tttactttcc agcttccctt ttgtggcccc aatgtcatca atcactttat gtgtgacttg 540
 taccggttac tggagcttgc ctgcactgat actcacatct ttggcctcat ggtggtcatc 600
 aacagtgggt ttatctgcat cataaacttc tcttgttgc ttgtctccta tgctgtcatc 660
 ttgctctctc tgagaacaca cagttctgaa gggcgctgga aagctctctc cacctgtgga 720
 tctcacattg ctgttgatgat tttgttcttt gtcccatgca tatttgtata tacacgacct 780
 ccatctgctt tttcccttga caaaatggcg gcaatatttt atatcatctt aaatcccttg 840
 ctcaatcctt tgatttacac tttcaggaat aaggaaagta aacaggccat gaggagaata 900
 tggaacagac tgatggtggt ttctgatgag aaagaaaata ttaactt 948

<210> 1063
 <211> 930
 <212> DNA
 <213> Unknown (H38g913 nucleotide)

<220>
 <223> Synthetic construct

<400> 1063

atgcaactga	ataataatgt	gactgagttc	attctgcttg	gattgacaca	ggatcctttt	60
tggaagaaaa	tagtgtttgt	tatttttttg	cgtctctact	tggaacact	gttgggtaat	120
ttgctaata	ttattagtg	caaggccagc	caggcactta	agaacccaat	gttcttcttc	180
cttttctact	tatecttate	tgatacttgc	ctctctactt	ccatagcccc	tagaatgatt	240
gtggatgccc	ttttgaagaa	gacaactatc	tccttcagcg	agtgcattgat	ccaagtcttt	300
tcaccccatg	tctttggctg	cctggagatc	ttcatcctca	tcctcacggc	tggtgaccgc	360
tatgtggaca	tctgtaagcc	cctgcactac	atgaccatca	taagccagtg	ggctctgtgg	420
gttttgatgg	ctgtggcctg	gggtgggatcc	tgtgtgcatt	ctttagttca	gatttttctt	480
gccctgagtt	tgccattctg	tgcccccaat	gtgatcaatc	actgtttctg	tgacttgcag	540
cccttggtga	aacaagcctg	ttcagaaacc	tatgtggtta	acctactcct	ggtttccaat	600
agtggggcca	tttgtgcagt	gagttatgtc	atgctaatat	tctcctatgt	catcttcttg	660
cattctctga	gaaaccacag	tgctgaagtg	ataaagaaag	cactttccac	atgtgtctcc	720
cacatcattg	tggtcatctt	gttcttttga	ccttgcatat	ttatgtacac	atgccctgca	780
accgtattcc	ccatggataa	gatgatagct	gtattttata	cagttggaac	atcttttctc	840
aaccctgtga	tttacacgct	gaagaatata	gaagtgaaaa	gtgccatgag	gaagctttgg	900
agcaagaaat	tgatcacaga	tgacaaaaga				930

<210> 1064

<211> 964

<212> DNA

<213> Unknown (H38g914 nucleotide)

<220>

<223> Synthetic construct

<400> 1064

atggagacaa	caaatacttc	tgccgtgact	gaattctttc	tggtggggct	ttcccaatat	60
ccagagctcc	agctttttct	gttctctgtc	tgccatcatc	tgtacatgat	aatcctcctg	120
ggaaatagct	tcctcattat	catcaccatc	ttggattctc	gcctccatac	ccccatgtat	180
ttctttcttg	gaaacctctc	attcttgggc	atctgttaca	catcatcatc	cattcctcca	240
atgcttatta	tatttgtatc	tgagagaaaa	tccatctcct	tcattggctg	tgctctgcag	300
atggttgtgt	cccttggctt	gggtccatt	gagtgatcc	tcctggctgt	gatggcctat	360
gaccgctatg	tgccatctg	caaccactg	aggtaactcc	tcacatgaa	cagagtgtctg	420
tatgtgcaaa	tggtgtcatg	gtcctggatc	ataggctgtc	tgacctccct	attgcgaaca	480
gttctgacaa	tgatgttgcc	tttctgtggg	aataatatca	ttgatcatct	tacctgtgag	540
atcctggctc	ttcttaaagt	catatgtctc	gatatctcca	taaatgtgtt	tataatgaca	600
gtgtcaagta	ttgttttatt	gggtgattcct	cttaattttt	atctcctatg	tgtttattct	660
ctcttccatc	ttgagaatta	attctgtctg	gggaagaaag	aaagcctttt	ttacctgttc	720
agcgcaactg	actgtgtgca	tcttattcta	tggttcagtt	cttttcatgc	acatgaagcc	780
caaatcaaatg	ttgcacaacag	catctgatga	aatcattgga	ttgtcttatg	aagtgtatcac	840
cccaatgaac	cccatcatct	acagcctgag	gaataaggag	ataaaagaag	ctgtgaagaa	900
aatcctcagc	agacacgtgc	atctatggaa	aatatgaaag	gccttgaggc	atgtgacgtt	960
ctca						964

<210> 1065

<211> 620

<212> DNA

<213> Unknown (H38g915 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(620)

<223> n = A,T,C or G

<400> 1065

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ctttttcctg	aagaacctct	ctgttttggg	tctgtgctac	atctcagtc	ctgtgcctaa	120
atccatccgt	aactccctga	ctgcagaag	ctccatctct	tatcttggct	gtgtggctca	180
agcctatttt	ttctctgcct	ttgcatctgc	tgagctggcc	ttccttactg	tcattgtctta	240

tgaccgctat	gttgccattt	gccacccct	ccaatacaga	gccgtgatga	catcaggagg	300
gtgctatcag	atggcagtc	ccacctggct	aagctgcttt	tcctacgcag	ccgtccacac	360
tggcaacatg	tttcgggagc	acgtttgcag	atccaatgtg	atccaccagt	tcttccgtga	420
catccctcag	gtgttgccc	tggtttcctg	ngagggtttc	tttgtagagc	tttgacceng	480
ccctgagcct	caatgcttgg	ntctgggatg	ctttattccc	atgatgatct	ccnattttcc	540
anatcttctn	aanggggctc	nagaatccct	tnaggaccag	antcnagcta	aaagcctttn	600
cccnnctgct	tccccccacg					620

<210> 1066

<211> 611

<212> DNA

<213> Unknown (H38g916 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(611)

<223> n = A,T,C or G

<400> 1066

gatgcatgct	cgagcggccg	ccagtgtgat	ggatatctgc	agaattcgcc	cttccaatgt	60
atattttct	ctctgacctc	tccttcttgg	acctctgctt	taccacaagt	tgtgtccccc	120
agatgctggt	caacctctgg	ggcccaaaga	agaccatcag	cttcctggga	tgtctgtgcc	180
agctcttcat	cttctgtgcc	ctggggacca	ctgagtgcac	cctcctgaca	gtgatggcct	240
ttgaccgata	cgtggctgtc	tgccagcccc	tccactatgc	caccatcatc	cacccccgcc	300
tgtgctggca	gctggcatct	gtggcctggg	ttatgagtct	ggttcaatcg	atagtccaga	360
catcatccac	cctccacttg	cccttctgtc	cccaccagca	gatagatgac	tttttatgtg	420
aggtcccatc	tctgattcga	ctctcctgng	gagatacctc	ctacaatgaa	atccagttgn	480
ctgtgtccag	tgtcatcttt	ggtggntgtg	cctctcagcc	tcctccttgc	ctcttatgga	540
gccactgccc	aggcnggggc	tgaggattaa	ctttgccnna	gccatggaag	aaaggtcttt	600
nggacctngn	n					611

<210> 1067

<211> 619

<212> DNA

<213> Unknown (H38g917 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(619)

<223> n = A,T,C or G

<400> 1067

gatgcatgct	cgagcggccg	ccagtgtgat	ggatatctgc	agaattcgcc	ctttctttat	60
ttcgaagagt	atacactagt	ggattgaaga	gaaacaaata	cataggaagg	gcgaattcca	120
gcacactggc	ggccgttact	agtggatccg	agctcggtag	caagcttgat	gcatagcttg	180
agtattctaa	cgcgctacct	aaatagcttg	gcgtaatcat	ggatcatagct	gtttcctgtg	240
tgaaattggt	atccgctcac	aattccacac	aacatacgag	cgggaagcat	aaagtgtaaa	300
gcctggggtg	cctaattgagt	gagctaactc	acattaattg	cgttgcgctc	actgtccgct	360
ttccagtcgg	gaaacctgtc	gtgccagctg	cattaatgaa	tcggccaacg	cgcggnnaga	420
ggccggnttg	cgtattgggc	gctcttccgc	ttctcgctca	ctgactcgct	gcgctcggga	480
cgtccggctg	cggcgagcgg	tatcagctta	ctcaanggcc	gtantacggt	tattcncagg	540
aatnnggggt	taacgcncng	naaagaacat	tgtgngccan	angncaagcn	taatgcccag	600
gaaccgntan	aacgntccc					619

<210> 1068

<211> 621

<212> DNA

<213> Unknown (H38g918 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(621)

<223> n = A,T,C or G

<400> 1068

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gnnnnttntt cantccattg ggccctctag atgcatgctc gagcgccgc cagtgtgatg      60
gatatctgca gaattcgccc ttattccgga gggatatacat gaagggattg gtaactagac      120
gtaaaactcga agccaagaac agaatttctc ttagaaaaga gaattgaaac taaagagaaa      180
gaactagcaa agaaggaaat attgaatata caagagagag gagacagatg atggaacaag      240
actctgaaag aggtggaagg gattgaatac aatcaaaagt atgggtgactg ctagttccaa      300
gatggtggcg taggggcaag ctggctttgc ttacccccct ggcagaaaac caaaaacaaa      360
tagcaccaag attatcacta gcaatatccc agaactcaca tataaggatg agacagttcc      420
cagggcccag agaagatcag aagcacaagt gggagaagtc agctttggat gctactttgt      480
tctaaggag acaagttggg aggatgattg cagatgtata ttcaatgtta taaaacagcc      540
cataaaacaa agattgaaa atgttgaaat ttgcaaccag gagcaaatat tgggaaaggc      600
gaattccagc cacttgcnge c                                     621

```

<210> 1069

<211> 615

<212> DNA

<213> Unknown (H38g919 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1069

```

gnnnnttnan tcantgccct ngggccctct agatgcatgc tcgagcgcc gccagtgtga      60
tgatattctg cagaattcgc ccttggttgc caaggtgtaa atgaaaggt ttgcgaggga      120
gtaaatgaag ggattacgca ggagtaaatg aagggattac gcaggagtaa atgaaggat      180
tacgcaggag taaatgaagg gattacgcag gagtaaatga agggattacg caggagtaaa      240
tgaagggatt acgcaggagt aaatgaaggg attacgcagg agtaaatgaa gggattacgc      300
aggagtaaat gaagggatta cgcaggagta aatgaaggga ttacgcagga gtaaatgaag      360
ggattacgca ggagcaaata cataggaagg gcgaattcca gcacactggc ggccgttact      420
agtggatccg agctcggtac caagcttgat gcatagcttg agtattctaa cgcgctcacct      480
aaatagcttg gcgtaatcat ggtcatagct gtttcctgtg tgaaattgtt atccgctcac      540
aattccacac aacatacgag cccggaagca taaagtgtaa agnctggggg gcctaattgag      600
tgacttactc catta                                     615

```

<210> 1070

<211> 614

<212> DNA

<213> Unknown (H38g920 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(614)

<223> n = A,T,C or G

<400> 1070

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ggnnnttnant cattgccccg ctngatgcat gctcgagcgg ccgccagtgt gatggatatt      60

```

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tgcagaattc gcccttccga tgtattttct tctacgttaa ggtattttta attgttacta 120
atgcataagg gcaacacatt ctgtaatgct gacaagatga aagagccaaa agtaattaat 180
gatgctgtta cctcaciaat atgtatgtgt ggatgtatat atatctattc aatatatgta 240
actatacata tgtctgtttc taattgaaaa caccaggtaa ttatcatctg tagaaaccct 300
agtgtctcag ataagttggc tagttttttg ttccacataa aggaacaaac atttatagat 360
ttatatgtat attaaaaatg gtaaaaattg gctgggtgca gtgggtcatg cctataatac 420
cagcactttg ggaagccgag gtgggaggat tacttgaggt aaggagccca gcctgaccaa 480
caaggtgaaa ccccatccct actaaaaata caagaattag cccggggatg gtgggtggcca 540
cctgtaatcc cagctacttg ggagactgaa gccaggaaaa tcacttgacc caggaagcng 600
aggttgcagg ngag 614

```

<210> 1071

<211> 857

<212> DNA

<213> Unknown (H38g921 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(857)

<223> n = A,T,C or G

<400> 1071

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atggnnnnnn nntttnnnaa anttttnccc antttgggcc gnccccccct tctttaaggn 60
aatgggcccc ttgggccctt cccggaaggc cggggggcnc cgggccccaa aggtttgggt 120
tggaagatgg ggggaattta aattcctttg ggccaaggna aaaattttcc ngccccctt 180
tttttcccc tttggttttt anccggggga angggggggt tgattaatta atcgggaagn 240
tnggggggaa nttttttaa aaaaacctg ggggaagggt ccaaccaaac aaggttggtt 300
ttccanaggga ccgttgggac caggcttttn gaatcaagaa tcccaaaggg cattcttttg 360
gattaaggaa nggtgccggg accggtgaaa gggaaaaaac tgggtggacc cataccaaaa 420
tgagaaccac ggtgagatgc cgaggagcac gtggagaaag gctttgcttc cggccactgg 480
cagaggggat cctgaggatg gtgcttgatg atgtacacat agggagacaa ggggtgatgag 540
gcatgaactc aggataacca caacagcnat cacaaaggcc acaaagctct actgcctgtg 600
tgttgggtgc aggccagggc aatccagggg tgcaatgtca caagaaagaa agtgggtgat 660
ggcacgggng ggccacagaa ggacaggcca cttgatgaag ggcttggtgg cactgcaatg 720
gccacgaaac caccagaccc aggaacccan ggccaagctt gcgcctgaag agcaaggcta 780
ctcatgaatg gcttccgtag tngtaaagga tagcaagatg gcaaaggcaa gccggtcatn 840
aagccatggc ttgccng 857

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<210> 1072

<211> 593

<212> DNA

<213> Unknown (H38g922 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(593)

<223> n = A,T,C or G

<400> 1072

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aacgcagagt accgccact acgtaatctg tacatgaaag ggtttaaaag agactgggaa 60
gagaggaatt ggcaagatca agcagaggca actccttcta gtccttctag taccgcaagg 120
ggcagataaa tggaatgggt aacacctaga ggaaagtata cttgccaaaa gcaaatncat 180
aggggggagt acattatcgg gttgaaaaaa gtattccatg cagataaaaa ccaaaagcaa 240
atacatcggg ggcgtacttc tgcgtcttt gagcgtactg atggtacca gcttttgnct 300
ctttagttag ggttaattgc gcgcttgagg taatcatggt catagctggt ttctgtgtga 360
aattgttate ccgctcaciaa ttcacacaac atacgagccc gggagcataa agtgtaaagc 420
ctgggggtgcc taatgagtg agcttactta cattaaattg cgttgcgctc actggccgct 480

```

tttccaagtc gggaaacctg tcgtgncagc ttcantaatg aatcggccaa cgccgcgggg 540
agaggcggtg tgcgtattgg gcgctcttcc gcttcttngt tnactgactt cgg 593

<210> 1073

<211> 624

<212> DNA

<213> Unknown (H38g923 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(624)

<223> n = A,T,C or G

<400> 1073

gnnntttaac nccgnggctn cnagcagtgg aacaacgcag agtacgcccc cgatgtactt 60
tctttttcag tctcaagtct tctcttctc caaagatttt gtcttttcta ctacctgagc 120
taccaaatcc cttgtcatca atttcaataa ctgtattctc ttcattcatt caacttcaaa 180
cgtgtcatct cagaacaagc ttcattgtac ttccaatttt atccttcttg tttgctgatt 240
ccaagaattc cagtcccatc taggccccga atgcattgtt cctgccaccc ttttcataac 300
ctcaattccc ttgtatcatc actttctctt tatatagcac agattccatg attcataaca 360
ataaattatg ttttttttgc atgtgctctt aatttctctt cttgctccta ttatcttcta 420
tcatactttt ctggaaacac taattctggt gaaatatact ctttgtggac tttgcactta 480
tgctcagtc gctgaagatg atggctagac aaatactcac aatcatgctg actggcccaa 540
tttatagtc tgaccaccga ttacaaaccc cttcatttat tctccgcaac aggggcgtct 600
tctgcgcttg agcgtccggt gggg 624

<210> 1074

<211> 637

<212> DNA

<213> Unknown (H38g924 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(637)

<223> n = A,T,C or G

<400> 1074

ttatnnccat tggagctcca aagcagtggg aacaaccgca gagtacgccc cccatgtatt 60
ttctttttct tgggnagct gnatgcttcc tncgtgttac catggnatat gaccggctat 120
gngnccatct gcagtcctt gnnctcccag tcattatgaa ccaaaggaca cgggccaaac 180
tggctgggtg ttctgggtc ccaagcttct ctgnagctac tngcaagac cacaatggct 240
cttnagnntt ccattctgng gcaccaacaa ggtgaaccac ttntttctgn gacagccggc 300
tgtgctgaaa gctggtctgn tgcaagacac agcactgtt gagatctacg ccatcgctcg 360
aaccattctg gtggtcaatg aacccttctg tgctgatctt gngttcctat actcgnattg 420
gtgctgctat ccctcaagaa cccatcaagc taaangggaa gcaataaagn cttttctcta 480
cgtgctcctt aacacctccc ttggtggcct ctcttttcta atataatcnt ctaagcctca 540
acctacttct tgggcctnaa ntcaataaaa ttcttctgga gaggcaagaa ggtggtattc 600
atztatncta cactggtngn gactccatgn tggaaact 637

<210> 1075

<211> 621

<212> DNA

<213> Unknown (H38g925 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature
 <222> (1)...(621)
 <223> n = A,T,C or G

<400> 1075
 gtnatncnt ttaatncnt tggagctcca agcagtggta acaacgcaga gtacgcccgt 60
 tcctcagaca gtatatgaat ggggttaaaaa tgggccagag cagatgcagg aagatcaaatt 120
 aggaggctac tgcagtagag tcaaatctag ggctgatggt ttcttgggat gcatagtaat 180
 aggtagatag agaaagtctt taggaggtag aatggacagg acttcacaat gcattaaatg 240
 tagggagaaa aaaaatgatt cctgggtttc tagcttgagc tagtagggat agtggtagaa 300
 ttacttgata tggaaaactg gaggaaaaag agtttggaag agaaagatgg caagttaaatt 360
 acctgtggga aatataatca cagacactaa ataggcagct gtgtgggtgg caaaggagag 420
 ccatgggcta ggaacataca gtgggattcc ctggcatgctc attggttact gaagtcagag 480
 tgtatgagac agcctaagga gagaatncac acaggagaag aaagaactaa acattcagtg 540
 gctggccaga ggatgagaaa cccaagagat tggactgttt aggagcaaca gtgttgngaa 600
 aaggagagaaa nggttgaaat t 621

<210> 1076
 <211> 631
 <212> DNA
 <213> Unknown (H38g926 nucleotide)

<220>
 <223> Synthetic construct

<221> misc_feature
 <222> (1)...(631)
 <223> n = A,T,C or G

<400> 1076
 ggntttannc nctggagctc caaagcagng gtaacaacgc agagtacgcc cattgcgtag 60
 cgtgtacata aaggggttgg agctgaagga ggagataaag aagaagacag ccagaacctt 120
 gtccctctgtc ggagatcgca gggatcttgg gccgtagata ggtataagca aaggggtgcat 180
 agtagaaaagt cactacagtg aggtgggtgc tgcaggtcga ataggccttc ttctccctt 240
 ctgcagagtg catgtggttag acagcaagga gaatccggcc ataggaacat gcaatacaaa 300
 tgaagggaaa cacaagaaaa atgggtggtgc tcaaaaacac cgtgcactca tagaccagg 360
 tatccgtgca ggctagggtc aacatagctg gaacatcaca gaaaaaatga ttgatggctc 420
 tggacttgca atatgggata cggagtgcac ataccgtgtg agcacaagag ttgatggagc 480
 ctatcatcca agatcctgtt atcatcagtg cacacactct ttttctcata cggatgagat 540
 agtggagagg aaagcaata gccacataac gatcataggc cattgatgtc aggagcagcg 600
 cttctgcacc tgctaaagtc aggaagaaga t 631

<210> 1077
 <211> 620
 <212> DNA
 <213> Unknown (H38g927 nucleotide)

<220>
 <223> Synthetic construct

<221> misc_feature
 <222> (1)...(620)
 <223> n = A,T,C or G

<400> 1077
 tgttantccn ntttncntcc attggagctc ccaagcagtg gtaacaacgc agagtacgcc 60
 ctcttctgtt ctgagagtgt agatgaaggg gttataggag ataaagatca gggcaatatg 120
 taggacaagg acacagacac tgacaacaaa gttgattatc tcattgacag tgggtgtctgt 180
 gcaggccagc ttcagcaggg gtctcacatc acagaagaag tgggagatga caaagtcac 240
 acaaaagggc aggccaaaca tagatgttac ttggacaata gccatgccca ggccaatcct 300
 cagtgaacca gatcccgatc agacacaagc cctcttacct atgaataccg taagggttg 360

cagaagacca	catagcaatc	atatcccatg	gctatgagaa	gaaagcagtt	gttgatgcc	420
aaagtcacat	agaagagctg	agtgcacacg	ccttgcatga	caataagcta	gtgaggattc	480
aagaggcgag	aaagcatatg	gggagtaatg	gccaccatgt	agcaggctctc	agagatagac	540
agcaatgctt	agggaaaaagt	acatgggccc	tactttctgtc	gtcttgagcg	tactgatggt	600
accagctttt	tgttcccttt					620

<210> 1078

<211> 627

<212> DNA

<213> Unknown (H38g928 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(627)

<223> n = A,T,C or G

<400> 1078

tgtagctcca	aagcagtgg	aacaacgcag	agtacgcct	cttggttacg	taagggaata	60
gatgatggg	ttcagcatgg	gggtgactac	agtgtacatg	acagtggcca	cacgggtcca	120
ctctgctcg	gtcgggacgt	ggcctggaag	tagactgcaa	tgactgtcct	atagaaagag	180
gctcaccaca	nccaggtggg	agccacaggt	gggncacaag	tcccggagcc	tcccagaggc	240
ttgagggcag	ctggagcacg	ggnaagcttg	ntatggncct	acaaggaggc	gaggatgagc	300
agnaagggag	tgaccaccac	ttgengcgcc	ctnggtgaag	atgagcagct	tgatgtggt	360
ggntgtcaga	gcacgagagc	ctttaagaga	ggcttggtgg	gtcacagaag	aagtgggngc	420
actttgtggg	aaagcacaga	aaggacaagc	gagccatgag	caggatatac	aggagggagt	480
tgctcgtggg	acaccagcca	tgccattcca	accagggctg	cgccatngc	cggggacatt	540
ctcgtgggat	aagggaaggg	gtgccggatn	ggcacgtatc	agtcataaggc	cttggnccgc	600
agaagacagc	tttnaattta	ccccagg				627

<210> 1079

<211> 549

<212> DNA

<213> Unknown (H38g929 nucleotide)

<220>

<223> Synthetic construct

<400> 1079

gcagtggtaa	caacgcagag	taccgcccc	tatgtacttt	ttcttgggaa	acttgtctgt	60
gtttgacatg	ggtttctcct	cagtgcattg	tcccaaaatg	ctgctctacc	ttatggggct	120
gggccgactc	atctcctaca	aagactgtgt	ctgccagctt	ttcttcttcc	atttcctcgg	180
gagcattgag	tgcttcttgt	ttacgggtgat	ggcctatgac	cgcttcactg	ccatctgtta	240
tcctctgcga	tacacagtca	tcatgaacct	aaggatctgt	gtggccctgg	ctgtgggcac	300
atggctgtta	gggtgcattc	attccagtat	cttgacctcc	ctcaccttca	ccttgccaca	360
ctgtgtgccc	aatgaagtgg	atcacttctt	ctgtgacatt	ccagcactgt	tgcccttggc	420
ctgtgctgac	acatccttag	cccagagggt	gagcttcacc	aacgttggcc	tcatactct	480
ggctgcttct	tgctaaatct	tttatcctac	actagaatca	caaatatcta	tcttaagcat	540
tcgtacaac						549

<210> 1080

<211> 616

<212> DNA

<213> Unknown (H38g930 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(616)

<223> n = A,T,C or G

<400> 1080

gnnnnnnnt	tcattccatt	gggcccctcta	gatgcatgct	cgagcggccg	ccagtgtgat	60
ggatatctgc	agaattcgcc	cttggtgctt	agagtgtaaa	taaaaggggt	aacattggct	120
tagagggtgaa	gagtaaatac	ataggaagg	cgaattccag	cacactggcg	gccgttacta	180
gtggatccga	gctcgggtacc	aagcttgatg	catagcttga	gtattctaac	gcgtcaccta	240
aatagcttgg	cgtaatcatg	gtcatagctg	tttctgtgt	gaaattgtta	tccgctcaca	300
attccacaca	acatacgagc	cggaagcata	aagtgtaaag	cctgggggtgc	ctaattgagt	360
agctaactca	cattaattgc	gttgcgctca	ctgcccgcct	tccagtcggg	aaacctgtcg	420
tgccagctgc	attaatgaat	cggccaacgc	gcggggagag	gcgggttgcg	tattgggcgc	480
tcttcgctt	cctcgctcac	tgactcgctg	cgctcggtcg	ntcggctgcg	gcgagcggta	540
tcaagctcac	tcaaaggcgg	taatacgggt	atccacagaa	tcagggggat	acgcangaaa	600
gaacatgtga	gcaaat					616

<210> 1081

<211> 615

<212> DNA

<213> Unknown (H38g931 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1081

ngnnnnttna	ntcnangccn	ngngccctct	agatgcatgc	tcgagcggcc	gccagtgtga	60
tggatatctg	cagaattcgc	ccttccaatg	tatttacttc	tcagccagct	ctcccttatg	120
gacctgatgt	acatctccac	caccgtcccc	aagatggcgt	acaacttcct	gtccggccag	180
aaaggcatct	ccttctggg	atgtggtgtg	caaagcttct	tcttctgac	catggcgtgt	240
tctgaaggct	tactcctgac	ctccatggcc	tacgaccgtt	atttggccat	ctgccactct	300
ctctattatc	ctatccgcat	gagtaaaatg	atgtgtgtga	agatgattgg	aggctcttgg	360
acactgggg	ccatcaactc	cttggcacac	acagtctttg	cccttcatat	tccctactgc	420
aggtctaggg	ctattgacca	tttcttctgc	gatgtcccag	ccatgttgc	tcttgctgta	480
cagatacttg	ggtctatgaa	tatatggttt	ttgtaaggac	aaagcctctt	tcttcttttn	540
cctttcattg	gcatacttc	ttctgngggc	cgagtcctaa	ttgctggcta	tataatgcac	600
tcaaaggagg	ggagg					615

<210> 1082

<211> 628

<212> DNA

<213> Unknown (H38g932 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(628)

<223> n = A,T,C or G

<400> 1082

ngnnnnnat	ttnatgccnt	tnttgattcc	cnttnnnnnn	ncaagcagng	gtaacaacgc	60
agagtacgcc	ccctatgtat	ttcttcctaa	gatccaaata	ttaaaataaa	agacagtcac	120
cccaccacta	actaaagtag	tgtttccac	acttctctat	taagaagcat	gtgagatact	180
tgttacaac	ataacatcct	ggtcacccc	caaagccact	caatcaata	ctccagggaa	240
gggatctagg	aattcgtagg	tttaacgagt	gccccaaaat	gattattacc	tggtggagaa	300
tctaggcaac	aatgaattaa	ggaaagctct	ctaccatttg	gtactgggtac	cagggttgag	360
gatcacaggg	aagagggtaa	gcatacaga	ctagcagagc	tgccagaact	cgggctttca	420
aaagagaggt	gccaccctct	cccattgtcca	tgtaagtagc	aaacaaccct	ctcatgtaca	480

ctctgaggaa	caagggggcg	tactttctgtc	gtcttgagcg	tactgatggg	accagcttt	540
tgccccctta	gtgagggtta	attgcgcgct	tggcgtaatc	atgggcatag	ctgtttcctg	600
tgtgaaattg	ttatccgctc	acaattct				628

<210> 1083

<211> 613

<212> DNA

<213> Unknown (H38g933 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(613)

<223> n = A,T,C or G

<400> 1083

annncentng	gagctccaaa	gcagtggtaa	caacgcagag	tacgccccct	atgtacttac	60
ttttgttaag	tccaacctcc	atcctccttg	gccttttgat	tcaattgac	actccttcc	120
cctcaaaaaca	ccttggttcac	tcatecttcc	tcagtctcct	ttgtggattc	ttcctcattt	180
atttgacctc	ttgctgggtga	accctttcat	atacactctc	cgtaacaaaag	agggcgctact	240
tctgtcgtct	tgagcgnact	gatggnaccc	agcttttggt	cccttttagtg	agggntaatt	300
gcgcgcttgg	cgnaatcatg	gncatagctg	nttncctgng	gaaantgnta	tttcgntnac	360
aattncacac	aacatacnag	ccgggagcat	aaaggggnnaa	gncctggggg	gcctaataag	420
ggagcttact	cacaataatt	ggggtgngcc	cactggcccc	ttttcaggcg	ggaaaacctn	480
gcggggccag	ctggaataaa	tgaatcgggc	cacgcgccgg	ggaggagggc	gggttnngga	540
attgggcgct	ttttccnttt	ctnggttaat	ggactnggtn	ggcnnngtcc	gttcgggttg	600
gggggancgg	nnt					613

<210> 1084

<211> 886

<212> DNA

<213> Unknown (H38g934 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(886)

<223> n = A,T,C or G

<400> 1084

ggteccntcg	ngtatnctt	naccctctga	tgtgtctcga	gcggccggca	gggtgatgga	60
tatctgcaga	attcgccctt	ctgttacgca	ggaatatata	aaggggttac	tgaggaataa	120
ataaatgggt	tactgaggaa	taaataaatg	ggttactgag	gaacaaatac	ataggggttg	180
aagaactgta	aaatagaaaa	aggaccttnt	gctgtctctc	aggatggcgg	nacttagggg	240
ccatgtacat	gacgatgnng	ctgccnntna	agagtccac	tnctcancng	cctcagcccg	300
ncttttttct	cacnnccnt	ntttntctnc	cctcttnnnc	tcttttcttc	ctattccccc	360
cccttccnct	cctccctttt	gentnaccat	tgncctnat	ccctttaatt	cnntcnntcn	420
tctccctctc	attccttcnn	tnctcgnctt	cantctctnc	ctctttctcc	ccnctttct	480
ctctctctct	cttctctctg	tcatectnct	tcntctctct	ncctanttcc	ctctancctt	540
ntcttattnc	tcctctatnc	cctctcatct	caentctctn	cctctctctn	tacttnnctc	600
nnctcttccn	ctccgtctnc	cnctttctct	tcntnacgcc	acccctcnnn	cntnctctct	660
ntctctctct	cactctctcc	tctccctnct	cntcaatntt	ctccnctctc	acntcctatn	720
ctcnctctct	nncttnactt	tgtaacgctc	tcctctctct	ctctacgcac	nttttatctc	780
ttatctctcn	catcnccctc	ntttctncac	ncattnactt	ctttctctnc	atactntatn	840
ctcctntcnn	cttanatcnc	ctcccttctn	tnancnntc	actgcn		886

<210> 1085

<211> 125

<212> PRT

<213> Unknown (H38g1 protein)

<220>

<223> Synthetic construct

<400> 1085

```

Leu Ala Cys Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Pro Asp
 1          5          10          15
Val Gly Leu Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr
          20          25          30
Thr Arg Ile Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg
          35          40          45
Arg Arg Ala Phe Ser Thr Cys Ser Ala His Leu Ile Ala Ile Leu Cys
          50          55          60
Ala Tyr Gly Pro Ile Ile Thr Val Tyr Leu Gln Pro Thr Pro Asn Pro
          65          70          75          80
Met Leu Gly Thr Val Val Gln Ile Leu Met Asn Leu Val Gly Pro Met
          85          90          95
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Thr Ala
          100          105          110
Leu Lys Thr Ile Leu His Arg Thr Gly His Val Pro Glu
          115          120          125

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<210> 1086

<211> 322

<212> PRT

<213> Unknown (H38g2 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1086

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His Thr Glu Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
          20          25          30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Met Arg Asn Leu Leu Ser
          35          40          45
Ile Leu Thr Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe
          50          55          60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
          65          70          75          80
Val Pro Thr Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Pro
          85          90          95
His Ala Gly Cys Leu Thr Gln Met Tyr Phe Leu Val Phe Phe Ala Cys
          100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
          115          120          125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
          145          150          155          160
Leu His Ser Xaa Ile Val Leu Gln Phe Asn Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
          180          185          190
Ser Asp Ser Val Ile Asn Ile Ile Phe Ile Tyr Phe Asp Ser Thr Met

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      195              200              205
Phe Ala Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
  210              215              220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ser
  225              230              235              240
Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly
      245              250              255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
      260              265              270
Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
  275              280              285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asn Ile Gln Ser Ala Leu
  290              295              300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Arg
  305              310              315              320
Phe Ser

```

<210> 1087

<211> 312

<212> PRT

<213> Unknown (H38g3 protein)

<220>

<223> Synthetic construct

<400> 1087

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
  1              5              10              15
Ile Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
      20              25              30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
      35              40              45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50              55              60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
      65              70              75              80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
      85              90              95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
      100              105              110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys Cys
      115              120              125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
      130              135              140
Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
      145              150              155              160
Phe Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
      165              170              175
Leu Phe Cys Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr
      180              185              190
His Ile Ile His Thr Ala Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
      195              200              205
Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
      210              215              220
Ile Leu Gln Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr
      225              230              235              240
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
      245              250              255
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
      260              265              270

```

Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Arg Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu
 290 295 300
 Trp Arg Pro Phe Gln Arg Pro Lys
 305 310

<210> 1088

<211> 305

<212> PRT

<213> Unknown (H38g4 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(305)

<223> Xaa = Any Amino Acid

<400> 1088

Met Arg Asn His Thr Leu Leu Asn Glu Phe Ile Leu Arg Gly Ile Pro
 1 5 10 15
 Gln Thr Glu Gly Leu Glu Ala Val Leu Cys Ala Val Phe Ser Phe Ile
 20 25 30
 Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Ile Ala Ile Phe
 35 40 45
 Leu His Thr Pro Met Tyr Phe Leu Gly Arg Leu Ser Thr Phe Asp
 50 55 60
 Ile Leu Phe Pro Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu Ser
 65 70 75 80
 Gly Gln Ser Pro Val Ile Ser Phe Lys Gly Cys Ala Ser Gln Leu Phe
 85 90 95
 Phe Tyr Gln Leu Leu Gly Ser Ala Glu Gly Cys Leu Tyr Ser Val Met
 100 105 110
 Ser Tyr Asp Arg Phe Val Ala Ile His His Thr Leu Arg Tyr Met Leu
 115 120 125
 Ile Met Lys Pro Gly Val Cys Val Gly Leu Val Val Val Pro Trp Leu
 130 135 140
 Val Gly Cys Leu His Ala Thr Ile Leu Thr Ser Phe Thr Phe Gln Leu
 145 150 155 160
 Ser Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile Pro
 165 170 175
 Ala Val Leu Pro Leu Ala Cys Thr Asp Ser Ala Leu Ala Gln Arg Val
 180 185 190
 Gly Ser Ile Asn Val Gly Phe Leu Ala Leu Thr Leu Leu Ile Ser Val
 195 200 205
 Cys Val Cys Tyr Thr Ser Ile Gly Ile Ala Ile Leu Arg Ile Arg Ser
 210 215 220
 Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala His Leu Val
 225 230 235 240
 Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Ile Ile Tyr Leu Lys Ser
 245 250 255
 Thr Pro Asn Pro Leu Leu Gly Gly Gln Val Gln Ile Leu Asn Asn Val
 260 265 270
 Val Ser Pro Met Leu Asn Ser Leu Ile Tyr Ser Leu Arg Asn Lys Glu
 275 280 285
 Val Lys Arg Ser Leu Lys Arg Val Phe Xaa Asn Val Leu Leu Thr Val
 290 295 300
 Cys
 305

<210> 1089
 <211> 317
 <212> PRT
 <213> Unknown (H38g5 protein)

<220>
 <223> Synthetic construct

<400> 1089

```

Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu
      20           25           30
Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
      35           40           45
Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50           55           60
Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
      65           70           75           80
Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
      85           90           95
Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
      100          105          110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
      115          120          125
Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
      130          135          140
Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr
      145          150          155          160
Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His
      165          170          175
Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
      180          185          190
Ser Ser Asn Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met
      195          200          205
Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
      210          215          220
Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr
      225          230          235          240
Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile
      245          250          255
Phe Thr Tyr Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys
      260          265          270
Leu Phe Ser Val Phe Tyr Ala Ile Leu Thr Pro Met Leu Asn Pro Met
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu
      290          295          300
Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr
      305          310          315

```

<210> 1090
 <211> 342
 <212> PRT
 <213> Unknown (H38g6 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(342)
 <223> Xaa = Any Amino Acid

<400> 1090
 Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Ile Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Glu Lys Leu Leu Ile Ile Met
 35 40 45
 Ala Val Ser Pro Asp Phe His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100 105 110
 Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile
 115 120 125
 Cys His Pro Pro Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly
 130 135 140
 Phe Gln Asp Leu Leu Ser Leu Phe Phe Phe Ser Phe Phe Phe Phe
 145 150 155 160
 Leu Arg Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met
 165 170 175
 Thr Cys Phe Lys Asp Val Glu Ile Ser Asn Val Phe Trp Glu Pro Ser
 180 185 190
 Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn
 195 200 205
 Leu Tyr Phe Pro Ala Ala Val Leu Gly Phe Leu Pro Ile Ser Gly Thr
 210 215 220
 Leu Phe Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser
 225 230 235 240
 Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser
 245 250 255
 Ala Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu Gly Ser
 260 265 270
 Asp Val Ser Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met Tyr
 275 280 285
 Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn
 290 295 300
 Arg Asp Met Lys Ser Val Leu Arg Arg Pro His Ser Ser Thr Val Xaa
 305 310 315 320
 Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Gly Trp Val Lys
 325 330 335
 Lys Gly Ser Lys Val Lys
 340

<210> 1091

<211> 313

<212> PRT

<213> Unknown (H38g7 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1091

Met Val Lys Gly Asn His Ser Thr Val Thr Glu Phe Asn Leu Ala Gly


```

1           5           10           15
Leu Thr Asp Lys Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
20           25           30
Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Ser Met Ile Thr Leu
35           40           45
Ile Gly Phe Ser Ser His Leu His Thr Pro Met Tyr His Phe Leu Ser
50           55           60
Ser Leu Ser Phe Ile Asp Leu Cys Gln Ser Ser Val Ile Thr Pro Lys
65           70           75           80
Met Leu Val Asn Phe Val Ser Glu Arg Asn Ile Ile Ser Tyr Pro Ala
85           90           95
Cys Met Thr Gln Leu Tyr Phe Phe Leu Val Leu Val Ile Ser Glu Cys
100          105          110
His Met Leu Ala Ala Met Ala Tyr Asp His Tyr Ile Ala Ile Cys Asn
115          120          125
Pro Leu Leu Tyr His Val Ala Met Ser Tyr Gln Val Cys Ser Trp Met
130          135          140
Val Val Glu Val Tyr Phe Met Gly Phe Ile Gly Ala Ser Ala His Thr
145          150          155          160
Val Cys Met Leu Arg Val Leu Phe Cys Lys Ala Asp Val Ile Asn His
165          170          175
Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu Ser Arg Ser Ser Ile
180          185          190
Ser Ile Asn Glu Ile Val Val Cys Ala Cys Ser Ala Phe Asn Ile Leu
195          200          205
Phe Arg Ser Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Val Ala Ser
210          215          220
Ile Leu Cys Ile Arg Ser Thr Glu Gly Arg Ser Lys Thr Phe Ser Thr
225          230          235          240
Cys Ser Ser His Ile Ser Ala Val Ser Val Phe Phe Gly Ser Ala Ala
245          250          255
Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys
260          265          270
Val Ser Ser Val Phe Tyr Ala Thr Val Val Pro Met Leu Asn Pro Leu
275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Ile Lys Phe
290          295          300
Leu Glu Lys Arg Ser Phe Leu Xaa Lys
305          310

```

<210> 1092

<211> 328

<212> PRT

<213> Unknown (H38g8 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1092

```

Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val Ser Glu Phe Ile Leu
1           5           10           15
Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val Ser Leu Phe Ala Leu
20           25           30
Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly Asn Thr Leu Ile Leu
35           40           45
Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro Met Tyr Phe Ser
50           55           60

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Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr Thr Lys Ser Ile Val
65          70          75          80
Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg Lys Ser Ile Pro Phe
85          90          95
Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser Leu Ala Leu Cys Gly Ser
100        105        110
Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Tyr Val Ala Val
115        120        125
Cys His Pro Leu His Tyr Thr Val Ile Met His Gly Gly Leu Cys Leu
130        135        140
Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe Ser Asn Ser Leu Met
145        150        155        160
Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser Arg Phe Ile Asn His
165        170        175
Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu Ala Cys Val Asp Val
180        185        190
Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly Phe Leu Val Ile Leu
195        200        205
Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala Cys Ile Val Ala Thr
210        215        220
Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys Lys Ala Phe Gly Thr
225        230        235        240
Cys Ala Ser His Leu Ile Val Val Cys Met Cys Phe Gly Ala Thr Ile
245        250        255
Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser Ala Glu Glu Glu Lys
260        265        270
Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro Met Leu Asn Pro Leu
275        280        285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala Ala Val Arg Lys Val
290        295        300
Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu Arg Thr Ser Cys Tyr
305        310        315        320
Leu Ser Ser Lys Pro Lys Arg Arg
325

```

<210> 1093

<211> 318

<212> PRT

<213> Unknown (H38g9 protein)

<220>

<223> Synthetic construct

<400> 1093

```

Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly
1          5          10          15
Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala
20        25        30
Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala
35        40        45
Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg
50        55        60
Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln
65        70        75        80
Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly
85        90        95
Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys
100       105       110
Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys
115       120       125
Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met

```

```

      130              135              140
Ile Ile Met Ile Trp Ser Ile Ser Leu Ala Asn Ser Val Val Leu Cys
145              150              155              160
Thr Leu Thr Leu Asn Leu Pro Thr Cys Gly Asn Asn Ile Leu Asp His
      165              170              175
Phe Leu Cys Glu Leu Pro Ala Leu Val Lys Ile Ala Cys Val Asp Thr
      180              185              190
Thr Thr Val Glu Met Ser Val Phe Ala Leu Gly Ile Ile Ile Val Leu
      195              200              205
Thr Pro Leu Ile Leu Ile Leu Ile Ser Tyr Gly Tyr Ile Ala Lys Ala
      210              215              220
Val Leu Arg Thr Lys Ser Lys Ala Ser Gln Arg Lys Ala Met Asn Thr
225              230              235              240
Cys Gly Ser His Leu Thr Val Val Ser Met Phe Tyr Gly Thr Ile Ile
      245              250              255
Tyr Met Tyr Leu Gln Pro Gly Asn Arg Ala Ser Lys Asp Gln Gly Lys
      260              265              270
Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro Leu
      275              280              285
Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Leu
      290              295              300
Met Arg Phe His His Lys Ser Thr Lys Ile Lys Arg Asn Cys
305              310              315

```

<210> 1094

<211> 324

<212> PRT

<213> Unknown (H38g10 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1094

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Ser Val Leu Ala Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Thr Tyr Leu Ala Thr Val Leu Arg Asn Val Leu Asn
      35      40      45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
      50      55      60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
      65      70      75      80
Val Pro Lys Met Ile Val Asp Met Gln Ser Tyr Ser Arg Val Ile Ser
      85      90      95
His Glu Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100      105      110
Ile Glu Gly Met Ile Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115      120      125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130      135      140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
      145      150      155      160
Leu His Ser Xaa Ile Val Leu Gln Phe Asn Ile Ile Lys Asn Val Glu
      165      170      175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Phe Leu Lys Leu Ala Cys
      180      185      190

```

```

Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser Thr Met
    195                200                205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Phe Ser Xaa Phe Lys Ile
    210                215                220
Val Thr Phe Ile Leu Trp Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
    225                230                235                240
Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
    245                250                255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
    260                265                270
Asn Gly Val Val Ala Ser Met Met Tyr Ala Val Val Thr Pro Met Leu
    275                280                285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
    290                295                300
Arg Arg Leu Leu Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
    305                310                315                320
Phe Phe Leu Cys

```

<210> 1095

<211> 311

<212> PRT

<213> Unknown (H38g11 protein)

<220>

<223> Synthetic construct

<400> 1095

```

Met Glu Leu Glu Asn Gln Thr Arg Val Thr Lys Phe Ile Leu Val Gly
  1          5          10          15
Phe Pro Gly Ser Leu Ser Met Arg Ala Ala Met Phe Leu Ile Phe Leu
    20          25          30
Val Ala Tyr Ile Leu Thr Val Ala Glu Asn Val Ile Ile Ile Leu Leu
    35          40          45
Val Leu Gln Asn Arg Pro Leu His Lys Pro Met Tyr Phe Phe Leu Ala
    50          55          60
Asn Leu Ser Phe Leu Glu Thr Trp Tyr Ile Ser Val Thr Val Pro Lys
    65          70          75          80
Leu Leu Phe Ser Phe Trp Ser Val Asn Asn Ser Ile Ser Phe Thr Leu
    85          90          95
Cys Met Ile Gln Leu Tyr Phe Phe Ile Ala Leu Met Cys Thr Glu Cys
    100         105         110
Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
    115         120         125
Pro Leu His Tyr Pro Thr Ile Met Ser His Gly Leu Cys Phe Arg Leu
    130         135         140
Ala Leu Gly Ser Trp Ala Ile Gly Phe Gly Ile Ser Leu Ala Lys Ile
    145         150         155         160
Tyr Phe Ile Ser Cys Leu Ser Phe Cys Gly Pro Asn Val Ile Asn His
    165         170         175
Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ser Cys Thr Asp Met
    180         185         190
Ser Ile Thr Glu Leu Val Asp Phe Ile Leu Ala Leu Val Ile Phe Leu
    195         200         205
Phe Pro Leu Phe Ile Thr Val Leu Ser Tyr Gly Cys Ile Leu Ala Thr
    210         215         220
Ile Leu Cys Met Pro Thr Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala
    225         230         235         240
Ser His Leu Val Val Val Thr Ile Phe Tyr Ser Ala Ile Ile Phe Met
    245         250         255
Tyr Ala Arg Pro Arg Val Ile His Ala Phe Asn Met Asn Lys Ile Ile

```

```

                260                265                270
Ser Ile Phe Tyr Ala Ile Val Thr Pro Ser Leu Asn Pro Phe Ile Tyr
                275                280                285
Cys Leu Arg Asn Arg Glu Val Lys Glu Ala Leu Lys Lys Leu Ala Tyr
                290                295                300
Cys Gln Ala Ser Arg Ser Asp
305                310

```

<210> 1096
 <211> 313
 <212> PRT
 <213> Unknown (H38g12 protein)

<220>
 <223> Synthetic construct

```

<400> 1096
Met Glu Gln Val Asn Lys Thr Val Val Arg Glu Phe Val Val Leu Gly
 1          5          10          15
Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu
 20          25          30
Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ile Ser Thr
 35          40          45
Ile Val Leu Asp Arg Ala Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50          55          60
Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Val Ile Val Pro Lys
 65          70          75          80
Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly
 85          90          95
Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Phe Gly Ser Ser His Ser
100          105          110
Phe Leu Leu Ala Ala Met Gly Tyr Asp Arg Tyr Met Ala Ile Cys Asn
115          120          125
Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu
130          135          140
Met Ala Ala Ala Cys Ala Cys Gly Phe Thr Val Ser Leu Val Thr Thr
145          150          155          160
Ser Leu Val Phe His Leu Pro Phe His Ser Ser Asn Gln Leu His His
165          170          175
Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu Ala Ser Gln His Ser
180          185          190
Gly Phe Ser Gln Leu Val Ile Phe Met Leu Gly Val Phe Ala Leu Val
195          200          205
Ile Pro Leu Leu Leu Ile Leu Val Ser Tyr Ile Arg Ile Ile Ser Ala
210          215          220
Ile Leu Lys Ile Pro Ser Ser Val Gly Arg Tyr Lys Thr Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Ile Val Val Thr Val His Tyr Ser Cys Ala Ser
245          250          255
Phe Ile Tyr Leu Arg Pro Lys Thr Asn Tyr Thr Ser Ser Gln Asp Thr
260          265          270
Leu Ile Ser Val Ser Tyr Thr Ile Leu Thr Pro Leu Phe Asn Pro Met
275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Phe Lys Ser Ala Leu Arg Arg Thr
290          295          300
Ile Gly Gln Thr Phe Tyr Pro Leu Ser
305          310

```

<210> 1097
 <211> 318
 <212> PRT

<213> Unknown (H38g13 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1097

Cys	Val	Asp	Ser	Ser	Leu	Lys	Xaa	Glu	Ile	Thr	Gln	Xaa	Cys	Leu	Ser
1				5					10					15	
Leu	Leu	Leu	Xaa	Met	Ala	Glu	Gly	Trp	Arg	Leu	Tyr	Phe	Ile	Ile	Leu
			20					25					30		
Ile	Ile	Ser	Tyr	Lys	Phe	Cys	Thr	Leu	Leu	Gly	Asn	Val	Ile	Phe	Arg
		35					40					45			
Thr	Leu	Val	Cys	Ser	Leu	Gly	Phe	His	Thr	Ser	Cys	Met	Tyr	Phe	Phe
		50				55					60				
Pro	Xaa	Lys	Ile	Ser	Leu	Xaa	Leu	Ala	Xaa	Val	Cys	His	Ser	Ile	Ile
65					70					75					80
Ala	Leu	Pro	Ser	Thr	Gln	Lys	Xaa	Ala	Ile	Asn	Val	Gln	Gly	Ala	Ala
				85					90					95	
Val	His	Val	Phe	Ser	Phe	Pro	Cys	Leu	Tyr	Cys	Pro	Glu	Ile	Phe	Leu
			100					105					110		
His	Ser	Leu	Thr	Gln	Cys	His	Pro	Phe	Ile	Ala	Ile	Gly	Tyr	Pro	Leu
		115					120					125			
Gln	Gly	Met	His	Thr	Ile	Thr	His	Lys	Leu	Tyr	Ile	Leu	Leu	Thr	Thr
		130				135					140				
Gly	Pro	Trp	Arg	Gly	Cys	Xaa	Leu	His	Val	Asn	Leu	Leu	Thr	Ala	Ile
145					150					155					160
Leu	Gly	Ser	Tyr	Pro	Asn	Pro	Val	Pro	Thr	Lys	Leu	Trp	Leu	Ser	Phe
				165					170					175	
Pro	Ser	Ile	Pro	Glu	Val	Lys	Leu	Xaa	Pro	Met	Gln	Ala	Tyr	Thr	Lys
			180					185					190		
Pro	Tyr	Ala	Gly	Leu	Ser	Leu	Cys	Leu	Ser	Leu	Ser	Leu	Ser	Leu	Ser
		195					200					205			
Phe	Ser	Leu	Phe	Ser	Ile	Ile	Ser	Ile	Ser	Tyr	Ile	Cys	Asn	Glu	Ile
		210				215					220				
Asp	Ile	Pro	Lys	Ile	Ile	Ser	Ala	Asp	Ser	Val	His	Gly	Ala	Phe	Ser
225					230					235					240
Thr	Cys	Leu	Ala	His	Leu	Phe	Ala	Phe	Ser	Thr	Cys	Ile	Ala	Gln	Pro
				245						250				255	
Ala	Val	Cys	Asn	Ser	Leu	Trp	Pro	Trp	Thr	Glu	Ala	Gln	Thr	Glu	Ser
			260					265					270		
Ser	Arg	Asp	Ser	Val	Ile	Gln	Arg	Pro	Asn	Leu	Cys	Val	Thr	Ile	Ser
		275					280					285			
Leu	Asn	Ser	Leu	Ile	Ser	Ser	Leu	Arg	Asn	Glu	Ser	Val	Lys	Gln	Ala
		290				295					300				
Ser	His	Lys	Ile	Phe	Lys	Glu	Gln	Thr	Leu	Phe	Met	Lys	Ile		
305					310					315					

<210> 1098

<211> 333

<212> PRT

<213> Unknown (H38g14 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1098

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1          5          10          15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser
          20          25          30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
          35          40          45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
65          70          75          80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
          85          90          95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
          100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
          115          120          125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
130          135          140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
145          150          155          160
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
          165          170          175
Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
          195          200          205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr
210          215          220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
225          230          235          240
Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
          245          250          255
Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
          260          265          270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
          275          280          285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
290          295          300
Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
305          310          315          320
Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
          325          330

```

<210> 1099

<211> 322

<212> PRT

<213> Unknown (H38g15 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1099

```

His Thr Gly Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15

```

Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Thr Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr L u Val Thr Val Leu Arg Asn Leu Leu Ser
 35 40 45
 Il Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Xaa Ala Thr
 65 70 75 80
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Ala Val Cys Leu Ile Gln Met Ser Leu Leu Val Leu Phe Ala Cys
 100 105 110
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
 115 120 125
 Ile Cys Cys Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130 135 140
 Val Phe Phe Val Leu Val Ser Phe Leu Leu Ser Leu Leu Asp Ser Gln
 145 150 155 160
 Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
 165 170 175
 Ile Ser Asn Ser Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys
 180 185 190
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
 210 215 220
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
 245 250 255
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
 260 265 270
 Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
 275 280 285
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
 290 295 300
 Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Arg
 305 310 315 320
 Phe Ser

<210> 1100

<211> 279

<212> PRT

<213> Unknown (H38g16 protein)

<220>

<223> Synthetic construct

<400> 1100

Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile
 1 5 10 15
 Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 20 25 30
 Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu
 35 40 45
 Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu
 50 55 60
 Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu
 65 70 75 80
 Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu


```

      85      90      95
His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Thr
      100      105      110
Gly Ser Trp Val Val Ala Asn Ser Asn Ala Leu Leu His Thr Leu Leu
      115      120      125
Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His Ile Phe
      130      135      140
Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu
      145      150      155      160
Ser Glu Val Met Ile Leu Thr Glu Ala Ala Leu Val Thr Ile Thr Pro
      165      170      175
Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr Cys Val Val Leu
      180      185      190
Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly
      195      200      205
Ser His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr Ile Met Ser Pro
      210      215      220
Tyr Phe Arg Thr Ser Ser Ser His Ser Ala Gln Arg Asp Ile Ala Ala
      225      230      235      240
Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn Pro Leu Ile Tyr
      245      250      255
Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val Lys Val Val Ala
      260      265      270
Val Lys Phe Phe Ser Val Gln
      275

```

<210> 1101

<211> 257

<212> PRT

<213> Unknown (H38gl7 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(257)

<223> Xaa = Any Amino Acid

<400> 1101

```

Phe Ile Leu Trp Gly Phe Phe Asp His Pro Xaa Pro Glu Met Phe Leu
  1           5           10           15
Phe Ile Met Gly Leu Val Gly Leu Ser Leu His Thr Gly Gly Gln His
      20           25           30
Leu Asn Tyr Cys Gly Thr Gln Gly Ile Phe Xaa Gly Ser Thr Lys Cys
      35           40           45
Ile Ile Leu Ala Val Thr Ser Leu Asp Pro Tyr Ile Ala Ile Cys Lys
      50           55           60
His Leu Arg Tyr Pro Ala Ile Met His Gln Gln Leu Cys Val Leu Leu
      65           70           75           80
Val Ala Met Ala Trp Leu Ser Ser Leu Ala Asn Ser Leu Gln Ser Ser
      85           90           95
Leu Ala Val Gln Leu Pro Leu Gly Gly Asn Lys Val Asp Asp Phe Leu
      100           105           110
Cys Glu Val Ser Ala Met Ile Lys Ile Ser Arg Phe Asp Thr Thr Phe
      115           120           125
Asn Val Ser Met Leu Ser Ile Val Arg Ile Phe Xaa Ser Leu Val Leu
      130           135           140
Xaa Ser Ile Ile Phe Ala Tyr Cys Gly Phe Ile Val Ala Thr Val Leu
      145           150           155           160
Arg Ile Gln Ser Ser Gly Gly Lys Lys Glu Val Phe Asn Thr Cys Gly
      165           170           175

```

Ser His Ile Val Ser Leu Leu Tyr Gly Pro Val Ile Ser Met Tyr Val
 180 185 190
 Gln Pro Ser Ala Asn Ser Gln Asp Lys Asn Lys Phe Met Ser Leu Phe
 195 200 205
 Tyr Ser Leu Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Thr Leu Ser
 210 215 220
 Asn Arg Asp Ile Lys Gly Ala Met Arg Arg Leu Leu Val Phe Leu Tyr
 225 230 235 240
 His Gln Glu Glu Asn Lys Ser Asn Tyr Cys Leu Tyr Ser Thr Phe Phe
 245 250 255
 Ile

<210> 1102

<211> 334

<212> PRT

<213> Unknown (H38g18 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 1102

Ser Thr Asp Pro Gln Asn Val Thr Asp Val Ser Arg Phe Leu Leu Leu
 1 5 10 15
 Lys Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Pro Asp Ser His Leu His Thr Ser Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro
 65 70 75 80
 Lys Met Val Val Asp Ile Gln Ser His Arg Val Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu
 100 105 110
 Asn Met Leu Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys
 115 120 125
 His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe
 130 135 140
 Leu Leu Leu Leu Ser Phe Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu
 145 150 155 160
 His Asn Met Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile
 165 170 175
 Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys
 180 185 190
 Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Val Phe
 195 200 205
 Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val
 210 215 220
 Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Pro Cys
 225 230 235 240
 Ser Thr Cys Gly Ser His Leu Ser Val Phe Cys Xaa Phe Tyr Gly Thr
 245 250 255
 Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys
 260 265 270
 Ala Ala Val Ala Ser Leu Met Tyr Lys Met Val Thr Pro Met Leu Asn

275 280 285
 Pro Ser Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu Arg
 290 295 300
 Gln Pro His Gly Ser Thr Val Xaa Ser Gln Asp Leu Leu Ile Cys Ser
 305 310 315 320
 Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
 325 330

<210> 1103

<211> 333

<212> PRT

<213> Unknown (H38g19 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1103

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1 5 10 15
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35 40 45
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
 130 135 140
 Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
 145 150 155 160
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
 195 200 205
 Gly Thr Phe Phe Ile Leu Val Ile Ser Tyr Ile Phe Ile Leu Phe Thr
 210 215 220
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
 245 250 255
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
 290 295 300
 Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
 305 310 315 320

<400> 1104																
Asp 1	Thr	Asp	Pro	Gln 5	Ser	Leu	Thr	Asp	Val 10	Ser	Ile	Phe	Leu	Leu 15	Leu	
Glu	Leu	Ser	Glu	Asp 20	Pro	Glu	Leu	Gln 25	Pro	Val	Leu	Ala	Gly 30	Leu	Phe	
Leu	Ser	Met 35	Cys	Leu	Val	Thr	Val 40	Leu	Arg	Asn	Leu	Leu 45	Ile	Ile	Leu	
Ala	Ile 50	Ser	Pro	Asp	Ser	His 55	Leu	His	Thr	Pro	Met 60	Tyr	Phe	Phe	Leu	
Ser 65	Asn	Leu	Ser	Phe 70	Pro	Asp	Ser	Arg	Phe 75	Thr	Ser	Thr	Thr	Val	Pro 80	
Lys	Met	Ile	Val	Asp 85	Ile	Gln	Ser	His	Ser 90	Arg	Val	Ile	Ser	Tyr 95	Ala	
Gly	Cys	Leu	Thr 100	Gln	Met	Ser	Leu	Phe 105	Ala	Ile	Phe	Gly	Asp 110	Met	Glu	
Glu	Asn	Met 115	Phe	Leu	Ser	Val	Val 120	Ala	Tyr	Asp	Arg	Phe	Val 125	Ala	Ile	
Cys	His 130	Pro	Leu	Tyr	Arg	Ser	Ala 135	Ile	Leu	Asn	Pro 140	Cys	Phe	Cys	Gly	
Phe 145	Leu	Asp	Ser	Leu	Ser	Leu	Phe 150	Phe	Phe	Phe 155	Phe	Phe	Leu	Ser	Leu 160	
Leu	Asp	Ser	Gln	Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe 175	
Lys	Asp	Val	Glu	Ile 180	Pro	Asn	Phe	Phe 185	Trp	Glu	Pro	Ser	Gln	Leu	Pro 190	
His	Leu	Ala 195	Cys	Cys	Asp	Ile	Phe 200	Thr	Arg	Asn	Ile	Asn 205	Leu	Tyr	Phe	
Pro	Ala	Ala 210	Ile	Phe	Gly	Phe	Leu 215	Pro	Ile	Ser	Gly	Thr 220	Leu	Phe	Ser	
Tyr 225	Tyr	Lys	Ile	Val	Ser	Phe	Ile 230	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly 240	
Lys	Tyr	Lys	Ala	Phe 245	Ser	Ala	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Tyr 255	
Xaa	Val	Tyr	Gly	Thr 260	Gly	Phe	Gly	Gly	Tyr	Leu	Ser	Ser	Asp	Val	Ser 270	
Ser	Ser	Pro 275	Arg	Lys	Gly	Ala	Val 280	Ala	Ser	Val	Met	Tyr	Thr	Val	Val 285	
Thr	Pro	Met 290	Leu	Asn	Pro	Phe	Ile 295	Tyr	Ser	Leu	Arg	Asn	Gly	Asp	Ile 300	
Lys	Ser	Val	Leu	Arg	Gln	Pro	His 310	Gly	Ser	Thr	Val	Xaa	Ser	Gln	Tyr 320	
Leu	Leu	Ile	Cys	Ser	Ile	Pro	Phe	Val	Val	Trp	Val	Lys	Lys	Gly	Ser 335	
Lys Val Lys																

<210> 1105
 <211> 314
 <212> PRT
 <213> Unknown (H38g21 protein)

<220>
 <223> Synthetic construct

<400> 1105
 Met Glu Thr Arg Lys Tyr Ser Ala Met Thr Glu Phe Phe Leu Val Gly
 1 5 10 15
 Leu Ser Gln Tyr Pro Glu Leu Gln Leu Phe Leu Phe Leu Cys Leu
 20 25 30
 Ile Met Tyr Met Ile Ile Leu Leu Gly Asn Ser Leu Leu Ile Ile Ile
 35 40 45
 Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ser Ile Pro Pro
 65 70 75 80
 Met Leu Ile Ile Phe Met Ser Glu Arg Lys Ser Ile Ser Phe Ile Gly
 85 90 95
 Cys Ala Leu Gln Met Val Val Ser Leu Gly Leu Gly Ser Thr Glu Cys
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp His Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Ser Ile Ile Met Asn Gly Val Leu Tyr Val Gln Met
 130 135 140
 Ala Ala Trp Ser Trp Ile Ile Gly Cys Leu Thr Ser Leu Leu Gln Thr
 145 150 155 160
 Val Leu Thr Met Met Leu Pro Phe Cys Gly Asn Asn Val Ile Asp His
 165 170 175
 Ile Thr Cys Glu Ile Leu Ala Leu Leu Lys Leu Val Cys Ser Asp Ile
 180 185 190
 Thr Ile Asn Val Leu Ile Met Thr Val Thr Asn Ile Val Ser Leu Val
 195 200 205
 Ile Leu Leu Leu Leu Ile Phe Ile Ser Tyr Val Phe Ile Leu Ser Ser
 210 215 220
 Ile Leu Arg Ile Asn Cys Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Ser Ile Val Val Ile Leu Phe Tyr Gly Ser Ala Leu
 245 250 255
 Phe Met Tyr Met Lys Pro Lys Ser Lys Asn Thr Asn Thr Ser Asp Glu
 260 265 270
 Ile Ile Gly Leu Ser Tyr Gly Val Val Ser Pro Met Leu Asn Pro Ile
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Val Lys Lys Val
 290 295 300
 Leu Ser Arg His Leu His Leu Leu Lys Met
 305 310

<210> 1106
 <211> 319
 <212> PRT
 <213> Unknown (H38g22 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(319)
 <223> Xaa = Any Amino Acid

<400> 1106

```

Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr
1      5      10      15
Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu
20      25      30
Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Val Val Thr Ile Thr
35      40      45
Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu
50      55      60
Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ser Ala Pro Lys Leu Ile
65      70      75      80
Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met
85      90      95
Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu
100     105     110
Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu
115     120     125
His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val
130     135     140
Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe
145     150     155     160
Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
165     170     175
Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr
180     185     190
Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
195     200     205
Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys
210     215     220
Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser
225     230     235     240
His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
245     250     255
Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Ala Val Phe
260     265     270
Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
275     280     285
Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val
290     295     300
Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg
305     310     315

```

<210> 1107

<211> 311

<212> PRT

<213> Unknown (H38g23 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1107

```

Met Arg Asn Phe Ser Val Val Ser Glu Phe Ile Leu Leu Gly Ile Pro
1      5      10      15
His Thr Glu Gly Leu Glu Thr Ile Leu Leu Val Leu Phe Leu Ser Phe
20      25      30
Tyr Ile Phe Thr Leu Met Gly Asn Leu Leu Ile Leu Leu Ala Ile Val

```

```

      35              40              45
Ser Ser Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Cys Lys Leu
  50              55              60
Ser Val Phe Asp Leu Phe Phe Pro Ser Val Ser Ser Pro Lys Met Leu
  65              70              75              80
Cys Tyr Leu Ser Gly Asn Ser Arg Ala Ile Ser Tyr Ala Gly Cys Ala
      85              90              95
Ser Gln Leu Phe Phe Tyr His Phe Leu Gly Cys Thr Glu Cys Phe Leu
      100              105              110
Tyr Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
      115              120              125
Arg Tyr Thr Ile Ile Met Ser His Arg Ala Cys Ile Ile Leu Ala Met
      130              135              140
Gly Thr Ser Phe Phe Gly Cys Ile Gln Ala Thr Phe Leu Thr Thr Leu
      145              150              155              160
Thr Phe Gln Leu Pro Tyr Cys Val Pro Asn Glu Val Asp Tyr Tyr Phe
      165              170              175
Cys Asp Ile Pro Val Met Leu Lys Leu Ala Cys Ala Asp Thr Ser Ala
      180              185              190
Leu Glu Met Val Gly Phe Ile Ser Val Gly Leu Met Pro Leu Ser Cys
      195              200              205
Phe Leu Leu Ile Leu Thr Ser Tyr Ser Gly Ile Val Phe Ser Ile Leu
      210              215              220
Xaa Ile Cys Ser Ala Glu Gly Arg Arg Arg Ala Phe Ser Thr Cys Ser
      225              230              235              240
Ala His Leu Thr Ala Ile Leu Leu Phe Tyr Met Pro Val Val Leu Ile
      245              250              255
Tyr Leu Arg Pro Thr His Ser Leu Trp Leu Asp Ala Thr Val Gln Ile
      260              265              270
Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
      275              280              285
Arg Asn Lys Glu Val Lys Leu Ser Leu Arg Lys Val Leu Tyr Gln Leu
      290              295              300
Gly Phe Leu Pro Glu Gln Leu
      305              310

```

<210> 1108

<211> 302

<212> PRT

<213> Unknown (H38g24 protein)

<220>

<223> Synthetic construct

<400> 1108

```

Met Asp Ile Pro Gln Asn Ile Thr Glu Phe Phe Met Leu Gly Leu Ser
  1              5              10              15
Gln Asn Ser Glu Val Gln Arg Val Leu Phe Val Val Phe Leu Leu Ile
      20              25              30
Tyr Val Val Thr Val Cys Gly Asn Met Leu Ile Val Val Thr Ile Thr
      35              40              45
Ser Ser Pro Thr Leu Ala Ser Pro Val Tyr Phe Phe Leu Ala Asn Leu
      50              55              60
Ser Phe Ile Asp Thr Phe Tyr Ser Ser Ser Met Ala Pro Lys Leu Ile
      65              70              75              80
Ala Asp Ser Leu Tyr Glu Gly Arg Thr Ile Ser Tyr Glu Cys Cys Met
      85              90              95
Ala Gln Leu Phe Gly Ala His Phe Leu Gly Gly Val Glu Ile Ile Leu
      100              105              110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115              120              125

```

```

His Asn Thr Thr Ile Met Thr Arg His Leu Cys Ala Met Leu Val Gly
  130                135                140
Val Ala Trp Leu Gly Gly Phe Leu His Ser Leu Val Gln Leu Leu Leu
 145                150                155                160
Val Leu Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe Ala
                165                170                175
Cys Asp Leu Tyr Pro Leu Leu Glu Val Ala Cys Thr Asn Thr Tyr Val
                180                185                190
Ile Gly Leu Leu Val Val Ala Asn Ser Gly Leu Ile Cys Leu Leu Asn
                195                200                205
Phe Leu Met Leu Ala Ala Ser Tyr Ile Val Ile Leu Tyr Ser Leu Arg
 210                215                220
Ser His Ser Ala Asp Gly Arg Cys Lys Ala Leu Ser Thr Cys Gly Ala
 225                230                235                240
His Phe Ile Val Val Ala Leu Phe Phe Val Pro Cys Ile Phe Thr Tyr
                245                250                255
Val His Pro Phe Ser Thr Leu Pro Ile Asp Lys Asn Met Ala Leu Phe
                260                265                270
Tyr Gly Ile Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
                275                280                285
Asn Glu Glu Val Lys Asn Ala Met Arg Lys Leu Phe Thr Trp
 290                295                300

```

<210> 1109

<211> 266

<212> PRT

<213> Unknown (H38g25 protein)

<220>

<223> Synthetic construct

<400> 1109

```

Met Ile Thr Leu Ile Gly Leu Ser Ser His Leu His Thr Pro Met Tyr
  1                5                10                15
Tyr Phe Leu Ser Ser Leu Ser Phe Ile Asp Phe Cys His Ser Thr Val
                20                25                30
Ile Thr Pro Lys Met Leu Val Asn Phe Ala Thr Glu Lys Asn Ile Ile
 35                40                45
Ser Tyr Pro Glu Cys Met Ala Gln Leu Tyr Leu Phe Ser Ile Phe Ala
 50                55                60
Ile Ala Glu Cys His Met Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val
 65                70                75                80
Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His His
                85                90                95
Cys Phe Trp Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly Ser
 100                105                110
Thr Ile His Thr Ser Phe Met Leu Arg Leu Phe Leu Cys Lys Thr Asn
 115                120                125
Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Gly Leu Ser
 130                135                140
Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser Ala
 145                150                155                160
Phe Asn Ile Leu Met Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile Phe
                165                170                175
Ile Ile Ala Ser Ile Leu Arg Ile His Ser Thr Glu Gly Arg Ser Lys
                180                185                190
Ala Phe Ser Thr Cys Ser Ser His Ile Leu Ala Val Ala Val Phe Phe
 195                200                205
Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met
 210                215                220
Asp Gln Arg Lys Val Ser Ser Val Phe Tyr Thr Thr Ile Val Pro Met

```


225					230					235				240	
Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Leu	Ala
				245					250					255	
Val	Lys	Lys	Ile	Leu	His	Gln	Thr	Ala	Cys						
			260					265							

<210> 1110

<211> 318

<212> PRT

<213> Unknown (H38g26 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1) ... (318)

<223> Xaa = Any Amino Acid

<400> 1110

Met 1	Gly	Asn	Ser	Asn 5	Gln	Ser	Phe	Met	Thr 10	Glu	Phe	Val	Leu 15	Gly
Leu	Ser	Gly	Tyr 20	Pro	Glu	Leu	Glu	Ala 25	Ile	Tyr	Phe	Val	Leu 30	Val
Cys	Met	Tyr 35	Leu	Val	Ile	Leu	Leu 40	Gly	Asn	Gly	Val	Ile 45	Ile	Val
Ser	Val 50	Tyr	Asp	Thr	His	Leu 55	His	Thr	Pro	Met	Tyr 60	Phe	Phe	Ser
Asn 65	Leu	Ser	Phe	Leu	Asp 70	Ile	Cys	Tyr	Thr	Ser	Ser	Ser	Ile	Pro
Phe	Leu	Ser	Ser	Phe 85	Leu	Thr	Ser	Lys	Lys 90	Thr	Ile	Ser	Phe	Gly
Cys	Gly	Val	Gln 100	Met	Phe	Leu	Ser	Phe 105	Ala	Met	Gly	Ala	Thr 110	Cys
Val	Leu	Leu	Ser	Met	Met	Ala	Phe 120	Asp	Cys	Tyr	Val	Ala 125	Ile	Asn
Pro	Leu 130	Xaa	Tyr	Pro	Ile 135	Ile	Met	Ser	Lys	Ala	Ser	Tyr 140	Met	Met
Ala 145	Ala	Gly	Ser	Trp	Ile 150	Gly	Gly	Gly	Ile	Asn	Ser	Val	Leu	Thr
Ser	Leu	Ala	Met	Arg 165	Leu	Pro	Phe	Cys	Gly 170	Asp	Asn	Val	Ile 175	His
Phe	Thr	Cys	Glu 180	Ile	Leu	Ala	Val	Leu 185	Lys	Leu	Ala	Cys	Ala 190	Ile
Ser	Ile	Asn 195	Ile	Ile	Ser	Met	Val 200	Val	Ala	Ser	Met	Ile 205	Phe	Val
Gly	Pro 210	Val	Leu	Phe	Ile 215	Phe	Val	Thr	Tyr	Val	Phe 220	Ile	Leu	Thr
Ile 225	Leu	Arg	Ile	Pro	Ser 230	Ala	Glu	Gly	Arg	His	Lys 235	Ala	Ser	Thr
Cys	Ser	Ala	His 245	Leu	Thr	Val	Val	Ile 250	Phe	Tyr	Arg	Thr	Ile 255	Leu
Phe	Met	Tyr 260	Ala	Lys	Pro	Lys	Ala	Lys 265	Asp	Ser	Ser	Gly	Ala 270	Lys
Glu	Gln	Val 275	Thr	Asp	Lys	Ile	Ile 280	Ser	Leu	Phe	Tyr	Gly 285	Val	Thr
Pro	Met 290	Leu	Asn	Pro	Leu 295	Ile	Tyr	Ser	Leu	Arg	Asn 300	Lys	Asp	Lys
Ala 305	Ala	Val	Lys	Ser	Ile 310	Leu	Xaa	Gln	Lys	Cys 315	Phe	Leu	Glu	

<210> 1111

<211> 329
 <212> PRT
 <213> Unknown (H38g27 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(329)
 <223> Xaa = Any Amino Acid

<400> 1111

Lys	Ser	Met	Lys	Lys	Met	Asn	Asn	Val	Ile	Glu	Phe	Ile	Leu	Leu	Gly	1	5	10	15
Leu	Thr	His	Asn	Pro	Glu	Leu	Gln	Lys	Phe	Leu	Phe	Val	Met	Phe	Leu	20	25	30	
Ile	Thr	Tyr	Leu	Ile	Thr	Leu	Ala	Gly	Asn	Leu	Phe	Ile	Ser	Val	Ile	35	40	45	
Ile	Phe	Ile	Ser	Pro	Ala	Leu	Gly	Ser	Pro	Met	Tyr	Ser	Phe	Pro	Ser	50	55	60	
Tyr	Leu	Phe	Ile	Ile	Asp	Ile	Phe	Cys	Ser	Ser	Ser	Ile	Ala	Pro	Lys	65	70	75	80
Met	Asn	Phe	Asp	Leu	Ile	Ser	Glu	Lys	Asn	Thr	Ile	Ser	Phe	Asn	Gly	85	90	95	
Cys	Met	Thr	Gln	Leu	Phe	Thr	Glu	His	Phe	Phe	Thr	Glu	His	Phe	Phe	100	105	110	
Glu	Ala	Ala	Glu	Ile	Ile	Leu	Leu	Ser	Val	Met	Ala	Tyr	Asp	His	Tyr	115	120	125	
Val	Ala	Ile	Arg	Lys	Pro	Leu	His	Tyr	Ala	Thr	Ile	Met	Ser	Gln	Pro	130	135	140	
Met	Cys	Gly	Phe	Leu	Met	Val	Val	Ala	Gly	Ile	Leu	Gly	Phe	Val	His	145	150	155	160
Gly	Gly	Ile	Gln	Thr	Leu	Phe	Ile	Ala	Gln	Leu	Pro	Phe	Cys	Gly	Pro	165	170	175	
Asn	Val	Ile	Asn	His	Phe	Met	Cys	Asp	Leu	Val	Pro	Leu	Leu	Glu	Leu	180	185	190	
Ala	Cys	Thr	Asp	Thr	His	Thr	Leu	Gly	Pro	Leu	Ile	Ala	Ala	Asn	Ser	195	200	205	
Gly	Ser	Leu	Cys	Phe	Leu	Ile	Phe	Ser	Met	Leu	Val	Ala	Ser	Tyr	Val	210	215	220	
Ile	Ile	Leu	Cys	Phe	Leu	Arg	Thr	His	Ser	Ser	Glu	Gly	Arg	Arg	Lys	225	230	235	240
Ala	Leu	Ser	Ser	Cys	Ala	Ser	His	Ile	Phe	Ile	Val	Ile	Leu	Phe	Phe	245	250	255	
Val	Pro	Phe	Ser	Tyr	Leu	Tyr	Leu	Arg	Pro	Ile	His	Ser	Phe	Pro	Thr	260	265	270	
Asp	Lys	Ala	Val	Thr	Val	Phe	Cys	Thr	Leu	Phe	Thr	Pro	Met	Leu	Asn	275	280	285	
Pro	Leu	Ile	Tyr	Thr	Leu	Lys	Asn	Lys	Glu	Val	Lys	Asn	Val	Ile	Lys	290	295	300	
Lys	Leu	Trp	Lys	Gln	Ile	Met	Thr	Thr	Asp	Asp	Lys	Xaa	Val	Leu	Xaa	305	310	315	320
His	Lys	His	Leu	Gly	Lys	Asn	Ile	Trp								325			

<210> 1112
 <211> 318
 <212> PRT
 <213> Unknown (H38g28 protein)

<220>

<223> Synthetic construct

<400> 1112

```

Met Glu Trp Glu Asn His Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1      5      10      15
Leu Ser Gly His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
      20      25      30
Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
      35      40      45
Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
      50      55      60
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
      65      70      75      80
Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Leu Ser Gly
      85      90      95
Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys
      100      105      110
Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
      115      120      125
Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asp Ala Tyr Val Pro Met
      130      135      140
Ala Ala Gly Ser Trp Ile Ile Gly Ala Val Asn Ser Ala Val Gln Ser
      145      150      155      160
Val Phe Val Val Gln Leu Pro Phe Cys Arg Asn Asn Ile Ile Asn His
      165      170      175
Phe Thr Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile
      180      185      190
Ser Asp Asn Glu Phe Ile Met Leu Val Ala Thr Thr Leu Phe Ile Leu
      195      200      205
Thr Pro Leu Leu Leu Ile Ile Val Ser Tyr Thr Leu Ile Ile Val Ser
      210      215      220
Ile Phe Lys Ile Ser Ser Ser Glu Gly Arg Ser Lys Ala Ser Ser Thr
      225      230      235      240
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
      245      250      255
Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp
      260      265      270
Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
      275      280      285
Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290      295      300
Glu Ala Val Lys His Leu Leu Asn Arg Arg Phe Phe Ser Lys
      305      310      315

```

<210> 1113

<211> 264

<212> PRT

<213> Unknown (H38g29 protein)

<220>

<223> Synthetic construct

<400> 1113

```

Met Val Asp Asn Leu Ile Ile Val Val Thr Ile Thr Thr Ser Pro Ala
 1      5      10      15
Leu Asp Ser Pro Val Tyr Phe Phe Leu Ser Phe Phe Ser Phe Ile Asp
      20      25      30
Gly Cys Ser Ser Ser Thr Met Ala Pro Lys Met Ile Phe Asp Leu Leu
      35      40      45
Thr Glu Lys Lys Thr Ile Ser Phe Ser Gly Cys Met Thr Gln Leu Phe
      50      55      60

```

```

Val Glu His Phe Phe Gly Gly Val Glu Ile Ile Leu Leu Val Val Met
65          70          75          80
Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu Tyr Tyr Leu Ile
85          90          95
Thr Met Asn Arg Gln Val Cys Gly Leu Leu Val Ala Met Ala Trp Val
100        105        110
Gly Gly Phe Leu His Ala Leu Ile Gln Met Leu Leu Ile Val Trp Leu
115        120        125
Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile Cys Asp Leu Phe
130        135        140
Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr His Val Phe Gly Leu Phe
145        150        155        160
Val Ala Ala Asn Ser Gly Leu Met Cys Met Leu Ile Phe Ser Ile Leu
165        170        175
Ile Thr Ser Tyr Val Leu Ile Leu Cys Ser Gln Arg Lys Ala Leu Ser
180        185        190
Thr Cys Ala Phe His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys
195        200        205
Ile Leu Val Tyr Leu Arg Pro Met Ile Thr Phe Pro Ile Asp Lys Ala
210        215        220
Val Ser Val Phe Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu Ile
225        230        235        240
Tyr Thr Leu Arg Asn Thr Glu Val Lys Asn Ala Met Lys Gln Leu Trp
245        250        255
Ser Gln Ile Ile Trp Gly Asn Asn
260

```

<210> 1114

<211> 312

<212> PRT

<213> Unknown (H38g30 protein)

<220>

<223> Synthetic construct

<400> 1114

```

Met Trp Pro Asn Ile Thr Ala Ala Pro Phe Leu Leu Thr Gly Phe Pro
1          5          10          15
Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Val
20        25        30
Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Leu Ile Lys
35        40        45
His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu
50        55        60
Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met
65        70        75        80
Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe
85        90        95
Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser
100       105       110
Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu
115       120       125
Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val
130       135       140
Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg
145       150       155       160
Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe
165       170       175
Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe
180       185       190
Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp

```

```

      195              200              205
Ser Leu Ile Ile Leu Phe Ser Tyr Ile Leu Ile Leu Asn Thr Val Ile
  210              215              220
Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys Ile
  225              230              235              240
Ser His Ile Ser Cys Val Leu Ile Phe Tyr Val Thr Val Met Gly Leu
      245              250              255
Thr Phe Ile Tyr Arg Phe Gly Lys Asn Val Pro Glu Val Val His Ile
      260              265              270
Ile Met Ser Tyr Ile Tyr Phe Leu Phe Pro Pro Leu Met Asn Pro Val
      275              280              285
Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr Gly Ile Ile Arg Leu
      290              295              300
Leu Ser Lys His Arg Phe Ser Arg
  305              310

```

<210> 1115

<211> 285

<212> PRT

<213> Unknown (H38g31 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(285)

<223> Xaa = Any Amino Acid

<400> 1115

```

Asp Thr Glu Pro Gln Asn Leu Thr Ala Val Ser Glu Phe Leu Leu Leu
  1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Phe
      20              25              30
Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35              40              45
Ala Ile Gly Ser Asp Ser His Leu Asp Thr Pro Met Tyr Phe Phe Leu
      50              55              60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
      65              70              75              80
Lys Met Ile Glu Glu Met Gln Ser His Ser Arg Val Ile Tyr His Gly
      85              90              95
Asp Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Lys Asp
      100              105              110
Asp Met Ile Leu Thr Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys
      115              120              125
His Pro Leu Asn Tyr Pro Gly Ile Met Asn Pro His Leu Cys Val Leu
      130              135              140
Leu Val Leu Val Pro Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
      145              150              155              160
Asn Leu Ile Val Leu Gln Phe Ile Cys Phe Lys Asn Val Glu Ile Ser
      165              170              175
Asn Phe Phe Cys Asp Pro Phe Gln Arg Leu Asn Leu Ala Cys Ser Asp
      180              185              190
Ser Asp Ile Asn Asn Ile Tyr Ile Tyr Leu Asp Ser Thr Ile Phe Gly
      195              200              205
Phe Leu Arg Ile Ser Gly Ile Leu Leu Cys Tyr Tyr Thr Val Val Phe
      210              215              220
Pro Ile Leu Arg Ile Pro Ser Ser Asp Gly Asn Tyr Lys Ala Phe Ser
      225              230              235              240
Thr Xaa Gly Ser Arg Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245              250              255

```

Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Ser Ser Pro Arg Asn Asp
 260 265 270
 Val Val Ala Ser Val Met Tyr Ala Val Val Val Thr Pro
 275 280 285

<210> 1116
 <211> 317
 <212> PRT
 <213> Unknown (H38g32 protein)

<220>
 <223> Synthetic construct

<400> 1116
 Met Gly Glu Ile Asn Gln Thr Leu Val Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Gly Tyr Pro Lys Ile Glu Ile Val Tyr Phe Ala Leu Ile Leu
 20 25 30
 Val Met Tyr Leu Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala
 35 40 45
 Ser Ile Phe Asp Ser His Phe His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ser Val Pro Ser
 65 70 75 80
 Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly
 85 90 95
 Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys
 100 105 110
 Leu Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Ile Ile Leu Ser Lys Val Ala Tyr Val Leu Met
 130 135 140
 Ala Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Ala Val Gln Thr
 145 150 155 160
 Leu Leu Ala Met Arg Leu Pro Phe Cys Gly Asn Asn Ile Ile Asn His
 165 170 175
 Phe Ala Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile
 180 185 190
 Ser Leu Asn Ile Ile Thr Met Val Ile Ser Asn Met Ala Phe Leu Val
 195 200 205
 Leu Pro Leu Met Val Ile Phe Phe Ser Tyr Met Phe Ile Leu Tyr Thr
 210 215 220
 Ile Leu Gln Met Asn Ser Ala Thr Gly Arg Arg Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe
 245 250 255
 Phe Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Ile Gly Glu Glu Lys
 260 265 270
 Leu Gln Ala Leu Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val Thr
 275 280 285
 Pro Met Leu Asn Pro Ile Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300
 Ala Ala Val Lys Tyr Leu Leu Asn Lys Lys Pro Ile His
 305 310 315

<210> 1117
 <211> 309
 <212> PRT
 <213> Unknown (H38g33 protein)

<220>

<223> Synthetic construct

<400> 1117

```

M t Gly Ala Lys Asn Asn Val Thr Glu Phe Val Leu Phe Gly Leu Phe
 1          5          10          15
Glu Ser Arg Glu Met Gln His Thr Cys Phe Val Val Phe Phe Leu Phe
 20          25          30
His Val Leu Thr Val Leu Gly Asn Leu Leu Val Ile Ile Thr Ile Asn
 35          40          45
Ala Arg Lys Thr Leu Lys Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu
 50          55          60
Ser Phe Ala Asp Ile Cys Tyr Pro Ser Thr Thr Ile Pro Lys Met Ile
 65          70          75          80
Ala Asp Thr Phe Val Glu His Lys Ile Ile Ser Phe Asn Gly Cys Met
 85          90          95
Thr Gln Leu Phe Ser Ala His Phe Phe Gly Gly Thr Glu Ile Phe Leu
100          105          110
Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu
115          120          125
His Tyr Thr Ala Ile Met Asp Cys Arg Lys Cys Gly Leu Leu Ala Gly
130          135          140
Ala Ser Trp Leu Ala Gly Phe Leu His Ser Ile Leu Gln Thr Leu Leu
145          150          155          160
Thr Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp Asn Phe Phe
165          170          175
Cys Asp Val His Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr Tyr Met
180          185          190
Val Gly Leu Ile Val Val Ala Asn Ser Gly Met Ile Ser Leu Ala Ser
195          200          205
Phe Phe Ile Leu Ile Ile Ser Tyr Val Ile Ile Leu Leu Asn Leu Arg
210          215          220
Ser Gln Ser Ser Glu Asp Arg Arg Lys Ala Val Ser Thr Cys Gly Ser
225          230          235          240
His Val Ile Thr Val Leu Leu Val Leu Met Pro Pro Met Phe Met Tyr
245          250          255
Ile Arg Pro Ser Thr Thr Leu Ala Ala Asp Lys Leu Ile Ile Leu Phe
260          265          270
Asn Ile Val Met Pro Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg
275          280          285
Asn Asn Asp Val Lys Asn Ala Met Arg Lys Leu Phe Arg Val Lys Arg
290          295          300
Ser Leu Gly Glu Lys
305

```

<210> 1118

<211> 329

<212> PRT

<213> Unknown (H38g34 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1118

```

Ala Thr Cys His Leu Xaa Thr His Asn Ala Ala Pro Phe Leu Leu Pro
 1          5          10          15
Gly Phe Ser Val Leu Glu Ala Thr Tyr His Ser Ile Ser Ile Pro Phe
 20          25          30

```

Phe Ala Val Tyr Val Cys Val Leu Leu Gly Asn Gly Lys Leu Leu Tyr
 35 40 45
 Leu Ile Lys His Asp His Ser Leu His Glu Pro Met Tyr Cys Phe Leu
 50 55 60
 Ala Thr Leu Arg Gln Asp Leu Met Val Lys Leu Thr Met Met Pro Thr
 65 70 75 80
 Val Met Gly Val Leu Trp Met Asn His Lys Glu Val Ile His Gly Ala
 85 90 95
 Cys Phe Leu Gln Val Tyr Ile Ile His Ser His Tyr Pro Leu Ala Glu
 100 105 110
 Ser Gly Ile Leu Leu Ser Met Ala Tyr Asp Arg Phe Ile Ile Ile His
 115 120 125
 Met Leu Leu Arg Tyr Asn Ser Ile Ser Thr Lys Ser Trp Val Lys Ile
 130 135 140
 Glu Leu Trp Leu Phe Met Arg Asp Phe Leu Ser Leu Val Pro Pro Ile
 145 150 155 160
 Leu Pro Leu His Cys Phe Pro Tyr Cys His Ser His Val Leu Phe His
 165 170 175
 Thr Phe Phe Leu His Gln Asp Val Leu Lys Leu Ala Cys Ala Asp Ile
 180 185 190
 Thr Phe Asn His Leu Tyr Pro Ala Ile Leu Val Ala Leu Ile Phe Phe
 195 200 205
 Leu Asp Ala Leu Ile Ile Val Phe Ser Tyr Ile Leu Ile Leu Lys Thr
 210 215 220
 Val Ile Gly Ile Ala Ser Arg Lys Glu Gln Ala Lys Ala Leu Asn Met
 225 230 235 240
 Cys Val Ser His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Ile
 245 250 255
 Ser Glu Thr Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val
 260 265 270
 His Ile Thr Val Ser Tyr Asp Ser Phe Leu Phe Pro Pro Phe Met Asn
 275 280 285
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Val
 290 295 300
 Arg Leu Phe Ser Gly His Arg Met Ala Xaa Ala Leu Phe Ser Glu Phe
 305 310 315 320
 Cys Asp Leu His Asp Phe Trp Ala Phe
 325

<210> 1119

<211> 296

<212> PRT

<213> Unknown (H38g35 protein)

<220>

<223> Synthetic construct

<400> 1119

Leu Leu Leu Leu Val Leu Leu Leu Pro Thr Phe Leu Leu Ser Leu Met
 1 5 10 15
 Gly Asn Met Leu Ile Ile Ser Thr Val Leu Ser Cys Ser Arg Leu His
 20 25 30
 Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Ile Leu Asp Ile Leu
 35 40 45
 Phe Thr Ser Val Ile Ser Pro Lys Val Leu Ala Asn Leu Gly Ser Arg
 50 55 60
 Asp Lys Thr Ile Ser Phe Ala Gly Cys Ile Thr Gln Cys Tyr Phe Tyr
 65 70 75 80
 Phe Phe Leu Gly Thr Val Glu Phe Leu Leu Thr Val Met Ser Tyr
 85 90 95
 Asp Cys Tyr Ala Ala Ile Cys Cys Pro Leu Arg Tyr Thr Thr Ile Met


```

      100      105      110
Arg Pro Tyr Val Cys Ile Gly Thr Val Val Phe Ser Trp Val Gly Gly
      115      120      125
Phe Leu Ser Val Leu Phe Pro Thr Ile Leu Ile Ser Gln Leu Pro Phe
      130      135      140
Cys Gly Ser Asn Ile Ile Asn His Phe Phe Cys Asp Ser Gly Pro Leu
145      150      155      160
Leu Ala Leu Ala Cys Ala Asp Thr Thr Ala Ile Glu Leu Met Asp Phe
      165      170      175
Met Leu Ser Ser Met Val Ile Leu Cys Cys Ile Val Leu Val Ala Tyr
      180      185      190
Ser Tyr Thr Tyr Ile Ile Leu Thr Ile Met Arg Ile Pro Ser Ala Ser
      195      200      205
Gly Arg Lys Lys Ala Phe Asn Thr Cys Ala Ser His Leu Thr Ile Val
      210      215      220
Ile Ile Ser Ser Gly Ile Thr Val Phe Ile Tyr Val Thr Pro Ser Gln
225      230      235      240
Lys Glu Tyr Leu Glu Ile Asn Lys Ile Pro Ser Val Leu Ser Ser Leu
      245      250      255
Val Thr Pro Phe Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn Asp Thr
      260      265      270
Val Gln Gly Val Leu Arg Asp Val Trp Val Arg Val Arg Gly Val Phe
      275      280      285
Glu Lys Arg Met Arg Ala Val Leu
      290      295

```

<210> 1120

<211> 310

<212> PRT

<213> Unknown (H38g36 protein)

<220>

<223> Synthetic construct

<400> 1120

```

Met Trp Tyr Asn Asn Ser Ala Gly Pro Phe Leu Leu Thr Gly Phe Leu
1      5      10      15
Gly Ser Glu Ala Val His Tyr Arg Ile Ser Met Ser Phe Phe Val Ile
      20      25      30
Tyr Phe Ser Val Leu Phe Gly Asn Gly Thr Leu Leu Val Leu Ile Trp
      35      40      45
Asn Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
      50      55      60
Ala Asp Thr Asp Leu Gly Met Thr Phe Thr Thr Met Pro Thr Val Leu
      65      70      75      80
Gly Val Leu Leu Leu Asp Gln Arg Glu Ile Ala His Ala Ala Cys Phe
      85      90      95
Thr Gln Ser Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Ile Leu
      100      105      110
Leu Val Leu Ala Tyr Asp Cys Phe Ile Ala Ile Arg Thr Pro Leu Arg
      115      120      125
Tyr Asn Cys Ile Leu Thr Asn Ser Arg Val Met Asn Ile Gly Leu Gly
      130      135      140
Val Leu Met Arg Gly Phe Met Ser Ile Leu Pro Ile Ile Leu Ser Leu
145      150      155      160
Tyr Cys Tyr Pro Tyr Cys Gly Ser Arg Ala Leu Leu His Thr Phe Cys
      165      170      175
Leu His Gln Asp Val Ile Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn
      180      185      190
His Ile Tyr Pro Ile Ile Gln Thr Ser Leu Thr Val Phe Leu Asp Ala
      195      200      205

```

```

Leu Ile Ile Ile Phe Ser Tyr Ile Leu Ile Leu Lys Thr Val Met Gly
 210                215                220
Ile Ala Ser Gly Gln Glu Glu Ala Lys Ser Leu Asn Thr Cys Val Ser
225                230                235                240
His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Met Gly Leu Ser
                245                250                255
Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val Pro Ile Thr
                260                265                270
Met Ser Tyr Val His Phe Leu Phe Pro Pro Phe Val Asn Pro Ile Ile
                275                280                285
Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Ile Arg Leu Phe
                290                295                300
Ser Gly Gln Ser Arg Ala
305                310

```

<210> 1121

<211> 332

<212> PRT

<213> Unknown (H38g37 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(332)

<223> Xaa = Any Amino Acid

<400> 1121

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1                5                10                15
Gly Leu Pro Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
                20                25                30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile
                35                40                45
Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe
                50                55                60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65                70                75                80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ala Ile Ser
                85                90                95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Phe Leu Phe Ala Cys
                100                105                110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
                115                120                125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys
                130                135                140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145                150                155                160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Phe Lys Asn Val Glu
                165                170                175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
                180                185                190
Ser Asp Gly Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
                195                200                205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
                210                215                220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225                230                235                240
Phe Ser Thr Cys Gly Ser His Gln Ala Val Val Cys Xaa Phe Tyr Arg
                245                250                255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg

```

```
<210> 1122
<211> 310
<212> PRT
<213> Unknown (H38g38 protein)
```

<400> 1122

<210> 1123

<211> 323
 <212> PRT
 <213> Unknown (H38g39 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(323)
 <223> Xaa = Any Amino Acid

<400> 1123

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Ile Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Thr
      20           25           30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
      35           40           45
Ala Val Ser Ser Asp Ser His Leu His Thr Ser Met Tyr Phe Val Leu
      50           55           60
Ser Asn Leu Arg Trp Val Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
      65           70           75           80
Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85           90           95
Gly Cys Leu Thr Gln Met Ser Phe Leu Val Phe Phe Ala Cys Ile Glu
      100          105          110
Asp Met Leu Leu Thr Val Met Ser Tyr Asp Gln Phe Leu Ala Ile Cys
      115          120          125
His Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys Val Phe
      130          135          140
Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
      145          150          155          160
Arg Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
      165          170          175
Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
      180          185          190
Ser Val Ile Asn Ile Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Gly
      195          200          205
Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
      210          215          220
Ser Ile Leu Arg Met Ser Leu Ser Asp Val Lys Tyr Lys Ala Phe Ser
      225          230          235          240
Thr Cys Gly Ser His Leu Ala Val Phe Cys Leu Phe Tyr Gly Ala Gly
      245          250          255
Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Ser Gly Asn Gly
      260          265          270
Val Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275          280          285
Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Pro Trp Arg
      290          295          300
Leu Arg Ser Thr Thr Val Glu Ser Pro Xaa Ser Leu Pro Ser Phe Phe
      305          310          315          320
Leu Cys Leu

```

<210> 1124
 <211> 320
 <212> PRT
 <213> Unknown (H38g40 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1124

```

His Thr Glu Pro Gln Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser
 20           25           30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
 35           40           45
Ala Val Ser Ser Asp Pro His Leu His Thr Pro Met Cys Phe Phe Leu
 50           55           60
Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro
 65           70           75           80
Lys Met Ile Val Asp Met Gln Ser His Thr Arg Val Ile Ser Tyr Glu
 85           90           95
Gly Cys Leu Thr Arg Ile Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 100          105          110
Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 115          120          125
Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe
 130          135          140
Phe Leu Leu Val Tyr Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145          150          155          160
Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu Ile Ser
 165          170          175
Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp
 180          185          190
Ser Val Ile Asn Ser Ile Phe Met Tyr Phe His Ser Thr Met Phe Gly
 195          200          205
Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
 210          215          220
Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser
 225          230          235          240
Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly Thr Gly
 245          250          255
Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly
 260          265          270
Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Leu
 275          280          285
Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg
 290          295          300
Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser
 305          310          315          320

```

<210> 1125

<211> 327

<212> PRT

<213> Unknown (H38g41 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1125

```

Ser Thr Asp Xaa Gln Ser Leu Thr Gly Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
          20          25          30
Leu Ser Met Cys Leu Val Lys Val Leu Gly Asn Leu Leu Ile Ile Leu
          35          40          45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro
65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
          85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
          115          120          125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Leu Ser Phe Ser Gln Leu His Asn
145          150          155          160
Leu Ile Ala Leu Lys Met Thr Cys Phe Lys Asn Val Gly Ile Pro Asn
          165          170          175
Phe Leu Cys Asp Pro Ser Gln Leu Pro His Leu Thr Cys Cys Asp Thr
          180          185          190
Phe Thr Asn His Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe
195          200          205
Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr His Val Ile Val Ser Ser
210          215          220
Ile Leu Arg Val Ser Ser Ser Arg Gly Arg Cys Lys Ala Phe Ser His
225          230          235          240
Leu Xaa Val Val Cys Xaa Tyr Tyr Gly Thr Gly Phe Gly Gly Tyr Leu
          245          250          255
Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala Val Ala Ser Val
260          265          270
Met Tyr Met Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu
275          280          285
Arg Asn Arg Asp Ile Lys Ser Val Val Gln Arg Pro His Gly Ser Thr
290          295          300
Val Xaa Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp
305          310          315          320
Val Lys Lys Gly Ser Lys Val
          325

```

<210> 1126

<211> 313

<212> PRT

<213> Unknown (H38g42 protein)

<220>

<223> Synthetic construct

<400> 1126

```

Met Gly Asn Trp Ser Thr Val Thr Glu Ile Thr Leu Ile Ala Phe Pro
 1          5          10          15
Ala Leu Leu Glu Ile Arg Ile Ser Leu Phe Val Val Leu Val Val Thr
          20          25          30
Tyr Thr Leu Thr Ala Thr Gly Asn Ile Thr Ile Ile Ser Leu Ile Trp
          35          40          45
Ile Asp His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
          50          55          60
Ser Phe Leu Asp Ile Leu Tyr Thr Thr Val Ile Thr Pro Lys Leu Leu

```

```

65          70          75          80
Ala Cys Leu Leu Gly Glu Glu Lys Thr Ile Ser Phe Ala Gly Cys Met
      85          90          95
Ile Gln Thr Tyr Phe Tyr Phe Phe Leu Gly Thr Val Glu Phe Ile Leu
      100        105        110
Leu Ala Val Met Ser Phe Asp Arg Tyr Met Ala Ile Cys Asp Pro Leu
      115        120        125
His Tyr Thr Val Ile Met Asn Ser Arg Ala Cys Leu Leu Leu Val Leu
      130        135        140
Gly Cys Trp Val Gly Ala Phe Leu Ser Val Leu Phe Pro Thr Ile Val
      145        150        155        160
Val Thr Arg Leu Pro Tyr Cys Arg Lys Glu Ile Asn His Phe Phe Cys
      165        170        175
Asp Ile Ala Pro Leu Leu Gln Val Ala Cys Ile Asn Thr His Leu Ile
      180        185        190
Glu Lys Ile Asn Phe Leu Leu Ser Ala Leu Val Ile Leu Ser Ser Leu
      195        200        205
Ala Phe Thr Thr Gly Ser Tyr Val Tyr Ile Ile Ser Thr Ile Leu Arg
      210        215        220
Ile Pro Ser Thr Gln Gly Arg Gln Lys Ala Phe Ser Thr Cys Ala Ser
      225        230        235        240
His Ile Thr Val Val Ser Ile Ala His Gly Ser Asn Ile Phe Val Tyr
      245        250        255
Val Arg Pro Asn Gln Asn Ser Ser Leu Asp Tyr Asp Lys Val Ala Ala
      260        265        270
Val Leu Ile Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Ser
      275        280        285
Leu Arg Asn Glu Lys Val Gln Glu Val Leu Arg Glu Thr Val Asn Arg
      290        295        300
Ile Met Thr Leu Ile Gln Arg Lys Thr
305          310

```

<210> 1127

<211> 247

<212> PRT

<213> Unknown (H38g43 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(247)

<223> Xaa = Any Amino Acid

<400> 1127

```

Met Gly Asn Ile Asn Ile Ser Leu Glu Asn Tyr Phe Ile Leu Leu Gly
1          5          10          15
Leu Ser Asn Xaa Pro Pro Leu Glu Ile Val Ile Phe Val Val Leu Leu
      20        25        30
Ile Phe Cys Phe Met Thr Leu Ile Gly Lys Leu Phe Ser Ile Ile Leu
      35        40        45
Ser Tyr Leu Asp Ser His Pro His Thr Pro Arg Tyr Leu Phe Ser Phe
      50        55        60
Leu Asp Phe Cys Tyr Thr Ile Ser Ser Ile Phe Xaa Leu Gln Tyr Asn
      65        70        75        80
Leu Trp Gly Pro Gln Lys Asn Ile Ser Tyr Ala Ser Gly Met Ile Gln
      85        90        95
Ile Tyr Phe Val Leu Thr Leu Gly Thr Met Asp Cys Ala Leu Leu Val
      100       105       110
Val Met Ser Arg Thr Val Tyr Ala Ala Gly His Arg His Leu Pro Tyr
      115       120       125

```

```

Thr Val Val Met Ala Val Ala Phe Trp Val Ser Ser Phe Thr Asn Ser
 130                      135                      140
Ala Phe Asp Ser Phe Phe Thr Phe Trp Val Thr Leu Cys Gly His His
145                      150                      155                      160
Tyr Tyr Ala Tyr Ile Phe Ile Phe Thr Ser Leu Leu Val Xaa Arg Trp
                      165                      170                      175
Phe Ile Asn Arg Lys Lys Gln Ser Val Phe Ser Leu Asn His Ala Ala
                      180                      185                      190
Leu Leu Thr Leu Ser Phe Pro Leu Xaa Asn Asp Cys Phe Gln Glu Ile
                      195                      200                      205
Glu Lys Asn Met Leu Arg Lys His Ser Ile Gly Glu Cys Xaa Lys His
210                      215                      220
Val Met Leu Val Gln Leu Asn Gln Val Ser Lys Thr Cys Ile Phe Met
225                      230                      235                      240
Arg Pro Ile Leu Gly Asn Ser
                      245

```

<210> 1128

<211> 316

<212> PRT

<213> Unknown (H38g44 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid.

<400> 1128

```

Asp Ile Gln Asn Gln Thr Thr Val Thr Glu Phe Thr Leu Thr Ala Phe
 1                      5                      10                      15
Pro Val Leu Gln Gln Leu Gln Ile Ser Leu Leu Ala Val Leu Trp Phe
                      20                      25                      30
Thr Tyr Met Leu Thr Leu Thr Gly Asn Val Ala Ile Ile Ser Leu Thr
                      35                      40                      45
Trp Ala Asn His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn
50                      55                      60
Trp Ser Ile Trp Asp Ile Phe Phe Thr Thr Ser Val Ile Pro Lys Leu
65                      70                      75                      80
Leu Ala Cys Leu Leu Gln Asp Lys Lys Thr Ile Ser Leu Ala Gly Cys
                      85                      90                      95
Ile Thr Gln Thr Tyr Phe Leu Gly Phe Leu Gly Thr Val Glu Phe Ile
                      100                      105                      110
Leu Trp Ala Val Met Ser Phe Asp Cys Tyr Val Ala Ile Cys Asp Pro
115                      120                      125
Leu His Tyr Thr Ile Ile Met Asn Ser Arg Ala Cys Leu Leu Leu Val
130                      135                      140
Leu Gly Cys Trp Val Gly Ala Phe Leu Ser Val Leu Cys Pro Thr Ile
145                      150                      155                      160
Val Val Ser Arg Leu Pro Phe Cys Tyr Lys Glu Ile Ser His Phe Phe
                      165                      170                      175
Cys Asp Ile Thr Pro Leu Leu His Val Ser Cys Ile Asp Thr His Phe
180                      185                      190
Ile Glu Met Ile Asn Phe Leu Leu Ser Ser Leu Ile Leu Leu Thr Ser
195                      200                      205
Leu Val Leu Thr Thr Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu
210                      215                      220
His Ile Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala
225                      230                      235                      240
Ser His Ile Thr Val Ile Ser Ile Ala Tyr Ile Ser Asn Ile Phe Arg

```



```

                245                250                255
Tyr Val Arg Pro Ser Gln Ser His Ser Met Gly Phe Asp Lys Val Thr
                260                265                270
Ala Val Pro Thr Met Val Thr Pro Leu Leu Asn Pro Phe Thr Tyr Ser
                275                280                285
Leu Arg Asn Glu Lys Val Lys Ala Val Leu Lys Glu Ala Val Ser Lys
                290                295                300
Ile Met Ser Ser Trp His Arg Arg Thr Xaa Asn Phe
305                310                315

```

<210> 1129

<211> 310

<212> PRT

<213> Unknown (H38g45 protein)

<220>

<223> Synthetic construct

<400> 1129

```

Met Glu Pro Gln Asn Thr Thr Gln Val Ser Met Phe Val Leu Leu Gly
 1                5                10                15
Phe Ser Gln Thr Gln Glu Leu Gln Lys Phe Leu Phe Leu Leu Phe Leu
                20                25                30
Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Ile Met Val Thr
                35                40                45
Val Thr Phe Asp Cys Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50                55                60
Asn Leu Ala Leu Ile Asp Leu Cys Tyr Ser Thr Val Thr Ser Pro Lys
65                70                75                80
Met Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly
                85                90                95
Cys Met Ala Gln Ile Phe Phe Phe His Leu Leu Gly Gly Gly Thr Val
                100                105                110
Phe Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln
                115                120                125
Pro Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu
130                135                140
Val Val Ala Ala Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu
145                150                155                160
Ala Leu Ile Leu Pro Leu Pro Phe Cys Asp Pro Asn Ile Ile Asp Asn
                165                170                175
Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr
180                185                190
Ser Leu Leu Glu Phe Leu Met Ile Phe Asn Ser Gly Leu Leu Val Ile
195                200                205
Ile Trp Phe Leu Leu Leu Leu Ile Ser Tyr Thr Val Ile Leu Val Met
210                215                220
Leu Arg Ser His Ser Gly Lys Ala Arg Arg Lys Ala Ala Ser Thr Cys
225                230                235                240
Thr Thr His Ile Ile Val Val Ser Met Ile Phe Ile Pro Cys Ile Tyr
                245                250                255
Ile Tyr Thr Trp Pro Phe Thr Pro Phe Leu Met Asp Lys Ala Val Ser
260                265                270
Ile Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr
275                280                285
Leu Arg Asn Gln Asp Met Lys Ala Ala Met Arg Arg Leu Gly Lys Cys
290                295                300
Leu Val Ile Cys Arg Glu
305                310

```

<210> 1130

<211> 311
 <212> PRT
 <213> Unknown (H38g46 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(311)
 <223> Xaa = Any Amino Acid

<400> 1130
 Asp Gln Glu Asn Gln Thr Ser Glu Val Thr Phe Ile Leu Leu Gly Phe
 1 5 10 15
 Ser Glu Tyr Pro Asp Leu Gln Thr Pro Leu Phe Leu Val Phe Leu Thr
 20 25 30
 Ile Tyr Thr Val Thr Val Leu Gly Asn Leu Gly Met Ile Ile Val Ile
 35 40 45
 Arg Ile Ser Pro Lys Leu His Thr Pro Met Cys Phe Phe Leu Ser His
 50 55 60
 Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu
 65 70 75 80
 Leu Glu Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys
 85 90 95
 Thr Met Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe
 100 105 110
 Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro
 115 120 125
 Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val
 130 135 140
 Ala Thr Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa
 145 150 155 160
 Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe
 165 170 175
 Val Cys Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys
 180 185 190
 Val Ser Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser
 195 200 205
 Ser Leu Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Thr Pro
 210 215 220
 Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu
 225 230 235 240
 Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val
 245 250 255
 Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe
 260 265 270
 Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg
 275 280 285
 Asn Lys Asp Val Lys Glu Thr Val Arg Arg Leu Leu Ile Thr Lys Leu
 290 295 300
 Leu Cys Leu Ile Leu Xaa Asn
 305 310

<210> 1131
 <211> 334
 <212> PRT
 <213> Unknown (H38g47 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 1131

```

Tyr Ala Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
1      5      10      15
Glu Val Ser Gly Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
20      25      30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
35      40      45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
85      90      95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
100     105     110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile
115     120     125
Cys His Pro Leu Tyr His Leu Thr Ile Met Asn Pro Cys Phe Cys Ala
130     135     140
Phe Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln
145     150     155     160
Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val Glu
165     170     175
Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Ser His Leu Ala Cys
180     185     190
Cys Asp Thr Phe Thr Ile Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
195     200     205
Phe Gly Phe Leu Pro Ile Leu Gly Thr Leu Phe Ser Phe Ser Lys Ile
210     215     220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225     230     235     240
Leu Ser Thr Cys Gly Ser Arg Leu Ser Val Val Cys Xaa Val Tyr Gly
245     250     255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
260     265     270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Leu Val Thr Pro Met Leu
275     280     285
Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Val Leu
290     295     300
Arg Gln Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Ile Cys Ser
305     310     315     320
Ile Pro Phe Val Val Trp Val Gln Lys Gly Ser Lys Val Lys
325     330

```

<210> 1132

<211> 307

<212> PRT

<213> Unknown (H38g48 protein)

<220>

<223> Synthetic construct

<400> 1132

```

Met Glu Thr Gly Asn Leu Thr Trp Val Ser Asp Phe Val Phe Leu Gly
1      5      10      15
Leu Ser Gln Thr Arg Glu Leu Gln Arg Phe Leu Phe Leu Met Phe Leu
20      25      30

```

Phe Val Tyr Ile Thr Thr Val Met Gly Asn Ile Leu Ile Ile Ile Thr
 35 40 45
 Val Thr Ser Asp Ser Gln Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50 55 60
 Asn Leu Ala Val Leu Asp Leu Cys Phe Ser Ser Val Thr Ala Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Tyr Gln Gly
 85 90 95
 Cys Met Gly Gln Ile Phe Phe Phe His Phe Leu Gly Gly Ala Met Val
 100 105 110
 Phe Phe Leu Ser Val Met Ala Phe Asp Arg Leu Ile Ala Ile Ser Arg
 115 120 125
 Pro Leu Arg Tyr Val Thr Val Met Asn Thr Gln Leu Trp Val Gly Leu
 130 135 140
 Val Val Ala Thr Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu
 145 150 155 160
 Ala Leu Met Leu Pro Leu Pro Phe Cys Gly Pro Asn Ile Leu Asp Asn
 165 170 175
 Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Leu Leu Glu Phe Leu Lys Ile Ser Asn Ser Gly Leu Leu Asp Val
 195 200 205
 Val Trp Phe Phe Leu Leu Leu Met Ser Tyr Leu Phe Ile Leu Val Met
 210 215 220
 Leu Arg Ser His Pro Gly Glu Ala Arg Arg Lys Ala Ala Ser Thr Cys
 225 230 235 240
 Thr Thr His Ile Ile Val Val Ser Met Ile Phe Val Pro Ser Ile Tyr
 245 250 255
 Leu Tyr Ala Arg Pro Phe Thr Pro Phe Pro Met Asp Lys Leu Val Ser
 260 265 270
 Ile Gly His Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Asp Met Gln Ala Ala Val Arg Arg Leu Gly Arg His
 290 295 300
 Arg Leu Val
 305

<210> 1133

<211> 316

<212> PRT

<213> Unknown (H38g49 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1133

His Thr Glu Pro Gln Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser
 35 40 45
 Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Asn Leu Cys
 50 55 60
 Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Ile Val
 65 70 75 80
 Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr

```
<210> 1135
<211> 356
<212> PRT
<213> Unknown (H38g51 protein)
```

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(356)

<223> Xaa = Any Amino Acid

<400> 1135

```

Met Ile Asn Asp Ser His Phe Ser Gly Phe Ile Leu Leu Gly Phe Thr
 1           5           10           15
Gly Gln Pro Gln Leu Gln Met Met Ile Ser Gly Val Val Phe Phe
 20           25           30
Tyr Thr Ile Ala Phe Met Gly Asn Met Ala Ile Ile Leu Leu Ser Phe
 35           40           45
Leu Asp Asp His Leu Gln Val Pro Met Tyr Phe Phe Leu Arg Asn Leu
 50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
 65           70           75           80
Val Ser Ile Trp Gly Lys Asp Lys Arg Ile Thr Phe Gly Gly Cys Ala
 85           90           95
Phe Gln Leu Phe Ile Asp Val Ala Leu Tyr Ser Val Glu Cys Ile Leu
 100          105          110
Leu Ser Met Met Ser Tyr Asp Arg Leu Asn Ala Ile Cys Lys Pro Leu
 115          120          125
His His Met Thr Ile Met Asn Leu Gln Leu Cys Gln Gly Leu Val Val
 130          135          140
Ile Ser Trp Val Val Gly Val Ile Asn Cys Ile Ile Pro Ser Pro Tyr
 145          150          155          160
Ala Thr Ser Leu Pro Arg Cys Arg Asn His His Leu Asp His Phe Phe
 165          170          175
Val Cys Val Lys Cys Leu Gln Xaa Ser Arg Phe Lys Ile Ala Cys Val
 180          185          190
Asp Thr Thr Ala Met Glu Val Thr Thr Phe Ala Met Cys Leu Ile Ile
 195          200          205
Val Leu Val Pro Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
 210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
 225          230          235          240
Gly Thr Cys Ser Ser His Leu Val Val Val Ser Ile Phe Cys Gly Thr
 245          250          255
Val Thr Tyr Met Tyr Ile Gln Pro Gly Asn Ser Pro Asn Gln Asn Glu
 260          265          270
Gly Lys Leu Leu Ser Ile Phe Tyr Ser Ile Val Thr Pro Ser Leu Asn
 275          280          285
Pro Leu Ile Tyr Thr Val Arg Asn Lys Glu Phe Lys Gly Ala Met Lys
 290          295          300
Arg Leu Thr Gly Lys Glu Lys Asp Cys Met Glu Lys Arg Gly His Xaa
 305          310          315          320
Phe Phe Leu Pro Ala Ile Ser Asn Met Ala Ile Asp Leu Pro Asn Leu
 325          330          335
Lys Cys Arg Gln Phe Ile Leu Xaa Ile Asn Cys Leu His Leu Arg Xaa
 340          345          350
Arg Xaa Tyr Pro
 355

```

<210> 1136

<211> 317

<212> PRT

<213> Unknown (H38g52 protein)

<220>

<223> Synthetic construct

<400> 1136

```

Met Ile Asn Asp Ser Tyr Phe Gly Trp Leu Met Leu Leu Gly Phe Pro
1      5      10      15
Gly Lys Pro Gln Leu Glu Met Ile Ile Ser Gly Val Val Phe Phe Phe
20      25      30
Tyr Ala Ile Ser Leu Met Gly Asn Met Val Leu Ile Leu Leu Pro Leu
35      40      45
Leu Asp Lys His Leu Gln Thr Pro Ile Tyr Phe Phe Leu Arg Asn Leu
50      55      60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
65      70      75      80
Val Asn Ala Trp Gly Lys Asp Lys Lys Ile Thr Phe Gly Gly Cys Ala
85      90      95
Phe Gln Leu Phe Thr Asn Val Thr Leu Cys Thr Val Glu Cys Met Leu
100     105     110
Leu Ala Val Met Ser Tyr Asp Pro Phe Asn Ala Val Cys Lys Pro Leu
115     120     125
Asp Tyr Met Thr Ile Met Asn Pro Gln Leu Cys Gln Gly Leu Val Ala
130     135     140
Met Thr Trp Leu Ile Gly Val Thr Asn Cys Met Ile Leu Ser Pro Cys
145     150     155     160
Pro Val Ser Leu Pro Arg Cys Gly Asp His His Leu Asp His Tyr Phe
165     170     175
Cys Glu Ile Ser Ala Met Val Lys Ile Ala Cys Gly Ala Thr Thr Val
180     185     190
Met Glu Glu Lys Pro Tyr Leu His Cys Val Val Val Val Val Phe Ile
195     200     205
Phe Leu Ala Ser Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
210     215     220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
225     230     235     240
Gly Thr Cys Phe Ser His Leu Ile Val Val Ser Ile Phe Tyr Gly Thr
245     250     255
Val Arg Tyr Met Tyr Ile Glu Pro Gly Asn Ser Pro Ser Gln Asp Glu
260     265     270
Gly Lys Leu Leu His Ile Phe Tyr Ser Ile Val Thr Pro Thr Leu Asn
275     280     285
Pro Tyr Pro Leu Arg Asn Lys Glu Phe Lys Trp Ala Met Lys Arg Leu
290     295     300
Ile Gly Lys Glu Lys Gly Ser Gly Asp Thr Ile Gly His
305     310     315

```

<210> 1137

<211> 312

<212> PRT

<213> Unknown (H38g53 protein)

<220>

<223> Synthetic construct

<400> 1137

```

Met Val Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
1      5      10      15
Glu His Pro Gly Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
20      25      30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
35      40      45
Leu Asp Pro Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
50      55      60

```

```

Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
65          70          75          80
Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
      85          90          95
Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
      100          105          110
Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
      115          120          125
His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
      130          135          140
Val Ala Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser
145          150          155          160
Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
      165          170          175
Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
      180          185          190
Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
      195          200          205
Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
210          215          220
Arg Ile Asn Ser Ala Lys Gly Arg Arg Lys Ala Phe Gly Thr Cys Ser
225          230          235          240
Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
      245          250          255
Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe
      260          265          270
Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr
      275          280          285
Thr Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Gly
290          295          300
Lys Glu Met Gly Leu Thr Gln Ser
305          310

```

<210> 1138

<211> 343

<212> PRT

<213> Unknown (H38g54 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(343)

<223> Xaa = Any Amino Acid

<400> 1138

```

Met Val Asn Gln Ser Ser Ala Pro Gly Phe Leu Leu Leu Gly Phe Ser
1          5          10          15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
      20          25          30
Tyr Leu Leu Thr Leu Gly Gly Leu Ile Ile Leu Leu Ser Val Leu Asp
      35          40          45
Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe
50          55          60
Leu Asp Leu Cys Phe Thr Ile Ser Cys Val Pro Gly Met Leu Val Asn
65          70          75          80
Leu Trp Glu Pro Lys Lys Thr Ile Ile Leu Leu Gly Cys Ser Val Gln
      85          90          95
Phe Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr
      100          105          110
Val Met Ala Phe Asp Arg Tyr Met Ala Ile Phe Lys Pro Leu Arg His

```



```

      115      120      125
Ala Thr Ile Val His Leu Cys Leu Cys Trp Gln Leu Ala Ser Val Ala
  130      135      140
Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser Thr Leu
  145      150      155      160
Arg Leu Pro Phe Cys Pro His Gln Gln Val Asp Asp Phe Val Cys Glu
      165      170      175
Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr Asn Glu
      180      185      190
Ile Gln Met Ala Val Ala Ser Val Phe Ile Leu Ala Val Pro Ser Leu
      195      200      205
Ile Leu Val Ser Tyr Gly Ala Ile Ala Trp Ala Val Leu Arg Ile Thr
      210      215      220
Ala Lys Gly Gln Arg Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr
  225      230      235      240
Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro
      245      250      255
Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr
      260      265      270
Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275      280      285
Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Ala Lys Glu Met Gly
      290      295      300
Leu Ile Gln Ser Xaa Gly Arg Ala Val Xaa Cys Ala Phe Xaa Ile Lys
  305      310      315      320
Lys Lys Leu Phe Ile Leu Leu Xaa Thr Ser Leu Ser Ser Gln Val Tyr
      325      330      335
Tyr Leu Ser Tyr Thr His His
      340

```

<210> 1139

<211> 291

<212> PRT

<213> Unknown (H38g55 protein)

<220>

<223> Synthetic construct

<400> 1139

```

Met Phe Ala Ala Leu Val Leu Leu Cys Tyr Leu Leu Thr Leu Thr Gly
  1      5      10      15
Asn Ser Ala Leu Val Leu Leu Ala Val Arg Asp Pro Arg Leu His Thr
      20      25      30
Pro Met Tyr Tyr Phe Leu Cys His Leu Ala Leu Val Asp Ala Gly Phe
      35      40      45
Thr Thr Ser Val Val Pro Pro Leu Leu Ala Asn Leu Arg Gly Pro Ala
      50      55      60
Leu Trp Leu Pro Arg Ser His Cys Thr Ala Gln Leu Cys Ala Ser Leu
  65      70      75      80
Ala Leu Gly Ser Ala Glu Cys Val Leu Leu Ala Val Met Ala Leu Asp
      85      90      95
Arg Ala Ala Lys Lys Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser
      100      105      110
Leu Gly Arg Gly Gln Ala Gly Gln Ser Ala Ser Trp Leu Ser Gly Leu
      115      120      125
Thr Asn Ser Val Ala Gln Thr Ala Leu Leu Ala Glu Arg Pro Leu Cys
      130      135      140
Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala Leu Leu
  145      150      155      160
Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln Met Phe
      165      170      175

```

Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala
 180 185 190
 Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly
 195 200 205
 Gly Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val
 210 215 220
 Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln
 225 230 235 240
 Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr Thr Val
 245 250 255
 Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Lys
 260 265 270
 Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser Leu Gly Arg Gly Gln
 275 280 285
 Ala Gly Gln
 290

<210> 1140

<211> 307

<212> PRT

<213> Unknown (H38g56 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(307)

<223> Xaa = Any Amino Acid

<400> 1140

Glu Leu Ile Thr Asn Ser Ser Ser Val Pro Ser Cys Glu Arg Thr Ile
 1 5 10 15
 Gln Ile Phe Leu Phe Ser Leu Ile Thr Thr Ile Tyr Ala Leu Thr Ile
 20 25 30
 Thr Gly Asn Gly Ala Ile Ala Phe Ala Leu Trp Cys Asp Arg Arg Leu
 35 40 45
 His Thr Pro Met Tyr Met Phe Leu Gly Asp Phe Ser Phe Leu Glu Ile
 50 55 60
 Trp Tyr Val Phe Ser Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser
 65 70 75 80
 Glu Lys Thr Asn Ile Ser Phe Ala Gly Cys Phe Leu Gln Ile Tyr Phe
 85 90 95
 Phe Phe Ser Leu Asn Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala
 100 105 110
 Phe Asp Gln Asn Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Asn Ile
 115 120 125
 Met Thr Gly His Leu Cys Ala Lys Leu Ala Ile Leu Cys Trp Val Cys
 130 135 140
 Gly Phe Leu Trp Phe Leu Ile Pro Ile Val Leu Ile Ser Gln Met Pro
 145 150 155 160
 Phe Cys Gly Pro Asn Ile Ile Asp His Val Val Cys Asp Pro Gly Pro
 165 170 175
 Leu Phe Ala Leu Asp Cys Val Ser Ala Pro Arg Ile Gln Leu Phe Cys
 180 185 190
 Tyr Thr Leu Ser Ser Leu Val Ile Phe Gly Asn Phe Leu Phe Ile Ile
 195 200 205
 Gly Ser Tyr Thr Ile Val Leu Lys Val Val Leu Gly Thr Pro Ser Ser
 210 215 220
 Thr Gly Arg His Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val
 225 230 235 240
 Val Ser Leu Cys Tyr Gly Ser Leu Met Val Met Tyr Val Ser Pro Gly

				245					250					255					
Leu	Gly	His	Ser	Thr	Glu	Met	Gln	Lys	Ile	Val	Thr	Leu	Phe	Tyr	Ala				
			260					265					270						
Met	Val	Thr	Ser	Leu	Phe	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Gln	Asn	Lys				
		275					280					285							
Glu	Ile	Lys	Ala	Ala	Leu	Arg	Lys	Val	Leu	Val	Ser	Ser	Asn	Ile	Ile				
	290					295					300								
Xaa	Gly	Ile																	
305																			

<210> 1141

<211> 221

<212> PRT

<213> Unknown (H38g57 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(221)

<223> Xaa = Any Amino Acid

<400> 1141

Ala	Cys	Lys	His	Asp	Met	Ile	Leu	Thr	Val	Met	Ala	Tyr	Asp	Cys	Leu				
1				5					10					15					
Val	Ala	Ile	Cys	Arg	Pro	Leu	His	Tyr	Pro	Val	Ile	Val	Asn	Pro	His				
			20					25					30						
Leu	Cys	Val	Phe	Phe	Val	Leu	Val	Ser	Phe	Phe	Ile	Ser	Met	Xaa	Asp				
		35				40						45							
Ser	Gln	Leu	His	Ser	Xaa	Ile	Val	Leu	Gln	Phe	Thr	Ile	Ile	Lys	Asn				
	50					55					60								
Val	Glu	Ile	Ser	Asn	Phe	Val	Cys	Asp	Pro	Ser	Gln	Phe	Leu	Lys	Leu				
	65				70					75					80				
Ala	Cys	Ser	Asp	Ser	Val	Ile	Asn	Ser	Ile	Phe	Thr	Tyr	Phe	His	Ser				
			85					90						95					
Thr	Met	Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Ile	Leu	Leu	Ser	Tyr	Phe				
			100					105						110					
Lys	Ile	Val	Thr	Phe	Ile	Leu	Trp	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr				
		115				120						125							
Lys	Ala	Phe	Ser	Thr	Cys	Asp	Ser	His	Leu	Ala	Val	Val	Cys	Xaa	Phe				
	130					135					140								
Tyr	Gly	Thr	Gly	Ile	Gly	Val	Tyr	Leu	Thr	Ser	Ala	Leu	Ser	Pro	Pro				
	145				150					155				160					
Pro	Arg	Asn	Gly	Val	Met	Ala	Ser	Val	Met	Tyr	Ala	Val	Val	Thr	Pro				
			165					170						175					
Met	Leu	Asn	Leu	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Ser				
			180					185					190						
Ala	Leu	Trp	Arg	Leu	Leu	Ser	Arg	Thr	Val	Glu	Ser	His	Asp	Leu	Phe				
		195				200						205							
His	Pro	Phe	Ser	Cys	Val	Gly	Lys	Gly	Asn	His	Ile	Lys							
	210					215					220								

<210> 1142

<211> 314

<212> PRT

<213> Unknown (H38g58 protein)

<220>

<223> Synthetic construct

<400> 1142

```

Met Ala Lys Asn Asn Leu Thr Arg Val Thr Glu Phe Ile Leu Met Gly
 1           5           10           15
Phe Met Asp His Pro Lys Leu Glu Ile Pro Leu Phe Leu Val Phe Leu
 20           25           30
Ser Phe Tyr Leu Val Thr Leu Leu Gly Asn Val Gly Met Ile Met Leu
 35           40           45
Ile Gln Val Asp Val Lys Leu Tyr Thr Pro Met Tyr Phe Phe Leu Ser
 50           55           60
His Leu Ser Leu Leu Asp Ala Cys Tyr Thr Ser Val Ile Thr Pro Gln
 65           70           75           80
Ile Leu Ala Thr Leu Ala Thr Gly Lys Thr Val Ile Ser Tyr Gly His
 85           90           95
Cys Ala Ala Gln Phe Phe Leu Phe Thr Ile Cys Ala Gly Thr Glu Cys
 100           105           110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Arg Asn
 115           120           125
Pro Leu Leu Tyr Thr Val Ala Met Asn Pro Arg Leu Cys Trp Ser Leu
 130           135           140
Val Val Gly Ala Tyr Val Cys Gly Val Ser Gly Ala Ile Leu Arg Thr
 145           150           155           160
Thr Cys Thr Phe Thr Leu Ser Phe Cys Lys Asp Asn Gln Ile Asn Phe
 165           170           175
Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180           185           190
Ala Asn Ile Glu Ile Val Ile Ile Phe Phe Gly Asn Phe Val Ile Leu
 195           200           205
Ala Asn Ala Ser Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile Lys Thr
 210           215           220
Ile Leu Lys Val Lys Ser Ser Gly Gly Arg Ala Lys Thr Phe Ser Thr
 225           230           235           240
Cys Ala Ser His Ile Thr Ala Val Ala Leu Phe Phe Gly Ala Leu Ile
 245           250           255
Phe Met Tyr Leu Gln Ser Gly Ser Gly Lys Ser Leu Glu Glu Asp Lys
 260           265           270
Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275           280           285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Arg Lys Val
 290           295           300
Ala Arg Arg Leu Gln Val Ser Leu Ser Met
305           310

```

<210> 1143

<211> 315

<212> PRT

<213> Unknown (H38g59 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1143

```

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1           5           10           15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
 20           25           30
Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
 35           40           45
Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe

```

```

      50      55      60
Phe Phe Leu Ser Thr Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser
65      70      75      80
Trp Glu Leu Xaa Val Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile
      85      90      95
Ser Tyr Asn Ser Cys Ser Val Gln Met Ile Thr His Leu Phe Leu Gly
      100      105      110
Thr Ala Gln Cys Leu Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val
      115      120      125
Glu Ile Ser Tyr Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val
      130      135      140
Cys Ile Gln Leu Ala Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala
145      150      155      160
Val Thr Leu Ile Ile Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val
      165      170      175
Ile Asn His Phe Thr Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys
      180      185      190
Ser Asp Thr Leu Val Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe
      195      200      205
Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile
      210      215      220
Phe Val Arg Ala Val Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly
225      230      235      240
Ser His Leu Thr Gly Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met
      245      250      255
Tyr Leu Lys Pro Gln Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val
      260      265      270
Ser Lys Leu Tyr Gly Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr
      275      280      285
Ile Gln Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys
      290      295      300
Gly Asn Glu Lys Ser Xaa Gln Phe Ser Leu Asn
305      310      315

```

<210> 1144

<211> 351

<212> PRT

<213> Unknown (H38g61 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(351)

<223> Xaa = Any Amino Acid

<400> 1144

```

Met Asp Ile Leu Val Ile Asp Asn Gly Ser Glu Val Thr Glu Phe Ile
1      5      10      15
Leu Val Gly Leu Tyr Asn His Pro Lys Phe Gln Ile Ala Phe Tyr Arg
      20      25      30
Thr Met Val Val Val Tyr Leu Ile Thr Phe Val Gly Ser Ser Leu Ile
      35      40      45
Ile Val Val Val Lys Val Asp Gly Trp Leu His Thr Pro Met Cys Phe
      50      55      60
Phe Leu Ser Asn Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Asn Ser
65      70      75      80
Val Pro Phe Leu Leu Phe Asn Gly Leu Arg Asp Tyr Pro Thr Ile Ser
      85      90      95
Tyr Asn Ser Cys Tyr Ala Gln Met Thr Ser Ala Phe Phe Leu Gly Met
      100      105      110

```

```

Thr Gly Cys Leu Leu Leu Ala Val Met Ala Tyr Glu Arg Phe Val Val
      115              120              125
Ile Ser Asn Pro Leu Arg Tyr Ile Ile Ile Met Asn Asn Lys Val Cys
      130              135              140
Ile Gln Leu Ala Met Val Thr Trp Ala Ser Ala Ser Pro Tyr Val Ile
145      150              155              160
Asn Thr Ile Ile Ala Ile Ile His Cys Asn Asn Thr Leu Ile Ala Met
      165              170              175
Ile Ala Leu Ser Ile Pro Ala His Phe Cys Gly His Asn Val Ile Asn
      180              185              190
His Phe Thr Cys Glu Val Gln Glu Leu Leu Lys Leu Val Cys Ser Asp
      195              200              205
Ile Pro Gly Ser Leu Ile Leu Gly Leu Val Ile Gly Ile Phe Thr Leu
      210              215              220
Ser Leu Pro Phe Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Phe Ala
225      230              235              240
Tyr Ala His Ile Val Val Ala Val Leu Arg Ile Asn Ser Ala Glu Ala
      245              250              255
Arg Leu Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Ile Ile
      260              265              270
Ile Phe Tyr Gly Thr Ala Thr Tyr Met Tyr Leu Lys Pro Gln Ser Arg
      275              280              285
Glu Ser Gln Asp Glu Gly Lys Val Ile Ser Val Phe Phe Leu Lys Val
      290              295              300
Glu Lys Gln His Gln Asn Asp Ser Ile Ser Val Phe Tyr Gly Val Val
305      310              315              320
Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asp Lys Asp Ala
      325              330              335
Lys His Ala Leu Arg Lys Ile Ile Arg Lys Lys Glu Ser Xaa Lys
      340              345              350

```

<210> 1145

<211> 318

<212> PRT

<213> Unknown (H38g62 protein)

<220>

<223> Synthetic construct

<400> 1145

```

Met Asp Lys Ile Asn Gln Thr Phe Val Arg Glu Phe Ile Leu Leu Gly
  1              5              10              15
Leu Ser Gly Tyr Pro Lys Leu Glu Ile Ile Phe Phe Ala Leu Ile Leu
      20              25              30
Val Met Tyr Val Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala
      35              40              45
Ser Ile Leu Asp Ser Arg Leu His Met Pro Met Tyr Phe Phe Leu Gly
      50              55              60
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Ile Pro Ser
      65              70              75              80
Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly
      85              90              95
Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys
      100              105              110
Phe Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
      115              120              125
Pro Leu Arg Tyr Pro Ile Ile Met Asn Lys Val Val Tyr Val Leu Leu
      130              135              140
Thr Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Thr Val Gln Thr
145      150              155              160
Ser Leu Ala Met Arg Trp Pro Phe Cys Gly Asn Asn Ile Ile Asn His

```

```

      165      170      175
Phe Leu Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ser Asp Ile
      180      185      190
Ser Val Asn Ile Val Thr Leu Ala Val Ser Asn Ile Ala Phe Leu Val
      195      200      205
Leu Pro Leu Leu Val Ile Phe Phe Ser Tyr Met Phe Ile Leu Tyr Thr
      210      215      220
Ile Leu Arg Thr Asn Ser Ala Thr Gly Arg His Lys Ala Phe Ser Thr
      225      230      235      240
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe
      245      250      255
Phe Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Leu Gly Lys Asp Asn
      260      265      270
Leu Gln Ala Thr Glu Gly Leu Val Ser Met Phe Tyr Gly Val Val Thr
      275      280      285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290      295      300
Ala Ala Ile Lys Tyr Leu Leu Ser Arg Lys Ala Ile Asn Gln
      305      310      315

```

<210> 1146

<211> 319

<212> PRT

<213> Unknown (H38g63 protein)

<220>

<223> Synthetic construct

<400> 1146

```

Met Phe Pro Ala Asn Trp Thr Ser Val Lys Val Phe Phe Phe Leu Gly
  1      5      10      15
Phe Phe His Tyr Pro Lys Val Gln Val Ile Ile Phe Ala Val Cys Leu
      20      25      30
Leu Met Tyr Leu Ile Thr Leu Leu Gly Asn Ile Phe Leu Ile Ser Ile
      35      40      45
Thr Ile Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Leu Asp Ile Trp Tyr Ser Ser Ala Leu Ser Pro
      65      70      75      80
Met Leu Ala Asn Phe Val Ser Gly Arg Asn Thr Ile Ser Phe Ser Gly
      85      90      95
Cys Ala Thr Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
      100      105      110
Val Leu Leu Pro Met Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115      120      125
Pro Leu Arg Tyr Pro Val Ile Met Asn Arg Arg Thr Cys Val Gln Ile
      130      135      140
Ala Ala Gly Ser Trp Met Thr Gly Cys Leu Thr Ala Met Val Glu Met
      145      150      155      160
Met Ser Val Leu Pro Leu Ser Leu Cys Gly Asn Ser Ile Ile Asn His
      165      170      175
Phe Thr Cys Glu Ile Leu Ala Ile Leu Lys Leu Val Cys Val Asp Thr
      180      185      190
Ser Leu Val Gln Leu Ile Met Leu Val Ile Ser Val Leu Leu Leu Pro
      195      200      205
Met Pro Met Leu Leu Ile Cys Ile Ser Tyr Ala Phe Ile Leu Ala Ser
      210      215      220
Ile Leu Arg Ile Ser Ser Val Glu Gly Arg Ser Lys Ala Phe Ser Thr
      225      230      235      240
Cys Thr Ala His Leu Met Val Val Val Leu Phe Tyr Gly Thr Ala Leu
      245      250      255

```

<210> 1148
<211> 321

<212> PRT

<213> Unknown (H38g65 protein)

<220>

<223> Synthetic construct

<400> 1148

```

Met Gly Met Glu Gly Leu Leu Gln Asn Ser Thr Asn Phe Val Leu Thr
 1           5           10           15
Gly Leu Ile Thr His Pro Ala Phe Pro Gly Leu Leu Phe Ala Ile Val
          20           25           30
Phe Ser Ile Phe Val Val Ala Ile Thr Ala Asn Leu Val Met Ile Leu
          35           40           45
Leu Ile His Met Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu
          50           55           60
Ser Gln Leu Ser Ile Met Asp Thr Ile Tyr Ile Cys Ile Thr Val Pro
65          70          75          80
Lys Met Leu Gln Asp Leu Leu Ser Lys Asp Lys Thr Ile Ser Phe Leu
          85          90          95
Gly Cys Ala Val Gln Ile Phe Leu Tyr Leu Thr Leu Ile Gly Gly Glu
          100         105         110
Phe Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
          115         120         125
Asn Pro Leu Arg Tyr Pro Leu Leu Met Asn Arg Arg Val Cys Leu Phe
130         135         140
Met Val Val Gly Ser Trp Val Gly Gly Ser Leu Asp Gly Phe Met Leu
145         150         155         160
Thr Pro Val Thr Met Ser Phe Pro Phe Cys Arg Ser Arg Glu Ile Asn
          165         170         175
His Phe Phe Cys Glu Ile Pro Ala Val Leu Lys Leu Ser Cys Thr Asp
          180         185         190
Thr Ser Leu Tyr Glu Thr Leu Met Tyr Ala Cys Cys Val Leu Met Leu
          195         200         205
Leu Ile Pro Leu Ser Val Ile Ser Val Ser Tyr Thr His Ile Leu Leu
210         215         220
Thr Val His Arg Met Asn Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala
225         230         235         240
Thr Cys Ser Ser His Ile Met Ala Val Ser Val Phe Tyr Gly Ala Ala
          245         250         255
Phe Tyr Thr Asn Val Leu Pro His Ser Tyr His Thr Pro Glu Lys Asp
          260         265         270
Lys Val Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro
          275         280         285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Ala Ala Leu Arg Lys
          290         295         300
Val Leu Gly Arg Cys Gly Ser Ser Gln Ser Ile Arg Val Ala Thr Val
305         310         315         320
Ile

```

<210> 1149

<211> 311

<212> PRT

<213> Unknown (H38g66 protein)

<220>

<223> Synthetic construct

<400> 1149

```

Met Ala His Thr Asn Glu Ser Met Val Ser Glu Phe Val Leu Leu Gly
 1           5           10           15

```

Leu Ser Asn Ser Trp Gly Leu Gln Leu Phe Phe Phe Ala Ile Phe Ser
 20 25 30
 Ile Val Tyr Val Thr Ser Val Leu Gly Asn Val Leu Ile Ile Val Ile
 35 40 45
 Ile Ser Phe Asp Ser His Leu Asn Ser Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Asn Leu Ser Phe Ile Asp Ile Cys Gln Ser Asn Phe Ala Thr Pro Lys
 65 70 75 80
 Met Leu Val Asp Phe Phe Ile Glu Arg Lys Thr Ile Ser Phe Glu Gly
 85 90 95
 Cys Met Ala Gln Ile Phe Val Leu His Ser Phe Val Gly Ser Glu Met
 100 105 110
 Met Leu Leu Val Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Ser Thr Ile Met Asn Arg Arg Leu Cys Val Ile Phe
 130 135 140
 Val Ser Ile Ser Trp Ala Val Gly Val Leu His Ser Val Ser His Leu
 145 150 155 160
 Ala Phe Thr Val Asp Leu Pro Phe Cys Gly Pro Asn Glu Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Leu Val Ile Glu Leu Ala Cys Met Asp Thr
 180 185 190
 Tyr Glu Met Glu Ile Met Thr Leu Thr Asn Ser Gly Leu Ile Ser Leu
 195 200 205
 Ser Cys Phe Leu Ala Leu Ile Ile Ser Tyr Thr Ile Ile Leu Ile Gly
 210 215 220
 Val Arg Cys Arg Ser Ser Ser Gly Ser Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Thr Ala His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Cys Ile Tyr
 245 250 255
 Phe Tyr Ile Trp Pro Phe Ser Arg Leu Pro Val Asp Lys Phe Leu Ser
 260 265 270
 Val Phe Tyr Thr Val Cys Thr Pro Leu Leu Asn Pro Ile Ile Tyr Ser
 275 280 285
 Leu Arg Asn Glu Asp Val Lys Ala Ala Met Trp Lys Leu Arg Asn Arg
 290 295 300
 His Val Asn Ser Trp Lys Asn
 305 310

<210> 1150

<211> 312

<212> PRT

<213> Unknown (H38g67 protein)

<220>

<223> Synthetic construct

<400> 1150

Met Asp Gln Lys Asn Gly Ser Ser Phe Thr Gly Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Pro Gln Leu Glu Leu Val Leu Phe Val Val Leu Leu
 20 25 30
 Ile Phe Tyr Ile Phe Thr Leu Leu Gly Asn Lys Thr Ile Ile Val Leu
 35 40 45
 Ser His Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Phe Ser
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Gly Ile Val Pro Gln
 65 70 75 80
 Leu Leu Val Asn Leu Arg Gly Ala Asp Lys Ser Ile Ser Tyr Gly Gly
 85 90 95
 Cys Val Val Gln Leu Tyr Ile Ser Leu Gly Leu Gly Ser Thr Glu Cys

100	105	110
Val Leu Leu Gly Val Met Val Phe Asp Arg Tyr Ala Ala Val Cys Arg		
115	120	125
Pro Leu His Tyr Thr Val Val Met His Pro Cys Leu Tyr Val Leu Met		
130	135	140
Ala Ser Thr Ser Trp Val Ile Gly Phe Ala Asn Ser Leu Leu Gln Thr		
145	150	155
Val Leu Ile Leu Leu Leu Thr Leu Cys Gly Arg Asn Lys Leu Glu His		
165	170	175
Phe Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Val Asp Thr		
180	185	190
Thr Met Asn Glu Ser Glu Leu Phe Phe Val Ser Val Ile Ile Leu Leu		
195	200	205
Val Pro Val Ala Leu Ile Ile Phe Ser Tyr Ser Gln Ile Val Arg Ala		
210	215	220
Val Met Arg Ile Lys Leu Ala Thr Gly Gln Arg Lys Val Phe Gly Thr		
225	230	235
Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ala Ile		
245	250	255
Tyr Ala Tyr Leu Gln Pro Gly Asn Asn Tyr Ser Gln Asp Gln Gly Lys		
260	265	270
Phe Ile Ser Leu Phe Tyr Thr Ile Ile Thr Pro Met Ile Asn Pro Leu		
275	280	285
Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Lys Val		
290	295	300
Leu Trp Lys Asn Tyr Asp Ser Arg		
305	310	

<210> 1151

<211> 313

<212> PRT

<213> Unknown (H38g68 protein)

<220>

<223> Synthetic construct

<400> 1151

Met Cys Ser Gly Asn Gln Thr Ser Gln Asn Gln Thr Ala Ser Thr Asp	
1	5
Phe Thr Leu Thr Gly Leu Phe Ala Glu Ser Lys His Ala Ala Leu Leu	
20	25
Tyr Thr Val Thr Phe Leu Leu Phe Leu Met Ala Leu Thr Gly Asn Ala	
35	40
Leu Leu Ile Leu Leu Ile His Ser Glu Pro Arg Leu His Thr Pro Met	
50	55
Tyr Phe Phe Ile Ser Gln Leu Ala Leu Met Asp Leu Met Tyr Leu Cys	
65	70
Val Thr Val Pro Lys Met Leu Val Gly Gln Val Thr Gly Asp Asp Thr	
85	90
Ile Ser Pro Ser Gly Cys Gly Ile Gln Met Phe Phe His Leu Thr Leu	
100	105
Ala Gly Ala Glu Val Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr	
115	120
Ala Ala Val Cys Arg Pro Leu His Tyr Pro Leu Leu Met Asn Gln Arg	
130	135
Val Cys Gln Leu Leu Val Ser Ala Cys Trp Val Leu Gly Met Val Asp	
145	150
Gly Leu Leu Leu Thr Pro Ile Thr Met Ser Phe Pro Phe Cys Gln Ser	
165	170
Arg Lys Ile Leu Ser Phe Phe Cys Glu Thr Pro Ala Leu Leu Lys Leu	
180	185
	190

```

Ser Cys Ser Asp Val Ser Leu Tyr Lys Met Leu Thr Tyr Leu Cys Cys
  195      200      205
Ile Leu Met Leu Leu Thr Pro Ile Met Val Ile Ser Ser Ser Tyr Thr
  210      215      220
Leu Ile Leu His Leu Ile His Arg Met Asn Ser Ala Ala Gly Arg Arg
  225      230      235      240
Lys Ala Leu Ala Thr Cys Ser Ser His Met Ile Ile Val Leu Leu Leu
      245      250      255
Phe Gly Ala Ser Phe Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr
      260      265      270
Ala Glu Gln Asp Met Met Val Ser Ala Phe Tyr Thr Ile Phe Thr Pro
      275      280      285
Val Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Thr Arg
      290      295      300
Ala Met Arg Ser Met Met Gln Ser Arg
  305      310

```

<210> 1152

<211> 314

<212> PRT

<213> Unknown (H38g69 protein)

<220>

<223> Synthetic construct

<400> 1152

```

Met Asp Val Gly Asn Lys Ser Thr Met Ser Glu Phe Val Leu Leu Gly
  1      5      10      15
Leu Ser Asn Ser Trp Glu Leu Gln Met Phe Phe Phe Met Val Phe Ser
      20      25      30
Leu Leu Tyr Val Ala Thr Met Val Gly Asn Ser Leu Ile Val Ile Thr
      35      40      45
Val Ile Val Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Thr
      50      55      60
Asn Leu Ser Ile Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys
      65      70      75      80
Met Ile Thr Asp Tyr Leu Thr Gly His Lys Thr Ile Ser Phe Asp Gly
      85      90      95
Cys Leu Thr Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile
      100      105      110
Ile Leu Leu Met Ala Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys
      115      120      125
Pro Leu His Tyr Ala Ser Val Ile Ser Pro Gln Val Cys Val Ala Leu
      130      135      140
Val Val Ala Ser Trp Ile Met Gly Val Met His Ser Met Ser Gln Val
      145      150      155      160
Ile Phe Ala Leu Thr Leu Pro Phe Cys Gly Pro Tyr Glu Val Asp Ser
      165      170      175
Phe Phe Cys Asp Leu Pro Val Val Phe Gln Leu Ala Cys Val Asp Thr
      180      185      190
Tyr Val Leu Gly Leu Phe Met Ile Ser Thr Ser Gly Ile Ile Ala Leu
      195      200      205
Ser Cys Phe Ile Val Leu Phe Asn Ser Tyr Val Ile Val Leu Val Thr
      210      215      220
Val Lys His His Ser Ser Arg Gly Ser Ser Lys Ala Leu Ser Thr Cys
      225      230      235      240
Thr Ala His Phe Ile Val Val Phe Leu Phe Phe Gly Pro Cys Ile Phe
      245      250      255
Ile Tyr Met Trp Pro Leu Ser Ser Phe Leu Thr Asp Lys Ile Leu Ser
      260      265      270
Val Phe Tyr Thr Ile Phe Thr Pro Thr Leu Asn Pro Ile Ile Tyr Thr

```

275 280 285
 Leu Arg Asn Gln Glu Val Lys Ile Ala Met Arg Lys Leu Lys Asn Arg
 290 295 300
 Phe Leu Asn Phe Asn Lys Ala Met Pro Ser
 305 310

<210> 1153

<211> 310

<212> PRT

<213> Unknown (H38g70 protein)

<220>

<223> Synthetic construct

<400> 1153

Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe
 1 5 10 15
 Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
 20 25 30
 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
 35 40 45
 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
 50 55 60
 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met
 65 70 75 80
 Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
 85 90 95
 Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu
 100 105 110
 Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
 115 120 125
 Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
 130 135 140
 Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val
 145 150 155 160
 Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
 165 170 175
 Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
 180 185 190
 Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
 195 200 205
 Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
 210 215 220
 Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys
 225 230 235 240
 Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile
 245 250 255
 Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
 260 265 270
 Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu
 290 295 300
 Gly Val Glu Arg Ala Leu
 305 310

<210> 1154

<211> 323

<212> PRT

<213> Unknown (H38g71 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1154

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Leu Pro Val Leu Ala Leu Leu Ser
 20      25      30
Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser
 35      40      45
Ile Leu Ala Val Ser Ser Asp Ser Pro His Thr Pro Val Tyr Phe Phe
 50      55      60
Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Pro Thr Val
 65      70      75      80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser His
 85      90      95
Ala Gly Cys Leu Ala Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile
 100      105      110
Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Ser Phe Val Ala Ile
 115      120      125
Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val
 130      135      140
Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
 145      150      155      160
His Gly Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu Ile
 165      170      175
Ser Asn Phe Leu Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser
 180      185      190
Asp Ser Val Thr Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe
 195      200      205
Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys Ile Val
 210      215      220
Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe
 225      230      235      240
Thr Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr
 245      250      255
Gly Ile Gly Met Tyr Leu Thr Ser Ala Leu Ser Pro Pro Pro Arg Asn
 260      265      270
Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn
 275      280      285
Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg
 290      295      300
Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe
 305      310      315      320
Phe Leu Cys

```

<210> 1155

<211> 315

<212> PRT

<213> Unknown (H38g72 protein)

<220>

<223> Synthetic construct

<400> 1155

```

Met Ala Trp Ser Asn Gln Ser Ala Val Thr Glu Phe Ile Leu Arg Gly

```

```

1           5           10           15
Leu Ser Ser Ser Leu Glu Leu Gln Ile Phe Tyr Phe Leu Phe Phe Ser
20           25           30
Ile Val Tyr Ala Ala Thr Val Leu Gly Asn Leu Leu Ile Val Val Thr
35           40           45
Ile Ala Ser Glu Pro His Leu His Ser Pro Thr Tyr Phe Leu Leu Gly
50           55           60
Asn Leu Ser Phe Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys
65           70           75           80
Met Ile Ala Asp Phe Leu Arg Glu His Lys Ala Ile Ser Phe Glu Gly
85           90           95
Cys Met Thr Gln Met Phe Phe Leu His Leu Leu Gly Gly Ala Glu Ile
100          105          110
Val Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Lys
115          120          125
Pro Leu His Tyr Leu Thr Ile Met Ser Arg Arg Met Cys Val Gly Leu
130          135          140
Val Ile Leu Ser Trp Ile Val Gly Ile Phe His Ala Leu Ser Gln Leu
145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Glu Val Asp Ser
165          170          175
Phe Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Val Asp Thr
180          185          190
Tyr Ile Leu Gly Val Phe Met Ile Ser Thr Ser Gly Met Ile Ala Leu
195          200          205
Val Cys Phe Ile Leu Leu Val Ile Ser Tyr Thr Ile Ile Leu Val Thr
210          215          220
Val Arg Gln Arg Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Cys
225          230          235          240
Ser Ala His Phe Thr Val Val Thr Leu Phe Phe Gly Pro Cys Thr Phe
245          250          255
Ile Tyr Val Trp Pro Phe Thr Asn Phe Pro Ile Asp Lys Val Leu Ser
260          265          270
Val Phe Tyr Thr Ile Tyr Thr Pro Leu Leu Asn Pro Val Ile Tyr Thr
275          280          285
Val Arg Asn Lys Asp Val Lys Tyr Ser Met Arg Lys Leu Ser Ser His
290          295          300
Ile Phe Lys Ser Arg Lys Thr Asp His Thr Pro
305          310          315

```

<210> 1156

<211> 321

<212> PRT

<213> Unknown (H38g73 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1156

```

Met Lys Lys Tyr Met Glu Arg Thr Asn Xaa Thr Thr Glu Phe Glu Leu
1           5           10           15
Ile Leu Ile Ser Leu Xaa Val Leu Ile Ser Xaa Gln Lys Leu Leu Phe
20           25           30
Val Thr Cys Leu Val Val Tyr Leu Val Thr Leu Leu Gly Asn Arg Ile
35           40           45
Gln Ile Ile Pro Thr Leu Leu Val Ser His Leu Tyr Leu Cys His Gly
50           55           60

```

```

Asn Pro Ser Phe Leu Asp Ile Gly Leu Thr Ser Ser Phe Thr Pro Ser
65          70          75          80
Ile Leu Ile Asn Phe Leu Ser Glu Gly Lys Lys Leu Ser Phe Thr Asp
      85          90          95
Cys Ile Ile Gln Met Ser Ile Phe Tyr Ser Met Gly Ser Thr Glu Cys
      100        105        110
Val Leu Leu Ala Val Met Ala Tyr Asp Asn Cys Val Val Ile Ser Lys
      115        120        125
Phe Leu Arg Tyr Pro Leu Ile Ile Asn Lys Val Asn Lys Ile Lys Lys
      130        135        140
Val Leu Cys Val Phe Met Ala Thr Val Ser Tyr Glu Leu Gly Phe Leu
145          150          155          160
Asn Arg Gln Asn Val Leu Ile Val Thr Tyr Ala Met His Phe Cys Gly
      165        170        175
Lys His Ile Ile Asn His Phe Tyr Lys Ile Leu Gln Leu Met Ala Leu
      180        185        190
Ala Cys Ile Asp Ile Ser Leu Asn Glu Asn Ile Ile Ile Leu Gly Lys
      195        200        205
Val Asn Phe Ser Phe Thr Leu Leu Leu Pro Phe Gln Phe Phe Ile Phe
      210        215        220
Ser Phe Leu Tyr Phe His His Leu Cys Cys Ile Glu Ile Asn Ser Ala
225          230          235          240
Glu Gly Arg Lys Lys Val Ser Ser Thr Cys Ser Ala His Ile Thr Val
      245        250        255
Val Ile Val Phe His Arg Thr Ile Leu Phe Met Tyr Ile Lys Ser Thr
      260        265        270
Ser Asn Gly Thr Thr Ser Glu Lys Leu Val Asp Leu Phe Cys Gly Val
      275        280        285
Val Met Leu Met Leu Asn Leu Ile Ile Tyr Ser Leu Gly Asn Met Glu
      290        295        300
Val Leu Gly Val Met Lys Lys Leu Ile Ser Met Ser Arg Pro Trp Cys
305          310          315          320
Trp

```

<210> 1157
 <211> 325
 <212> PRT
 <213> Unknown (H38g74 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(325)
 <223> Xaa = Any Amino Acid

```

<400> 1157
His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Met Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu
      35      40      45
Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Gln Leu His Thr Pro Met
      50      55      60
Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser
65          70          75          80
Pro Met Val Pro Lys Met Ile Met Asp Met Gln Ser His Ser Arg Val
      85          90          95
Ile Ser His Ala Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe

```



```

      100      105      110
Ala Cys Ile Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe
      115      120      125
Val Ala Ile Cys Arg Pro Leu His Tyr Pro Val Ile Met Asn Pro His
      130      135      140
Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp
      145      150      155      160
Ser Gln Leu His Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Asn Asn
      165      170      175
Val Glu Ile Ala Asn Phe Val Tyr Glu Pro Ser Gln Leu Leu Asn Leu
      180      185      190
Asp Cys Ser Asp Thr Val Ile Asn Ser Val Phe Ile Tyr Phe Asp Ser
      195      200      205
Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys
      210      215      220
Ile Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys
      225      230      235      240
Ala Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp
      245      250      255
Gly Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro
      260      265      270
Arg Asn Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met
      275      280      285
Leu Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala
      290      295      300
Leu Gln Arg Leu Ser Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro
      305      310      315      320
Ser Phe Phe Leu Cys
      325

```

<210> 1158

<211> 319

<212> PRT

<213> Unknown (H38g75 protein)

<220>

<223> Synthetic construct

<400> 1158

```

Met Gly Asn Trp Thr Ala Ala Val Thr Glu Phe Val Leu Leu Gly Phe
  1      5      10      15
Ser Leu Ser Arg Glu Val Glu Leu Leu Leu Val Leu Leu Leu Pro
      20      25      30
Thr Phe Leu Leu Thr Leu Leu Gly Asn Leu Leu Ile Ile Ser Thr Val
      35      40      45
Leu Ser Cys Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Cys Asn
      50      55      60
Leu Ser Ile Leu Asp Ile Leu Phe Thr Ser Val Ile Ser Pro Lys Val
      65      70      75      80
Leu Ala Asn Leu Gly Ser Arg Asp Lys Thr Ile Ser Phe Ala Gly Cys
      85      90      95
Ile Thr Gln Cys Tyr Phe Tyr Phe Phe Leu Gly Thr Val Glu Phe Leu
      100      105      110
Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Ala Thr Ile Cys Cys Pro
      115      120      125
Leu Arg Tyr Thr Thr Ile Met Arg Pro Ser Val Cys Ile Gly Thr Val
      130      135      140
Val Phe Ser Trp Val Gly Gly Phe Leu Ser Val Leu Phe Pro Thr Ile
      145      150      155      160
Leu Ile Ser Gln Leu Pro Phe Cys Gly Ser Asn Ile Ile Asn His Phe
      165      170      175

```

Phe Cys Asp Ser Gly Pro L u Leu Ala Leu Ala Cys Ala Asp Thr Thr
 180 185 190
 Ala Ile Glu Leu Met Asp Phe Met Leu Ser Ser Met Val Ile Leu Cys
 195 200 205
 Cys Ile Val Leu Val Ala Tyr Ser Tyr Thr Tyr Ile Ile Leu Thr Ile
 210 215 220
 Val Arg Ile Pro Ser Ala Ser Gly Arg Lys Lys Ala Phe Asn Thr Cys
 225 230 235 240
 Ala Ser His Leu Thr Ile Val Ile Ile Pro Ser Gly Ile Thr Val Phe
 245 250 255
 Ile Tyr Val Thr Pro Ser Gln Lys Glu Tyr Leu Glu Ile Asn Lys Ile
 260 265 270
 Pro Leu Val Leu Ser Ser Val Val Thr Pro Phe Leu Asn Pro Phe Ile
 275 280 285
 Tyr Thr Leu Arg Asn Asp Thr Val Gln Gly Val Leu Arg Asp Val Trp
 290 295 300
 Val Arg Val Arg Gly Val Phe Glu Lys Arg Met Arg Ala Val Leu
 305 310 315

<210> 1159

<211> 313

<212> PRT

<213> Unknown (H38g76 protein)

<220>

<223> Synthetic construct

<400> 1159

Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly
 1 5 10 15
 Leu Ser Gln Thr Arg Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu
 20 25 30
 Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr
 35 40 45
 Ile Arg Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ala Leu Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Lys
 65 70 75 80
 Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Leu Phe Phe Leu His Phe Val Gly Ala Ser Glu Met
 100 105 110
 Phe Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ala Thr Ile Met Asn Arg Arg Leu Cys Cys Ile Leu
 130 135 140
 Val Ala Leu Ser Trp Met Gly Gly Phe Ile His Ser Ile Ile Gln Val
 145 150 155 160
 Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser
 165 170 175
 Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr
 180 185 190
 Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val
 195 200 205
 Val Trp Phe Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu
 210 215 220
 Leu Lys Lys His Ser Gly Ser Asp Glu Asn Thr Asn Arg Ala Met Ser
 225 230 235 240
 Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser
 245 250 255
 Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val

<210> 1160
<211> 313
<212> PRT
<213> Unknown (H38g77 protein)

<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(313)
<223> Xaa = Any Amino Acid

<400>	1160																		
Met	Glu	Ser	Gln	Arg	Asn	Ile	Xaa	Lys	Phe	Ile	Leu	Met	Ser	Leu	Ser				
1				5					10					15					
Ser	Ile	Gln	Asn	Ile	Gln	Ile	Phe	Val	Phe	Val	Phe	Leu	Phe	Cys	Asn				
		20						25					30						
Val	Ala	Ile	Leu	Val	Gly	Asn	Phe	Leu	Ile	Leu	Ile	Ser	Ile	Xaa	Cys				
		35					40					45							
Ser	Pro	Leu	Phe	Asn	Gln	Pro	Met	His	Tyr	Phe	Leu	Gly	Tyr	Met	Asn				
	50					55					60								
Ile	Tyr	Tyr	Thr	Ser	Cys	Val	Thr	Pro	Lys	Ile	Ile	Gly	Asp	Leu	Val				
65					70					75					80				
Val	Gly	Arg	Ile	Asn	Ile	Ser	Tyr	Asp	Arg	Ile	Phe	Pro	Met	His	Phe				
				85					90					95					
Phe	Gly	Ile	Ile	Glu	Ile	Phe	Ile	Leu	Thr	Val	Met	Ala	Phe	Asp	His				
			100					105					110						
Tyr	Val	Ala	Ile	Cys	Lys	Pro	Pro	Arg	Tyr	Leu	Ile	Ile	Met	Asn	Arg				
		115					120					125							
Thr	Lys	Tyr	Asn	Thr	Leu	Ile	Ser	Val	Ala	Trp	Leu	Leu	Gly	Leu	Ile				
	130					135					140								
His	Ser	Leu	Phe	Gln	Phe	Ser	Met	Lys	Ile	Trp	Leu	Pro	Phe	Cys	Gly				
145					150					155					160				
Ser	Asn	Lys	Val	Asp	Asp	Xaa	Tyr	Xaa	Asp	Ile	Phe	Pro	Leu	Leu	Lys				
				165					170					175					
Val	Ala	Cys	Thr	Asp	Thr	Cys	Ile	Thr	Gly	Val	Leu	Val	Val	Ala	Asn				
			180					185					190						
Ser	Gly	Met	Phe	Ala	Leu	Val	Thr	Phe	Val	Leu	Ser	Phe	Gly	Ser	Tyr				
		195					200					205							
Val	Ile	Ile	Leu	Phe	Pro	Leu	Lys	Asn	His	Ser	Val	Glu	Gly	Arg	Cys				
	210					215					220								
Lys	Ala	Leu	Ser	Thr	Cys	Gly	Ser	His	Ile	Thr	Met	Val	Ile	Phe	Phe				
225					230					235					240				
Phe	Glu	Pro	Ser	Ile	Phe	Ala	Tyr	Leu	Arg	Pro	Ser	Thr	Phe	Pro	Glu				
				245					250					255					
Asp	Lys	Ile	Ser	Ala	Leu	Phe	Tyr	Thr	Ile	Ile	Ala	Pro	Met	Phe	Asn				
			260					265					270						
His	Leu	Ile	Tyr	Asn	Leu	Arg	Asn	Thr	Glu	Met	Lys	Lys	Ala	Met	Arg				
		275					280					285							
Lys	Val	Trp	Tyr	Gln	Ile	Ser	Phe	Ser	Glu	Glu	Lys	Gln	Leu	Ile	Cys				
</																			

<210> 1161
 <211> 304
 <212> PRT
 <213> Unknown (H38g78 protein)

<220>
 <223> Synthetic construct

<400> 1161
 Met Arg Asn Gly Thr Val Ile Thr Glu Phe Ile Leu Leu Gly Phe Pro
 1 5 10 15
 Val Ile Gln Gly Leu Gln Thr Pro Leu Phe Ile Ala Ile Phe Leu Thr
 20 25 30
 Tyr Ile Leu Thr Leu Ala Gly Asn Gly Leu Ile Ile Ala Thr Val Trp
 35 40 45
 Ala Glu Pro Arg Leu Gln Ile Pro Met Tyr Phe Phe Leu Cys Asn Leu
 50 55 60
 Ser Phe Leu Glu Ile Trp Tyr Thr Thr Thr Val Ile Pro Lys Leu Leu
 65 70 75 80
 Gly Thr Phe Val Val Ala Arg Thr Val Ile Cys Met Ser Cys Cys Leu
 85 90 95
 Leu Gln Ala Phe Phe His Phe Phe Val Gly Thr Thr Glu Phe Leu Ile
 100 105 110
 Leu Thr Ile Met Ser Phe Asp Arg Tyr Leu Thr Ile Cys Asn Pro Leu
 115 120 125
 His His Pro Thr Ile Met Thr Ser Lys Leu Cys Leu Gln Leu Ala Leu
 130 135 140
 Ser Ser Trp Val Val Gly Phe Thr Ile Val Phe Cys Gln Thr Met Leu
 145 150 155 160
 Leu Ile Gln Leu Pro Phe Cys Gly Asn Asn Val Ile Ser His Phe Tyr
 165 170 175
 Cys Asp Val Gly Pro Ser Leu Lys Ala Ala Cys Ile Asp Thr Ser Ile
 180 185 190
 Leu Glu Leu Leu Gly Val Ile Ala Thr Ile Leu Val Ile Pro Gly Ser
 195 200 205
 Leu Leu Phe Asn Met Ile Ser Tyr Ile Tyr Ile Leu Ser Ala Ile Leu
 210 215 220
 Arg Ile Pro Ser Ala Thr Gly His Gln Lys Thr Phe Ser Thr Cys Ala
 225 230 235 240
 Ser His Leu Thr Val Val Ser Leu Leu Tyr Gly Ala Val Leu Phe Met
 245 250 255
 Tyr Leu Arg Pro Thr Ala His Ser Ser Phe Lys Ile Asn Lys Val Val
 260 265 270
 Ser Val Leu Asn Thr Ile Leu Thr Pro Leu Leu Asn Pro Phe Ile Tyr
 275 280 285
 Thr Ile Arg Asn Lys Glu Val Lys Gly Ala Leu Arg Lys Ala Met Thr
 290 295 300

<210> 1162
 <211> 321
 <212> PRT
 <213> Unknown (H38g79 protein)

<220>
 <223> Synthetic construct

<400> 1162
 Met Thr Ile Leu Leu Asn Ser Ser Leu Gln Arg Ala Thr Phe Phe Leu
 1 5 10 15
 Thr Gly Phe Gln Gly Leu Glu Gly Leu His Gly Trp Ile Ser Ile Pro

<210> 1163
<211> 323
<212> PRT
<213> Unknown (H38g80 protein)

```
<220>  
<223> Synthetic construct  
  
<221> VARIANT  
<222> (1)...(323)  
<223> Xaa = Any Amino Acid
```

```

<400> 1163
Met Gly Asn His Thr Thr Val Thr Glu Phe Val Leu Leu Gly Leu Ser
 1          5          10          15
Glu Thr Cys Glu Leu Gln Met Leu Ile Phe Leu Gly Leu Leu Leu Thr
      20          25          30
Tyr Leu Leu Thr Leu Leu Gly Asn Leu Val Ile Val Val Ile Thr Leu
      35          40          45
Met Asp Arg Arg Leu His Thr Thr Met Tyr Tyr Phe Leu Arg Asn Phe
 50          55          60

```

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Ala Val Pro Glu Ile Trp Phe Thr Ser Val Ile Phe Pro Lys Val Leu
65          70          75          80
Ala Asn Ile Leu Thr Gly Tyr Lys Thr Ile Ser Leu Pro Gly Cys Phe
          85          90          95
Leu Gln Ser Leu Leu Tyr Phe Phe Leu Gly Thr Thr Glu Phe Phe Leu
          100         105         110
Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Asn Pro Leu
          115         120         125
His Tyr Ala Thr Ile Met Ser Lys Arg Val Cys Val Gln Leu Val Leu
          130         135         140
Cys Xaa Trp Met Thr Gly Phe Leu Leu Ile Ile Ile Pro Ser Phe Leu
145          150         155         160
Val Leu Gln Gln Pro Phe Cys Gly Pro Asn Ile Ile Asn His Phe Phe
          165         170         175
Cys Asp Asn Phe Pro Leu Leu Lys Leu Ile Cys Ala Asp Met Thr Leu
          180         185         190
Ile Glu Leu Leu Gly Phe Val Ile Ala Asn Val Ser Leu Leu Gly Thr
          195         200         205
Leu Ser Met Thr Ala Thr Cys Tyr Gly His Ile Leu His Ala Ile Leu
210         215         220
His Ile Pro Ser Ala Lys Glu Lys Gln Lys Ala Phe Ser Ala Cys Ser
225         230         235         240
Ser His Ile Ile Val Val Ser Leu Phe Tyr Gly Ser Cys Ile Phe Met
          245         250         255
Tyr Ile Gln Ser Gly Lys Ser Asp Gln Lys Glu Asp Arg Asn Lys Val
          260         265         270
Ala Ala Leu Leu Asn Thr Val Val Thr Leu Met Leu Asn Pro Phe Ile
          275         280         285
Tyr Thr Leu Arg Asn Lys Gln Val Lys Gln Val Phe Arg Gln Gln Val
          290         295         300
Ser Lys Leu Leu Ile Xaa Ser Cys Val Lys Lys Lys Leu Lys Leu Ser
305          310         315         320
Ile Pro Arg

```

<210> 1164

<211> 317

<212> PRT

<213> Unknown (H38g81 protein)

<220>

<223> Synthetic construct

<400> 1164

```

Glu Ile Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu
1          5          10          15
Gly Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile
          20          25          30
Leu Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe
          35          40          45
Thr Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu
          50          55          60
Gly Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro
65          70          75          80
Arg Met Leu Val Asp Phe Leu Ser Ala Lys Asn Val Ile Ser Tyr Arg
          85          90          95
Gly Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu
          100         105         110
Gly Leu Leu Leu Val Ile Val Ala Phe Asp Arg Tyr Ile Ala Ile Cys
          115         120         125
Arg Pro Leu His Tyr Ser Thr Leu Met Asn Pro Arg Ala Cys Tyr Ala

```

130	135	140
Met Met Leu Ala Leu Trp	Leu Gly Gly Phe Val His	Ser Ile Ile Gln
145	150	155
Val Val Leu Ile Leu Arg	Leu Pro Phe Cys Gly	Pro Asn Gln Leu Asp
165	170	175
Asn Phe Phe Cys Asp Val	Pro Gln Val Ile Lys	Leu Ala Cys Thr Asp
180	185	190
Thr Phe Val Val Glu Leu	Leu Met Val Phe Asn	Ser Gly Leu Met Thr
195	200	205
Leu Leu Cys Phe Leu Gly	Leu Leu Ala Ser Tyr	Ala Val Ile Leu Cys
210	215	220
His Val Arg Lys Ala Ala	Ser Glu Leu Lys Asn	Lys Ala Met Ser Thr
225	230	235
Cys Thr Thr His Val Ile	Ile Ile Leu Leu Met	Phe Gly Pro Ala Ile
245	250	255
Phe Ile Tyr Met His Pro	Phe Arg Ala Leu Pro	Ala Asp Lys Val Val
260	265	270
Ser Phe Phe His Thr Val	Ile Phe Pro Leu Met	Asn Pro Met Ile Tyr
275	280	285
Thr Leu Arg Asn Gln Glu	Val Lys Thr Ser Met	Lys Arg Leu Leu Ser
290	295	300
Arg His Val Val Cys Gln	Val Asp Phe Ile Ile	Arg Asn
305	310	315

<210> 1165

<211> 287

<212> PRT

<213> Unknown (H38g82 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(287)

<223> Xaa = Any Amino Acid

<400> 1165

Val Ile Arg Asn Gln Thr	Met Val Thr Glu Phe Thr	Leu Val Ser Leu
1	5	10
Pro Ala Val Gln Glu Leu	Gln Ile Trp Leu Cys Val	Leu Leu Trp Leu
20	25	30
Val His Met Leu Thr Ile	Thr Gly Asn Leu Phe Val	Ile Phe Leu Thr
35	40	45
Trp Thr Asp Asn Cys Leu	Gln Thr Pro Met Asp Leu	Phe Leu Glu Lys
50	55	60
Lys Val Ile Ser Phe Ser	Gly Cys Ile Thr Gln Ile	Tyr Phe Tyr Phe
65	70	75
Phe Leu Gly Thr Val Ala	Phe Ile Pro Leu Ala Val	Thr Ser Phe Lys
85	90	95
His Cys Met Ala Thr Cys	Asp Pro Leu Cys Ser Thr	Ile Ile Ala Lys
100	105	110
Ser Arg Ala Cys Leu Leu	Leu Ala Leu Gly Cys Trp	Met Gly Thr Phe
115	120	125
Leu Ala Val Leu Arg Leu	Thr Ile Val Val Ser Arg	Leu Pro Asp Cys
130	135	140
Thr Glu Lys Ile Ser Pro	Phe Phe Cys Asp Ile Ala	Ser Leu Leu Gln
145	150	155
Val Ala Cys Ile Asp Ile	His Phe Ile Glu Met Ile	Ser Phe Leu Xaa
165	170	175
Ser Ser Leu Met Val Leu	Thr Ser Leu Val Leu	Asn Ala Thr Ser Tyr
180	185	190

Ala	Tyr	Ile	Ile	Ser	Thr	Leu	Leu	Cys	Ile	Pro	Ser	Ala	Gln	Gly	Cys
	195						200					205			
Gln	Glu	Ala	Phe	Ser	Thr	Cys	Ala	Ser	His	Ile	Thr	Ile	Ile	Phe	Ile
	210					215					220				
Ala	Cys	Arg	Asn	Ser	Ile	Ser	Thr	Cys	Val	Arg	Pro	Asn	Pro	Arg	Tyr
225					230					235					240
Xaa	Leu	Asp	Phe	Asp	Lys	Val	Thr	Ala	Ile	Leu	Thr	Ile	Val	Val	Thr
			245						250					255	
Ser	Phe	Leu	Asn	Pro	Arg	Ile	Tyr	Ser	Leu	Arg	Xaa	Arg	Lys	Tyr	Glu
			260					265					270		
Gly	Ser	Thr	Ile	Cys	Thr	Ile	Leu	Ser	Pro	His	Ser	Lys	Gly	Thr	
	275						280					285			

<210> 1166

<211> 307

<212> PRT

<213> Unknown (H38g83 protein)

<220>

<223> Synthetic construct

<400> 1166

Met	Glu	Ser	Glu	Asn	Arg	Thr	Val	Ile	Arg	Glu	Phe	Ile	Leu	Leu	Gly
1				5					10				15		
Leu	Thr	Gln	Ser	Gln	Asp	Ile	Gln	Leu	Leu	Val	Phe	Val	Leu	Val	Leu
			20					25					30		
Ile	Phe	Tyr	Phe	Ile	Ile	Leu	Pro	Gly	Asn	Phe	Leu	Ile	Ile	Phe	Thr
		35					40					45			
Ile	Lys	Ser	Asp	Pro	Gly	Leu	Thr	Ala	Pro	Leu	Tyr	Phe	Phe	Leu	Gly
	50					55					60				
Asn	Leu	Ala	Phe	Leu	Asp	Ala	Ser	Tyr	Ser	Phe	Thr	Val	Ala	Pro	Arg
65					70					75					80
Met	Leu	Val	Asp	Phe	Leu	Ser	Ala	Lys	Lys	Ile	Ile	Ser	Tyr	Arg	Gly
			85						90					95	
Cys	Ile	Thr	Gln	Leu	Phe	Phe	Leu	His	Phe	Leu	Gly	Gly	Gly	Glu	Gly
			100					105					110		
Leu	Leu	Leu	Val	Val	Met	Ala	Phe	Asp	Arg	Tyr	Ile	Ala	Ile	Cys	Arg
			115					120					125		
Pro	Leu	His	Tyr	Pro	Thr	Val	Met	Asn	Pro	Arg	Thr	Cys	Tyr	Ala	Met
			130				135					140			
Met	Leu	Ala	Leu	Trp	Leu	Gly	Gly	Phe	Val	His	Ser	Ile	Ile	Gln	Val
145					150					155					160
Val	Leu	Ile	Leu	Arg	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Gln	Leu	Asp	Asn
			165						170					175	
Phe	Phe	Cys	Asp	Val	Pro	Gln	Val	Ile	Lys	Leu	Ala	Cys	Thr	Asp	Thr
			180					185					190		
Phe	Val	Val	Glu	Leu	Leu	Met	Val	Phe	Asn	Ser	Gly	Leu	Met	Thr	Leu
			195				200					205			
Leu	Cys	Phe	Leu	Gly	Leu	Leu	Ala	Ser	Tyr	Ala	Val	Ile	Leu	Cys	Arg
	210						215				220				
Ile	Arg	Gly	Ser	Ser	Ser	Glu	Ala	Lys	Asn	Lys	Ala	Met	Ser	Thr	Cys
225					230					235					240
Ile	Thr	His	Ile	Ile	Val	Ile	Phe	Phe	Met	Phe	Gly	Pro	Gly	Ile	Phe
			245						250					255	
Ile	Tyr	Thr	Arg	Pro	Phe	Arg	Ala	Phe	Pro	Ala	Asp	Lys	Val	Val	Ser
			260					265					270		
Leu	Phe	His	Thr	Val	Ile	Phe	Pro	Leu	Leu	Asn	Pro	Val	Ile	Tyr	Thr
		275					280					285			
Leu	Arg	Asn	Gln	Glu	Val	Lys	Ala	Ser	Met	Lys	Lys	Val	Phe	Asn	Lys
	290					295					300				
His	Ile	Ala													

305

<210> 1167

<211> 309

<212> PRT

<213> Unknown (H38g84 protein)

<220>

<223> Synthetic construct

<400> 1167

```

Met Glu Asn Gln Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1              5              10              15
Glu Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met
      20              25              30
Tyr Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile
      35              40              45
Thr Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu
      50              55              60
Ser Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile
      65              70              75              80
Val Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu
      85              90              95
Thr Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu
      100             105             110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115             120             125
His Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly
      130             135             140
Gly Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe
      145             150             155             160
Met Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile
      165             170             175
Cys Asp Leu Phe Gln Leu Leu Thr Leu Ala Cys Thr Asp Thr His Ile
      180             185             190
Leu Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile
      195             200             205
Phe Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys
      210             215             220
Ser Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser
      225             230             235             240
His Leu Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
      245             250             255
Met Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser
      260             265             270
Asp Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
      275             280             285
Asn Ala Glu Val Lys Ser Ala Met Lys Lys Leu Trp Met Lys Trp Glu
      290             295             300
Ala Leu Ala Gly Lys
305

```

<210> 1168

<211> 311

<212> PRT

<213> Unknown (H38g85 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1168

```

Val Glu Asp Met Val Pro Phe Ser Met Arg Ile Ser Gly Ile Phe Gln
 1          5          10          15
Ile Phe Phe Tyr Gly Tyr His His Leu Ile Tyr Xaa Tyr Ser Val Leu
          20          25          30
Thr Cys Val Pro Phe Gln Phe Thr Tyr Ser His Ile Val Lys Cys Xaa
          35          40          45
Leu Gln Gly Asn Leu Pro Gln Thr Gln Thr Ile Asn Val Thr Ser Glu
          50          55          60
Thr Ile Trp Ile Lys Ile Ile His Asp Phe Leu His Glu Pro Lys Thr
65          70          75          80
Ile Ser Phe Glu Gly Cys Met Ala Gln Ile Phe Leu Phe His Val Phe
          85          90          95
Ala Gly Gly Glu Met Val Leu Leu Val Ala Met Ala Tyr Asp Ile Tyr
          100          105          110
Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Asn Leu Cys
          115          120          125
Thr Cys Thr Gly Leu Val Val Gly Ser Trp Val Thr Gly Val Met His
          130          135          140
Ser Leu Ser Gln Leu Ala Phe Thr Val Ser Leu Pro Phe Cys Gly Pro
145          150          155          160
Asn Ile Val Asp Ser Tyr Tyr Cys Asp Leu Thr Leu Val Ile Lys Leu
          165          170          175
Ala Cys Thr Asp Thr Tyr Ile Pro Glu Ala Leu Met Leu Leu Asp Ser
          180          185          190
Gly Leu Met Gly Val Thr Ser Phe Leu Leu Leu Leu Ile Ser Tyr Thr
          195          200          205
Val Ile Leu Ile Thr Val Gln Arg Pro Ser Ser Ala Gly Met Ala Lys
          210          215          220
Ala Arg Ser Thr Leu Thr Ala His Val Thr Val Val Thr Leu Phe Phe
225          230          235          240
Gly Pro Cys Ile Phe Ile Tyr Ala Trp Pro Phe Ser Asn Leu Pro Val
          245          250          255
Asp Asn Ile Leu Ser Val Phe Ser Thr Val Phe Thr Pro Ile Leu Asn
          260          265          270
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Ser Ala Ile His
          275          280          285
Asn Leu Lys Thr Gln Tyr Val Thr Ser Arg Leu Ser Ser Gln Leu Ser
          290          295          300
Leu Ile Gly Leu Asp Leu Leu
305          310

```

<210> 1169

<211> 210

<212> PRT

<213> Unknown (H38g86 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(210)

<223> Xaa = Any Amino Acid

<400> 1169

```

Leu Gly Asn Val Ser Thr Glu Thr Thr Phe Ile Phe Val Cys Phe Thr
 1          5          10          15
Asn Gly Gln Gln Phe Gln Pro Val Cys Phe Ser Ser Phe Xaa Val Leu

```

```

      20      25      30
Gly His Ser Val Leu Gly Leu Ser Ser Leu Leu Asn Ile His Gly Glu
      35      40      45
Leu Val Phe Ser Leu Phe Ser Phe Val Phe Val Phe Gln Met Ser Tyr
      50      55      60
Ser Phe Val Ile Leu Ile Lys Met Ile Met Asn Ser Ile Ser Glu Arg
65      70      75      80
Tyr Ile Thr Thr Asn Leu Lys Cys Lys Thr Ser Ala Leu Val Phe Ile
      85      90      95
Cys Phe Ala Ile Ser Glu Thr Leu Ile Leu Leu Ala Trp Gly His Cys
      100      105      110
Gly Ile Cys Val Pro Gln Val Cys Ser Leu Thr Met Leu Gly Leu His
      115      120      125
Gly Val Gly Ile Asp Gly Val Met Ala His Pro Glu Ala Met Val Ser
      130      135      140
Leu Ser Phe Cys Asp Arg Ser Ile Ile Asn His Cys Val Trp His Thr
145      150      155      160
Ser Phe His Gln Thr Leu Leu Arg Ala Pro Ala Ser Gln Ala Gly Asp
      165      170      175
Phe Val Val Ile Ala Xaa Xaa Leu Ile Ile Phe Ile Ser Asp Ile Leu
      180      185      190
Ile Leu Ser Thr Ile Leu His Phe Leu Phe Pro Glu Ala Asn Ser Lys
      195      200      205
Ala Phe
      210

```

<210> 1170

<211> 274

<212> PRT

<213> Unknown (H38g87 protein)

<220>

<223> Synthetic construct

<400> 1170

```

Met Gly Asn Leu Gly Met Ile Met Val Ile Arg Ile Asn Pro Lys Leu
1      5      10      15
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ser Phe Val Asp Phe
      20      25      30
Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu Asn Leu Val Val
      35      40      45
Glu Asp Arg Ile Ile Ser Phe Thr Gly Cys Ile Met Gln Phe Phe Phe
      50      55      60
Ala Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu Ala Ala Met Ala
65      70      75      80
Tyr Asp Arg Phe Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala
      85      90      95
Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Ala Ser Tyr Ser Trp
      100      105      110
Ser Leu Val Cys Ser Leu Thr Tyr Thr Tyr Phe Leu Leu Thr Leu Ser
      115      120      125
Phe Cys Arg Thr Asn Phe Ile Asn Asn Phe Val Cys Glu His Ala Ala
      130      135      140
Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Met Ser Gln Lys Val Ile
145      150      155      160
Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Ile Leu
      165      170      175
Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr
      180      185      190
Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala
      195      200      205

```

```

Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn
 210                215                220
Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr
 225                230                235                240
Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys
                245                250                255
Asp Val Lys Glu Thr Val Arg Lys Leu Val Ile Thr Lys Leu Leu Cys
                260                265                270
His Lys

```

```

<210> 1171
<211> 348
<212> PRT
<213> Unknown (H38g88 protein)

```

```

<220>
<223> Synthetic construct

```

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<221> VARIANT
<222> (1)...(348)
<223> Xaa = Any Amino Acid

```

```

<400> 1171
Met Thr Asn Ser Ser Val Lys Gly Asp Phe Ile Leu Val Gly Phe Ser
 1                5                10                15
His Gln Pro His Leu Glu Lys Ile Leu Phe Val Ala Val Leu Ile Ser
                20                25                30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Val Ile Ile Leu Ile Cys Ser
 35                40                45
Val Asp Pro Lys Leu Lys Thr Pro Met Tyr Phe Phe Leu Ser His Leu
 50                55                60
Ser Leu Val Asp Ile Cys Phe Thr Thr Ser Ile Val Pro Gln Leu Leu
 65                70                75                80
Trp Asn Leu Lys Gly Pro Asp Lys Thr Ile Thr Phe Leu Gly Cys Val
                85                90                95
Ile Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys Val Leu
 100                105                110
Leu Ala Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu
 115                120                125
His Tyr Thr Ala Val Met Asn Pro Gln Leu Cys Gln Val Leu Ala Gly
 130                135                140
Val Ala Trp Leu Ser Gly Val Gly Asn Thr Leu Ile Gln Gly Thr Val
 145                150                155                160
Thr Leu Trp Leu Pro Arg Cys Gly His Arg Leu Leu Gln His Phe Phe
                165                170                175
Cys Glu Val Pro Ser Met Ile Lys Leu Ala Cys Val Asp Ile His Asp
                180                185                190
Asn Glu Val Gln Leu Phe Val Ala Ser Leu Val Leu Leu Leu Pro
 195                200                205
Leu Val Leu Ile Leu Leu Ser Tyr Gly His Ile Ala Lys Val Val Ile
 210                215                220
Arg Ile Lys Ser Val Gln Ala Trp Cys Lys Gly Leu Gly Thr Cys Gly
 225                230                235                240
Ser His Leu Ile Val Val Ser Leu Phe Cys Gly Thr Ile Thr Ala Val
                245                250                255
Tyr Ile Gln Ser Asn Ser Ser Tyr Ala His Ala His Gly Lys Phe Ile
 260                265                270
Ser Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Leu Ile Tyr
 275                280                285
Thr Leu Arg Asn Asn Asp Val Lys Gly Ala Leu Arg Leu Phe Asn Arg

```

```

      290              295              300
Asp Leu Gly Thr Xaa Lys Met Lys Gln Ser Thr Gln Arg Ser Thr Phe
305              310              315              320
Phe Thr Lys Gln Leu Xaa Arg Ser Tyr Leu Tyr Asn Phe Ser Leu Lys
              325              330              335
Asn Phe Ala Ser Leu Xaa Arg Lys Arg Cys Asn Leu
              340              345

```

<210> 1172

<211> 319

<212> PRT

<213> Unknown (H38g89 protein)

<220>

<223> Synthetic construct

<400> 1172

```

Met Asp Lys Ser Asn Ser Ser Val Val Ser Glu Phe Val Leu Leu Gly
1              5              10              15
Leu Cys Ser Ser Gln Lys Leu Gln Leu Phe Tyr Phe Cys Phe Phe Ser
              20              25              30
Val Leu Tyr Thr Val Ile Val Leu Gly Asn Leu Leu Ile Ile Leu Thr
              35              40              45
Val Thr Ser Asp Thr Ser Leu His Ser Pro Met Tyr Phe Leu Leu Gly
50              55              60
Asn Leu Ser Phe Val Asp Ile Cys Gln Ala Ser Phe Ala Thr Pro Lys
65              70              75              80
Met Ile Ala Asp Phe Leu Ser Ala His Glu Thr Ile Ser Phe Ser Gly
              85              90              95
Cys Ile Ala Gln Ile Phe Phe Ile His Leu Phe Thr Gly Gly Glu Met
              100              105              110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
              115              120              125
Pro Leu Tyr Tyr Val Val Ile Met Ser Arg Arg Thr Cys Thr Val Leu
130              135              140
Val Met Ile Ser Trp Ala Val Ser Leu Val His Thr Leu Ser Gln Leu
145              150              155              160
Ser Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Val Val Asp Ser
              165              170              175
Phe Phe Cys Asp Leu Pro Arg Val Thr Lys Leu Ala Cys Leu Asp Ser
              180              185              190
Tyr Ile Ile Glu Ile Leu Ile Val Val Asn Ser Gly Ile Leu Ser Leu
195              200              205
Ser Thr Phe Ser Leu Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Thr
210              215              220
Val Trp Leu Lys Ser Ser Ala Ala Met Ala Lys Ala Phe Ser Thr Leu
225              230              235              240
Ala Ser His Ile Ala Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe
              245              250              255
Ile Tyr Val Trp Pro Phe Thr Ile Ser Pro Leu Asp Lys Phe Leu Ala
260              265              270
Ile Phe Tyr Thr Val Phe Thr Pro Val Leu Asn Pro Ile Ile Tyr Thr
275              280              285
Leu Arg Asn Arg Asp Met Lys Ala Ala Val Arg Lys Ile Val Asn His
290              295              300
Tyr Leu Arg Pro Arg Arg Ile Ser Glu Met Ser Leu Val Val Arg
305              310              315

```

<210> 1173

<211> 312

<212> PRT

<213> Unknown (H38g90 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1173

```

Met Pro Ala Lys Asn Ser Ser Ser Val Thr Ala Phe Ile Leu Ser Gly
1          5          10          15
Leu Thr Asp Gln Pro Gly Leu Gln Ile Pro Ala Phe Phe Leu Phe Leu
20          25          30
Gly Phe Tyr Ala Val Thr Val Val Gly Asn Leu Gly Leu Ile Ile Leu
35          40          45
Ile Gly Leu Asn Ser Arg Leu His Ile Pro Met Tyr Phe Phe Pro Phe
50          55          60
Asn Leu Ser Phe Ile Asp Phe Ser Tyr Ser Thr Thr Leu Ala Pro Lys
65          70          75          80
Met Leu Met Ser Phe Val Ser Glu Asn Ile Ile Ser Tyr Ala Gly Cys
85          90          95
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Phe Ser Glu Ser Tyr
100         105         110
Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Gly Ile Cys Asn Pro
115         120         125
Leu Leu Tyr Thr Val Thr Met Ser Pro Gln Met Cys Leu Leu Leu Leu
130         135         140
Leu Gly Val Tyr Gly Met Gly Tyr Phe Gly Ala Val Ala His Met Gly
145         150         155         160
Asn Ile Met Phe Met Ser Phe Cys Gly Asp Asn Leu Val Asn His Tyr
165         170         175
Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Ser Ser Tyr
180         185         190
Ile Asn Leu Leu Val Val Phe Ile Ile Val Thr Val Gly Ile Gly Val
195         200         205
Pro Ile Val Thr Ile Phe Leu Ser Tyr Gly Phe Ile Leu Ser Ser Ile
210         215         220
Leu His Ile Ser Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
225         230         235         240
Ser Ser His Ile Ile Val Val Ser Leu Phe Phe Gly Ser Gly Ala Phe
245         250         255
Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu Asp Gln Gly Lys Val
260         265         270
Ser Ser Ile Phe Cys Thr Ala Val Val Pro Met Phe Asn Pro Leu Ile
275         280         285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Arg Thr Phe
290         295         300
Cys Arg Lys Leu Val Ser Xaa Lys
305         310

```

<210> 1174

<211> 357

<212> PRT

<213> Unknown (H38g91 protein)

<220>

<223> Synthetic construct

<400> 1174

```

Met Asn Trp Val Asn Lys Ser Val Pro Gln Glu Phe Ile Leu Leu Val

```

```

      1             5             10             15
Phe Ser Asp Gln Pro Trp Leu Glu Ile Pro Pro Phe Val Met Phe Leu
      20             25             30
Phe Ser Tyr Ile Leu Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
      35             40             45
Ser His Val Asp Phe Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50             55             60
Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln
      65             70             75             80
Met Leu Val Asn Ile Cys Asn Thr Arg Lys Val Ile Ser Tyr Gly Gly
      85             90             95
Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys
      100             105             110
Leu Leu Leu Ala Val Met Cys Phe Asp Arg Phe Val Ala Ile Cys Arg
      115             120             125
Pro Leu His Tyr Ser Ile Ile Met His Gln Arg Leu Cys Phe Gln Leu
      130             135             140
Ala Ala Ala Ser Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln Ser
      145             150             155             160
Thr Trp Thr Leu Lys Met Pro Leu Cys Gly His Lys Glu Val Asp His
      165             170             175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp Thr
      180             185             190
Thr Ala Asn Glu Ala Glu Leu Phe Phe Ile Ser Val Leu Phe Leu Leu
      195             200             205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln Ala
      210             215             220
Val Leu Arg Ile Gln Ser Ala Glu Gly Gln Arg Lys Ala Phe Gly Thr
      225             230             235             240
Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
      245             250             255
Ser Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly Lys
      260             265             270
Met Val Ser Leu Phe Cys Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
      275             280             285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Ala Phe Lys Arg Leu
      290             295             300
Val Ala Lys Ser Leu Leu Asn Gln Glu Ile Arg Asn Met Gln Met Ile
      305             310             315             320
Ser Phe Ala Lys Asp Thr Val Leu Thr Tyr Leu Thr Asn Phe Ser Ala
      325             330             335
Ser Cys Pro Ile Phe Val Ile Thr Ile Glu Asn Tyr Cys Asn Leu Pro
      340             345             350
Gln Arg Lys Phe Pro
      355

```

<210> 1175

<211> 320

<212> PRT

<213> Unknown (H38g92 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1175

```

His Thr Glu Pro Arg Asn Leu Thr Gly Ala Xaa Glu Leu Leu Leu Leu
  1             5             10             15

```

Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ser Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu
 50 55 60
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Arg Ser His Ser Gly Val Ile Ser Tyr Ala
 85 90 95
 Asp Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Val Glu
 100 105 110
 Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe
 130 135 140
 Leu Val Ser Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu Arg
 145 150 155 160
 Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Val Cys Asp Pro Ser Gln Pro Leu Lys Leu Ala Cys Ser Asp
 180 185 190
 Ser Ile Ile Asp Ser Met Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly
 195 200 205
 Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
 210 215 220
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Xaa Tyr Lys Ala Phe Ser
 225 230 235 240
 Ala Cys Gly Ser His Leu Pro Val Val Cys Leu Phe Tyr Gly Thr Gly
 245 250 255
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly
 260 265 270
 Val Val Ala Ser Val Thr Tyr Ala Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg
 290 295 300
 Leu Arg Ser Arg Thr Val Lys Ser His Asp Leu Phe His Pro Phe Ser
 305 310 315 320

<210> 1176

<211> 313

<212> PRT

<213> Unknown (H38g93 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1176

Met Glu Gly Phe Asn Cys Ser Arg Val Ser Glu Phe Met Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Ser Pro Glu Leu Gln Arg Phe Phe Phe Val Val Phe Ser
 20 25 30
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
 35 40 45
 Val Leu Ser Thr Ser His Leu His Ser Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Asn Leu Ser Leu Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys


```

65          70          75          80
Met Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly
      85          90
Cys Ile Ser Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile
      100          105          110
Val Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys
      115          120          125
Pro Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu
      130          135          140
Val Ala Val Ser Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
145          150          155          160
Ala Phe Thr Leu Tyr Leu Pro Phe Cys Gly Pro Asn Val Glu Ser Phe
      165          170          175
Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Met Asp Ile Tyr
      180          185          190
Val Leu Gly Ile Phe Met Ile Ser Thr Ser Gly Val Ile Ala Leu Ile
      195          200          205
Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Ile Thr Val
      210          215          220
Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys Thr
225          230          235          240
Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe Ile
      245          250          255
Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser Val
      260          265          270
Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu
      275          280          285
Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Xaa Leu Asn Ile Gln
      290          295          300
Tyr Phe Ser Leu Gly Lys Thr Ala Pro
305          310

```

<210> 1177

<211> 338

<212> PRT

<213> Unknown (H38g94 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(338)

<223> Xaa = Any Amino Acid

<400> 1177

```

Met Ile Leu Pro Ala Ser Phe Ser Xaa Gly Thr Met Glu Thr Ser Ser
  1          5          10          15
Val Ser Ser Gly Thr Asp Phe Ile Leu Leu Gly Phe Ser Asp Arg Pro
      20          25          30
Gln Leu Glu His Ile Ile Ser Val Val Phe Ile Ile Tyr Ile Val
      35          40          45
Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val Ser Tyr Leu Asp Thr
      50          55          60
Gln Leu His Thr Phe Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu
65          70          75          80
Asp Leu Cys Tyr Thr Thr Ser Ile Ile Pro Gln Met Leu Ala Asn Gln
      85          90          95
Trp Gly Pro Lys Lys Ser Ile Thr Tyr Gly Gly Cys Val Leu Gln Phe
      100          105          110
Phe Phe Val Leu Asp Leu Gly Ala Thr Glu Cys Leu Leu Leu Ala Val
      115          120          125

```

```

Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Gln Pro Leu His Tyr Thr
 130          135          140
Leu Lys Cys Thr Leu Ser Phe Ala Thr Ala Trp Leu Ser Gly Leu Ala
145          150          155          160
Ser Ala Leu Ile Val Cys Ser Leu Thr Leu Lys Leu Pro Arg Cys Gly
          165          170          175
His Arg Glu Val Asp Asn Phe Phe Cys Glu Met Pro Ala Leu Ile Lys
          180          185          190
Met Ala Cys Val Tyr Ser Lys Val Ile Glu Ile Val Val Phe Ala Phe
          195          200          205
Gly Val Val Phe Leu Phe Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr
210          215          220
Gly Val Ile Thr Gln Ala Val Met Arg Ile Lys Ser Ala Thr Arg Leu
225          230          235          240
Gln Lys Ile Leu Asn Thr Cys Gly Ser His Leu Thr Val Val Ile Leu
          245          250          255
Phe Tyr Gly Thr Ile Ile Tyr Ile Tyr Met Lys Pro Gln Asn Thr Ile
          260          265          270
Ser Gln Asp Glu Gly Lys Phe Ser Leu Phe Tyr Thr Ile Ile Thr Pro
          275          280          285
Ser Leu Asn Leu Pro Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ser
          290          295          300
Ala Leu Lys Arg Ile Leu Trp Met Lys Lys Ser Ser Ala Glu Xaa Met
305          310          315          320
Asn Xaa Met Glu Lys Ser Arg Met Xaa Ser Thr Lys Glu Ile Leu Ala
          325          330          335
Phe Ile

```

<210> 1178
 <211> 314
 <212> PRT
 <213> Unknown (H38g95 protein)

<220>
 <223> Synthetic construct

 <221> VARIANT
 <222> (1)...(314)
 <223> Xaa = Any Amino Acid

```

<400> 1178
Met His Gln Gly Asn Xaa Thr Thr Val Ser Lys Phe Phe Leu Leu Gly
 1          5          10          15
Ile Thr Thr Lys Pro Lys Glu Gln Gln Phe Ile Phe Met Leu Phe Leu
          20          25          30
Cys Thr Tyr Leu Val Thr Met Val Arg Asn Leu Leu Ile Ile Leu Ala
          35          40          45
Val Val Ser Asp Ala His Leu His Gly Pro Ile Tyr Phe Phe Leu Ala
          50          55          60
Asn Leu Ser Phe Thr Asn Val Cys Ile Thr Thr Thr Val Pro Lys
65          70          75          80
Ile Leu Ala Asp Ile Gln Ser Gln Asn Ser Thr Ile Ser Phe Glu Gly
          85          90          95
Cys Pro Ala Gln Met Xaa Phe Xaa Ile Phe Leu Val Asp Leu Asp Asn
          100          105          110
Phe Leu Leu Val Asp Met Ala Tyr Asn Xaa Tyr Ile Ala Ile Cys His
          115          120          125
Pro Leu His Tyr Thr Val Val Val Leu Ser Pro Lys Asn Cys Ala Leu
          130          135          140
Leu Val Val Thr Pro Trp Val Ile Ser Asn Leu Val Ser Ile Leu His

```

```

145          150          155          160
Leu Ser Leu Leu Ser His Leu Thr Phe Cys Ile Ser His Ile Phe Tyr
165          170          175
Asp Leu Glu Pro Ile Leu Gly Leu Ala Cys Ser Asp Thr Gln Ile Asn
180          185          190
Asn Leu Ile Ile Thr Ala Ile Gly Glu Val Val Ile Phe Ile Pro Phe
195          200          205
Thr Cys His Ile Leu Val Ser Tyr Gly Leu Ile Gly Ser Thr Met Leu
210          215          220
Gly Val Pro Ser Ala Lys Gly Lys Xaa Lys Thr Phe Ser Thr Cys Gly
225          230          235          240
Ser His Leu Ser Val Val Pro Gln Val Phe Tyr Gly Phe Ile Ile Gly
245          250          255
Val Tyr Phe Leu Ser Phe Phe Ala Tyr Ser Ala Glu Arg Asp Glu Val
260          265          270
Ala Ala Ile Met Tyr Thr Thr Val Thr His Leu Ile Lys Ser Phe Ile
275          280          285
Cys Ser Leu Arg Asn Glu Asp Met Lys Gly Ala Leu Arg Arg Pro Leu
290          295          300
Ser Arg Gln Gly Phe Ser Gly Val Val Ser
305          310

```

<210> 1179

<211> 314

<212> PRT

<213> Unknown (H38g96 protein)

<220>

<223> Synthetic construct

<400> 1179

```

Met Met Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly
1      5      10      15
Leu Pro Ile Gln Pro Glu Gln Arg Asn Leu Phe Tyr Ala Leu Phe Leu
20     25     30
Ala Val Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Val Ile Val Leu
35     40     45
Ile Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Cys Leu Ser
50     55     60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65     70     75     80
Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp
85     90     95
Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser
100    105    110
Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe
115    120    125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Cys Cys Leu Gly Leu
130    135    140
Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Thr Leu His Thr
145    150    155    160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Glu Asn Val Ile Pro His
165    170    175
Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asn Thr
180    185    190
Gln Val Asn Gly Trp Val Met Phe Phe Met Gly Gly Leu Ile Leu Val
195    200    205
Ile Pro Phe Leu Leu Leu Ile Met Ser Cys Ala Arg Ile Val Ser Thr
210    215    220
Ile Leu Arg Val Pro Ser Thr Gly Gly Ile Gln Lys Ala Phe Ser Thr
225    230    235    240

```

<400> 1180															
Met	Ala	Ala	Glu	Asn	Ser	Ser	Ser	Val	Thr	Glu	Phe	Ile	Leu	Ala	Gly
1				5					10					15	
Leu	Ile	His	Gln	Pro	Gly	Leu	Gln	Val	Pro	Val	Phe	Phe	Leu	Phe	Leu
			20					25					30		
Gly	Phe	Tyr	Ala	Val	Thr	Val	Val	Gly	Asn	Leu	Gly	Leu	Ile	Ile	Leu
		35					40					45			
Ile	Gly	Leu	Asn	Ser	Arg	Leu	His	Ile	Pro	Met	Tyr	Phe	Phe	Pro	Phe
	50					55					60				
Asn	Leu	Ser	Leu	Val	Asp	Phe	Ser	Phe	Ser	Thr	Thr	Ile	Ile	Pro	Lys
65					70					75					80
Met	Leu	Met	Ser	Phe	Val	Ser	Arg	Lys	Asn	Ile	Ile	Ser	Phe	Thr	Gly
				85					90					95	
Cys	Met	Ser	Gln	Phe	Phe	Phe	Phe	Cys	Phe	Phe	Val	Phe	Ser	Glu	Ser
			100					105					110		
Phe	Ile	Leu	Ser	Ala	Met	Val	Xaa	Asp	Arg	Tyr	Val	Gly	Ile	Cys	Asn
		115					120					125			
Pro	Leu	Leu	Tyr	Thr	Ile	Thr	Met	Ser	Pro	Gln	Val	Cys	Leu	Leu	Leu
	130					135					140				
Leu	Leu	Gly	Val	Tyr	Gly	Met	Gly	Val	Phe	Gly	Ala	Val	Ala	His	Thr
145					150					155					160
Gly	Asn	Ile	Val	Phe	Leu	Thr	Phe	Cys	Ala	Asp	Asn	Leu	Val	Asn	His
				165					170					175	
Tyr	Met	Cys	Asp	Ile	Leu	Pro	Leu	Leu	Glu	Leu	Ser	Cys	Asn	Gly	Ser
			180					185					190		
Tyr	Ile	Asn	Val	Leu	Val	Ile	Phe	Ile	Val	Val	Thr	Val	Gly	Ile	Gly
		195					200					205			
Val	Pro	Ile	Val	Ala	Val	Phe	Ile	Ser	Tyr	Gly	Phe	Ile	Leu	Ser	Ser
	210					215					220				
Ile	Leu	Arg	Val	Ser	Ser	Ala	Glu	Gly	Arg	Ser	Lys	Ala	Phe	Ser	Ser
225					230						235				240
Cys	Ser	Ser	Tyr	Ile	Ile	Ala	Val	Ser	Leu	Phe	Phe	Gly	Ser	Gly	Ala
				245					250					255	
Phe	Thr	Tyr	Leu	Lys	Pro	Pro	Ser	Ile	Leu	Pro	Leu	Asp	Gln	Gly	Lys
			260					265					270		
Val	Ser	Ser	Leu	Phe	Tyr	Thr	Thr	Val	Val	Pro	Met	Phe	Asn	Pro	Leu
	275						280					285			
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Leu	Ala	Leu	Lys	Arg	Thr

```

      290              295              300
Phe Ser Arg Ile Ser Phe Ser Glu Lys Asn Phe Arg Asn Arg Lys Glu
305              310              315              320
Ile Leu Gly Phe Phe Xaa Asn Gln Ile Ala Phe
              325              330

```

<210> 1181
 <211> 314
 <212> PRT
 <213> Unknown (H38g98 protein)

<220>
 <223> Synthetic construct

```

<400> 1181
Met Ser Asn Glu Asp Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu
 1              5              10              15
Phe Val Leu Thr Gly Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu
              20              25              30
Phe Leu Val Phe Leu Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu
              35              40              45
Gly Leu Ile Ala Leu Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met
              50              55              60
Tyr Phe Phe Leu Gly Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser
              65              70              75              80
Thr Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met
              85              90              95
Ile Ser Leu Ser Glu Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly
              100              105              110
Gly Thr Thr Glu Cys Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr
              115              120              125
Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser
              130              135              140
Leu Cys Ile Arg Leu Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His
              145              150              155              160
Ala Leu Ile His Glu Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser
              165              170              175
Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile
              180              185              190
Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser
              195              200              205
Gly Ser Ile Gln Val Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr
              210              215              220
Phe Ala Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg
              225              230              235              240
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
              245              250              255
Tyr Gly Pro Leu Ile Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala
              260              265              270
Asp Asp Gln Asp Met Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro
              275              280              285
Leu Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp
              290              295              300
Ser Phe Thr Lys Met Val Lys Arg Asn Val
305              310

```

<210> 1182
 <211> 313
 <212> PRT
 <213> Unknown (H38g99 protein)

<220>

<223> Synthetic construct

<400> 1182

```

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Cys Phe Leu Leu Gly
 1           5           10           15
Phe Ser Glu Gln Leu Glu Glu Gln Lys Pro Leu Phe Gly Ser Phe Leu
           20           25           30
Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
           35           40           45
Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
           50           55           60
Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
65           70           75           80
Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
           85           90           95
Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
           100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His
           115          120          125
Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Ile Phe Leu
           130          135          140
Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
145          150          155          160
Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His
           165          170          175
Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
           180          185          190
Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
           195          200          205
Ile Cys Val Leu Cys Leu Ile Ser Tyr Thr Asn Val Phe Ser Thr
           210          215          220
Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
           245          250          255
Cys Val Asp Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr
           260          265          270
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
           275          280          285
Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
           290          295          300
Ile Trp Val Arg Lys Ile His Ser Pro
305          310

```

<210> 1183

<211> 310

<212> PRT

<213> Unknown (H38g100 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1183

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15
Leu Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Thr Phe Leu

```

```

                20                25                30
Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Ala Val
   35                40                45
Ile Trp Lys Asp Pro His Leu Gln Ile Pro Met Tyr Leu Leu Leu Gly
   50                55                60
Asn Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys
   65                70                75                80
Met Leu Asn Asn Phe Leu Ala Lys Ser Lys Met Val Ser Leu Pro Glu
                85                90                95
Ser Lys Ile Gln Phe Phe Ser Phe Ala Ile Ser Val Thr Thr Glu Cys
                100                105                110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
                115                120                125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Asn Gly Leu Cys Ile Arg Leu
                130                135                140
Leu Gly Gly Leu Leu His Ala Leu Ile His Glu Gly Phe Leu Phe Arg
   145                150                155                160
Leu Thr Phe Cys Asn Ser Asn Val Val His His Ile Tyr Cys Asp Ile
                165                170                175
Ile Pro Leu Ser Lys Ile Ser Cys Thr Asp Ser Ser Ile Asn Phe Leu
                180                185                190
Met Val Phe Ile Phe Ser Gly Ser Ile Gln Val Phe Thr Ile Gly Thr
                195                200                205
Gly Leu Ile Ser Tyr Thr Phe Val Leu Phe Thr Ile Leu Lys Lys Lys
                210                215                220
Ser Val Lys Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ala His Leu
   225                230                235                240
Leu Ser Val Ser Leu Tyr His Gly Pro Leu Asp Phe Met Tyr Met Gly
                245                250                255
Ser Ala Ser Pro Gln Ala Asp Asp Glu Asp Met Met Glu Ser Leu Phe
                260                265                270
Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met Thr Tyr Ser Leu Arg
                275                280                285
Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met Phe Lys Arg Asn Asn
                290                295                300
Ile Xaa Ile Ser Tyr Ser
   305                310

```

<210> 1184

<211> 231

<212> PRT

<213> Unknown (H38g101 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(231)

<223> Xaa = Any Amino Acid

<400> 1184

```

Phe Cys Leu Phe Pro Ala Thr Val Ser Lys Ala Val Val Lys Phe Leu
   1                5                10                15
Ala Glu Thr Ile Ser Phe Ser Tyr Tyr Val Ile Gln Met Leu Val Phe
                20                25                30
Leu Phe Phe Val Thr Thr Glu Cys Asn Leu Leu Ala Ser Leu Gly Lys
                35                40                45
Asp Ile Tyr Met Pro Ile Arg Gln Pro Met Leu Tyr Pro Val Thr Met
                50                55                60
Ser Gln Val Cys Cys Ile Gln Leu Val Ala Ser Cys Tyr Gly His Gly
   65                70                75                80

```

```

Val Ile His Thr Met Phe Leu Gly Gly Ser Ile Ser Ile Phe Ala Phe
                        85                      90                      95
Cys Lys Ser Gln Thr Ile Ile Ser Phe Phe Gly Asp Ser Phe Pro Leu
                        100                     105                     110
Leu Val Leu Ser Cys Ser Asp Thr Tyr Ile Met Asn Ser Leu Phe Phe
                        115                     120                     125
Phe Thr Gly Cys Phe Ile Trp Met Ser Ser Xaa Pro Val Ile Leu Val
                        130                     135                     140
Ser His Met Phe Ile Ile Val Thr Phe Leu Arg Ile Phe Ser Val Val
                        145                     150                     155                     160
Val Glu Ser Lys Gly Phe Leu Ala Phe Ser Ser His Leu Thr Ala Ile
                        165                     170                     175
Ile Leu Phe Tyr Gly Asp Ile Met Ser Leu Tyr Met Xaa His Ser Ser
                        180                     185                     190
Asn Tyr Phe Leu Asn Gln Asp Gln Thr Val Ser Ile Phe Tyr Met Val
                        195                     200                     205
Arg Ile Leu Leu Leu Ser Pro Ile Ile Tyr Cys Leu Ile Lys Met Gln
                        210                     215                     220
Val Ile Cys Phe Leu Glu Asn
225                      230

```

<210> 1185

<211> 216

<212> PRT

<213> Unknown (H38g102 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(216)

<223> Xaa = Any Amino Acid

<400> 1185

```

Leu Phe Phe Phe Val Xaa His Ser Ile Leu Thr Xaa Xaa Glu Gly Val
  1           5           10           15
Lys Glu Ile Trp Tyr Phe Gln Glu Phe Leu Thr Tyr Pro Arg His Arg
      20           25           30
Xaa Leu Leu Phe Val Ser Ser Cys Met Tyr Tyr Ser Ser Arg Ile Phe
      35           40           45
Leu Arg Arg Thr Val Asn Ile Leu Phe Leu Leu Lys Val Ile Ser Leu
      50           55           60
Leu Cys Tyr Gly Ser Lys Leu Ser Leu Phe Ile Phe Val Val Thr Ala
      65           70           75           80
Glu Phe Xaa Leu Leu Ala Ser Arg Ile Cys His Cys Tyr Ile Ile Ile
      85           90           95
Cys Asn Pro Phe Ser Thr Gln Phe Ser His Xaa Lys Leu Leu Ile Ser
      100          105          110
Ile Leu Thr Ala His Tyr Asn Lys Arg Val Cys Ile Ser Ile Thr Thr
      115          120          125
Ser Asn Thr Met Ser Xaa Leu Phe Phe Gly Arg Ser Asn Val Val Asn
      130          135          140
Asn Phe Ser Asp Leu Leu Leu Leu Leu Asp Leu Ser Cys Thr Phe Val
      145          150          155          160
Ser Phe Xaa Ser Pro Ser Gln Leu Pro Asp His Ser Pro Gly Pro His
      165          170          175
Asn Phe Ile Ile Val Val Asn Ile Lys Ile Xaa Leu Ala Glu Gly Lys
      180          185          190
His Lys Asp Phe Ser Ile Cys Pro Leu Xaa Phe Ala Thr Val Ser Asn
      195          200          205
Phe Leu Met Ala His Ile His Ile

```


210

215

<210> 1186
 <211> 312
 <212> PRT
 <213> Unknown (H38g103 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(312)
 <223> Xaa = Any Amino Acid

<400> 1186
 Phe Met Glu Asn Arg Asn Ile Val Thr Val Phe Ile Leu Leu Gly Leu
 1 5 10 15
 Ser Gln Asn Lys Asn Ile Glu Val Phe Trp Phe Val Leu Phe Val Phe
 20 25 30
 Cys Tyr Ile Ala Ile Trp Met Glu Asn Phe Ile Ile Met Ile Ser Ile
 35 40 45
 Met Tyr Ile Xaa Leu Ile Asp Gln Pro Met Tyr Phe Phe Leu Asn Tyr
 50 55 60
 Leu Ala Leu Ser Asp Leu Cys Tyr Ile Ser Thr Val Ala Pro Lys Leu
 65 70 75 80
 Met Ile Asp Leu Leu Thr Glu Arg Lys Ile Val Ser Tyr Asn Asn Cys
 85 90 95
 Met Ile Gln Leu Phe Ile Thr His Phe Leu Gly Asp Ile Glu Ile Phe
 100 105 110
 Ile Leu Lys Ala Met Ala Tyr Asp His Tyr Ile Ala Ile Cys Lys His
 115 120 125
 Leu His Tyr Thr Ile Ile Thr Lys Gln Ser Cys Asn Thr Ile Ile
 130 135 140
 Ile Ala Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu
 145 150 155 160
 Leu Thr Ile Phe Leu Pro Phe Cys Gly Leu Asn Glu Ile Asp Gln Tyr
 165 170 175
 Phe Cys Tyr Val Tyr Pro Leu Leu Lys Leu Ala Arg Ile Asp Ile Tyr
 180 185 190
 Arg Ile Gly Phe Leu Val Ile Val Asn Ser Gly Leu Ile Ser Leu Leu
 195 200 205
 Ala Phe Val Ile Leu Met Val Ser Tyr Tyr Leu Ile Leu Ser Thr Ile
 210 215 220
 Arg Val Tyr Ser Ala Glu Ser His Thr Lys Ala Leu Ser Thr Cys Ser
 225 230 235 240
 Ser His Ile Ile Val Val Val Leu Phe Phe Val Pro Ala Leu Phe Ile
 245 250 255
 Tyr Ile Arg Pro Ala Ile Thr Phe Pro Glu Asp Lys Val Phe Val Leu
 260 265 270
 Phe Cys Ala Ile Ile Ala Pro Met Phe Ser Leu Leu Ile Tyr Met Leu
 275 280 285
 Arg Lys Val Glu Met Lys Asn Ala Val Arg Lys Met Trp Cys His Gln
 290 295 300
 Leu Leu Leu Ala Arg Lys Xaa Leu
 305 310

<210> 1187
 <211> 308
 <212> PRT
 <213> Unknown (H38g104 protein)

<220>

<223> Synthetic construct

<400> 1187

```

Met Ala Met Asp Asn Val Thr Ala Val Phe Gln Phe Leu Leu Ile Gly
 1           5           10           15
Ile Ser Asn Tyr Pro Gln Trp Arg Asp Thr Phe Phe Thr Leu Val Leu
          20           25           30
Ile Ile Tyr Leu Ser Thr Leu Leu Gly Asn Gly Phe Met Ile Phe Leu
          35           40           45
Ile His Phe Asp Pro Asn Leu His Thr Pro Ile Tyr Phe Phe Leu Ser
          50           55           60
Asn Leu Ser Phe Leu Asp Leu Cys Tyr Gly Thr Ala Ser Met Pro Gln
65           70           75           80
Ala Leu Val His Cys Phe Ser Thr His Pro Tyr Leu Ser Tyr Pro Arg
          85           90           95
Cys Leu Ala Gln Thr Ser Val Ser Leu Ala Leu Ala Thr Ala Glu Cys
          100          105          110
Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Val Val Ala Ile Ser Asn
          115          120          125
Pro Leu Arg Tyr Ser Val Val Met Asn Gly Pro Val Cys Val Cys Leu
          130          135          140
Val Ala Thr Ser Trp Gly Thr Ser Leu Val Leu Thr Ala Met Leu Ile
145          150          155          160
Leu Ser Leu Arg Leu His Phe Cys Gly Ala Asn Val Ile Asn His Phe
          165          170          175
Ala Cys Glu Ile Leu Ser Leu Ile Lys Leu Thr Cys Ser Asp Thr Ser
          180          185          190
Leu Asn Glu Phe Met Ile Leu Ile Thr Ser Ile Phe Thr Leu Leu Leu
          195          200          205
Pro Phe Gly Phe Val Leu Leu Ser Tyr Ile Arg Ile Ala Met Ala Ile
210          215          220
Ile Arg Ile Arg Ser Leu Gln Gly Arg Leu Lys Ala Phe Thr Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Ser Ala Ile Ser
          245          250          255
Met Tyr Met Lys Thr Gln Ser Lys Ser Tyr Pro Asp Gln Asp Lys Phe
          260          265          270
Ile Ser Val Phe Tyr Gly Ala Leu Thr Pro Met Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Lys Lys Asp Val Lys Arg Ala Ile Arg Lys Val Met
290          295          300
Leu Lys Arg Thr
305

```

<210> 1188

<211> 324

<212> PRT

<213> Unknown (H38g105 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1188

```

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu

```

```

                20                25                30
Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
                35                40                45
Val Ser Ser Asp Ser His Leu His Ser Pro Met Xaa Phe Phe Leu Ser
                50                55                60
Asn Leu Ser Phe Val Asp Thr Cys Phe Ile Cys Thr Thr Val Pro Lys
65                70                75                80
Met Leu Val Asn Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
                85                90                95
Cys Leu Thr Gln Val Tyr Phe Xaa Met Met Phe Ala Gly Met Asp Thr
                100                105                110
Phe Leu Leu Ala Val Ile Ala Tyr Asp Arg Phe Val Ala Ile Cys His
                115                120                125
Pro Leu Gln Tyr Met Val Ile Ile Asn Pro His Leu Cys Gly Leu Leu
                130                135                140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
145                150                155                160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
                165                170                175
Phe Phe Cys Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Ala
                180                185                190
Leu Leu Ile Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val
                195                200                205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
                210                215                220
Leu Met Arg Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr
225                230                235                240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
                245                250                255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
                260                265                270
Met Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
                275                280                285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Arg Leu
                290                295                300
Leu Ser Arg Ala Ala Ser Cys Pro Leu Thr Val His Asn Leu Arg Thr
305                310                315                320
Lys Arg Met Leu

```

<210> 1189

<211> 291

<212> PRT

<213> Unknown (H38g106 protein)

<220>

<223> Synthetic construct

<400> 1189

```

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
1                5                10                15
Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser
                20                25                30
Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
                35                40                45
Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser
                50                55                60
Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
65                70                75                80
Ile Met Asp Phe Phe Ala Leu Arg Asn Thr Ile Ser Phe Glu Gly Cys
                85                90                95

```

Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
 100 105 110
 Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
 115 120 125
 Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
 130 135 140
 Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
 145 150 155 160
 Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
 180 185 190
 Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu
 195 200 205
 Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile
 210 215 220
 Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser
 260 265 270
 Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
 275 280 285
 Leu Arg Asn
 290

<210> 1190

<211> 328

<212> PRT

<213> Unknown (H38g107 protein)

<220>

<223> Synthetic construct

<400> 1190

Tyr Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Glu
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp
 100 105 110
 Asp Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115 120 125
 His Pro Leu His Tyr Arg Ile Ile Met Asn Pro Arg Leu Cys Gly Phe
 130 135 140
 Leu Ile Leu Leu Ser Phe Phe Ile Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Asn Leu Ile Met Leu Gln Leu Thr Cys Phe Lys Asp Val Asp Ile Ser
 165 170 175
 Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu His Leu Arg Cys Ser Asp
 180 185 190
 Thr Phe Ile Asn Glu Met Val Ile Tyr Phe Met Gly Ala Ile Phe Gly

```

      195              200              205
Cys Leu Pro Ile Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser
 210              215              220
Pro Ile Leu Arg Val Pro Thr Ser Asp Gly Lys Tyr Lys Ala Phe Ser
 225              230              235              240
Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245              250              255
Leu Val Gly Tyr Leu Ser Ser Ala Val Leu Pro Ser Pro Arg Lys Ser
      260              265              270
Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275              280              285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Gln Ser Ala Leu Cys Arg
      290              295              300
Leu His Gly Arg Ile Ile Lys Ser His His Leu His Pro Phe Val Ile
 305              310              315              320
Trp Asp Arg Asn Gly Ser Lys Ile
      325

```

<210> 1191

<211> 325

<212> PRT

<213> Unknown (H38g108 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1191

```

Leu Thr Met Pro His Leu Ser Asn Thr Thr Ser Glu Phe Pro Ile Phe
 1              5              10              15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Phe His Ile Trp Ile Ser
      20              25              30
Ile Pro Phe Phe Leu Leu Ser Thr Val Ala Leu Leu Gly Asn Ser Met
      35              40              45
Ile Leu Leu Val Val Ile Leu Glu Pro Asn Leu His Glu Pro Met Tyr
      50              55              60
Cys Phe Leu Phe Met Leu Ser Ala Ala Asp Leu Gly Leu Thr Leu Ser
 65              70              75              80
Thr Met Pro Thr Thr Leu Ser Val Leu Trp Phe Ser Ala Arg Glu Ile
      85              90              95
Ile Leu Asn Ala Cys Ile Ile Gln Leu Phe Phe Leu His Ser Ser Gly
      100              105              110
Phe Met Glu Ser Ser Val Leu Met Ala Met Ala Phe Asp Arg Phe Val
      115              120              125
Ala Ile Cys Arg Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Ser Arg
      130              135              140
Ile Leu Lys Ile Gly Val Ala Ile Val Leu Arg Thr Leu Ile Ser Leu
 145              150              155              160
Ser Pro Ser Leu Phe Leu Ile Lys Arg Leu Ser Phe Cys Lys Val Asn
      165              170              175
Val Leu Ser His Ser Tyr Cys Phe His Pro Asp Ala Leu Lys Val Ala
      180              185              190
Cys Ser Asp Ser Arg Met Asn Ser Tyr Gly Gly Leu Ala Val Leu Ile
      195              200              205
Leu Val Thr Gly Val Gly Thr Pro Cys Val Ala Leu Ser Tyr Ile Leu
      210              215              220
Ile Ile His Ser Val Leu Asn Ile Ile Ser Ser Glu Gly Arg Arg Lys
 225              230              235              240

```

<210> 1192
<211> 295
<212> PRT
<213> Unknown (H38g109 protein)

```
<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(295)
<223> Xaa = Any Amino Acid
```

529

275 280 285
 Xaa Val Arg Lys Gly Ser Lys
 290 295

<210> 1193
 <211> 320
 <212> PRT
 <213> Unknown (H38g110 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

<400> 1193
 Tyr Thr Asp Ser Gln Asn Leu Thr Gly Val Leu Glu Phe Leu Phe Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Val Gly Leu Phe
 20 25 30
 Leu Ser Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Cys Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Ala Asp Ile Gly Leu Thr Ser Ala Thr Ile Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ile Ile Ser Tyr Glu
 85 90 95
 Gly Cys Leu Met Gln Met Tyr Phe Ile Tyr Phe Val Cys Met Asn Asp
 100 105 110
 Met Val Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu
 130 135 140
 Val Leu Val Ser Phe Ile Leu Ser Leu Leu Asn Ser Gln Leu His Asn
 145 150 155 160
 Gln Ile Val Leu Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Phe Asn
 165 170 175
 Phe Phe Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180 185 190
 Val Ile Asn Asn Ile Phe Met Tyr Leu Asp Ser Val Ile Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Ser Ser
 210 215 220
 Ile Leu Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Leu
 245 250 255
 Gly Ala Tyr Leu Ser Ser Ala Ala Ser Ser Phe Pro Arg Lys Gly Ala
 260 265 270
 Val Thr Ser Val Met Tyr Thr Val Val Ile Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Ala Leu Trp Arg Leu
 290 295 300
 His Ser Arg Thr Val Xaa Ser His Tyr Leu Phe His Pro Phe Cys Ser
 305 310 315 320

<210> 1194
 <211> 318
 <212> PRT

<213> Unknown (H38g111 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1194

```

His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
 1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu Phe
      20              25              30
Leu Ser Met Cys Leu Val Thr Met Leu Gly Asn Leu Leu Ile Ile Leu
      35              40              45
Ala Val Ser Pro Asp Ser His Leu His Ile Pro Met Tyr Phe Phe Leu
      50              55              60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Leu Ala Thr Val Pro
      65              70              75              80
Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala
      85              90              95
Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys Ile Asp
      100              105              110
Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala Ile Cys
      115              120              125
His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe
      130              135              140
Leu Val Leu Met Ser Phe Ile Leu Ser Leu Leu Asp Ser Xaa Leu His
      145              150              155              160
Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser Asn
      165              170              175
Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Val
      180              185              190
Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe Leu
      195              200              205
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile
      210              215              220
Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys
      225              230              235              240
Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
      245              250              255
Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val Val
      260              265              270
Ala Ser Val Leu Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe Ile
      275              280              285
Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu Cys
      290              295              300
Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser
      305              310              315

```

<210> 1195

<211> 350

<212> PRT

<213> Unknown (H38g112 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(350)

<223> Xaa = Any Amino Acid

<400> 1195

```

Met Ser Gln Leu Gly Arg Asp Asn Ile Thr Trp Val Ser Glu Phe Ile
 1          5          10          15
Leu Met Gly Leu Ser Ser Asp Arg Gln Thr Gln Ala Gly Leu Phe Ile
          20          25          30
Leu Phe Gly Ala Ala Tyr Leu Leu Thr Leu Leu Gly Asn Gly Leu Ile
          35          40          45
Leu Leu Leu Ile Trp Leu Asp Val Arg Leu His Leu Pro Met Tyr Phe
          50          55          60
Phe Leu Cys Asn Leu Ser Leu Val Asn Ile Cys Tyr Thr Ser Ser Arg
65          70          75          80
Val Pro Gln Met Leu Val His Leu His Gln Gln Arg Lys Thr Ile Ser
          85          90          95
Phe Ala Arg Cys Gly Thr Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly
          100          105          110
Thr Glu Phe Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala
          115          120          125
Val Cys Asp Pro Leu Cys Tyr Ile Ala Val Met Ser Pro Arg Leu Cys
130          135          140
Met Ala Leu Ala Ala Val Ser Trp Leu Val Gly Leu Ala Asn Ser Ala
145          150          155          160
Met Glu Thr Ala Leu Thr Met His Leu Pro Thr Cys Gly His Asn Val
          165          170          175
Leu Asn His Val Ala Cys Glu Thr Leu Ala Leu Val Arg Ser Ala Cys
          180          185          190
Val Asp Ile Thr Phe Asn Gln Val Val Ile Val Ala Ser Ser Val Val
          195          200          205
Val Leu Leu Val Pro Cys Cys Leu Val Ser Leu Ser Tyr Thr Leu Ile
          210          215          220
Val Val Ala Val Leu Gln Ile His Ser Thr Gln Gly His Arg Lys Ala
225          230          235          240
Phe Gly Thr Cys Ala Ser His Leu Thr Val Val Ser Ile Ser Tyr Gly
          245          250          255
Met Ala Leu Phe Thr Tyr Met Gln Pro Arg Ser Met Ala Ser Ala Glu
          260          265          270
Gln Glu Lys Val Met Val Leu Ser Tyr Ala Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu
          290          295          300
Ser Arg Ala Leu Met Arg Ser Ser Glu Leu Lys His Xaa Arg Val Val
305          310          315          320
Xaa Val Thr Arg Arg Pro His Ser Glu Asn Ser Gly His Trp Thr Val
          325          330          335
Leu Ser Ser Ile Thr Cys Val Arg Met Cys Val Tyr Val Cys
          340          345          350

```

<210> 1196

<211> 320

<212> PRT

<213> Unknown (H38g113 protein)

<220>

<223> Synthetic construct

<400> 1196

```

Met Asp Ser Pro Ser Asn Ala Thr Val Pro Cys Gly Phe Leu Leu Gln
 1          5          10          15
Gly Phe Ser Glu Phe Pro His Leu Arg Pro Val Leu Phe Leu Leu Leu
          20          25          30

```

```

Leu Gly Val His Leu Ala Thr Leu Gly Gly Asn Leu Leu Ile Leu Val
   35           40           45
Ala Val Ala Ser Met Pro Ser Arg Gln Pro Met Leu Leu Phe Leu Cys
   50           55           60
Gln Leu Ser Ala Ile Glu Leu Cys Tyr Thr Leu Val Val Val Pro Arg
   65           70           75           80
Ser Leu Val Asp Leu Ser Ser Arg Gly His Arg Arg Gly Ser Pro Ile
   85           90           95
Ser Phe Leu Ser Cys Ala Phe Gln Met Gln Met Phe Val Ala Leu Gly
  100           105           110
Gly Ala Glu Cys Phe Leu Leu Ala Met Ala Asn Asp Arg Tyr Val
  115           120           125
Ala Ile Cys His Pro Leu Arg Tyr Arg Ala Val Val Thr Pro Gly Leu
  130           135           140
Cys Ala Arg Leu Val Ser Gly Cys Cys Leu Arg Gly Leu Ala Val Ser
  145           150           155           160
Leu Gly Leu Thr Val Leu Ile Phe His Leu Pro Phe Cys Gly Ser Arg
  165           170           175
Leu Leu Leu His Phe Phe Cys Asp Ile Thr Ala Leu Leu His Leu Ala
  180           185           190
Cys Thr Arg Thr Thr Pro His Glu Leu Pro Leu Leu Gly Ala Cys Leu
  195           200           205
Val Leu Leu Leu Leu Pro Ser Val Leu Ile Leu Ala Ser Tyr Gly Ala
  210           215           220
Ile Ala Ala Ala Leu Val Arg Leu Arg Cys Pro Lys Gly Arg Gly Lys
  225           230           235           240
Ala Ala Ser Thr Cys Ala Leu His Leu Ala Val Thr Phe Leu His Tyr
  245           250           255
Gly Cys Ala Thr Phe Met Tyr Val Arg Pro Arg Ala Ser Tyr Ser Pro
  260           265           270
Arg Leu Asp Arg Thr Leu Ala Leu Val Tyr Thr Asn Val Thr Pro Leu
  275           280           285
Leu Cys Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Ile Thr Ala Ala
  290           295           300
Leu Ser Arg Val Leu Gly Arg Arg Arg Pro Gly Gln Ala Pro Gly Gly
  305           310           315           320

```

<210> 1197

<211> 315

<212> PRT

<213> Unknown (H38g114 protein)

<220>

<223> Synthetic construct

<400> 1197

```

Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu
   1           5           10           15
Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu
  20           25           30
Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu
  35           40           45
Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe
  50           55           60
Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu
  65           70           75           80
Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala
  85           90           95
Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu
  100           105           110
Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile

```

```

      115      120      125
Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly
  130      135      140
Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro
 145      150      155      160
Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu
      165      170      175
Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr
      180      185      190
Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr
      195      200      205
Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu
  210      215      220
Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu
 225      230      235      240
Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro
      245      250      255
Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro
      260      265      270
Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro Val
      275      280      285
Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Arg Leu Gly
  290      295      300
Ile Leu His Lys Phe Val Leu Arg Arg Arg Phe
 305      310      315

```

<210> 1198

<211> 289

<212> PRT

<213> Unknown (H38g115 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(289)

<223> Xaa = Any Amino Acid

<400> 1198

```

Phe His Gly Trp Ile Ser Met Pro Phe Cys Cys Ile Tyr Leu Met Pro
  1      5      10      15
Leu Leu Ser Asn Ala Thr Ile Leu Leu Thr Ile Trp Ser Asp Arg Thr
      20      25      30
Leu Arg Asp Pro Met Phe Tyr Phe Leu Ala Ile Leu Ser Ala Ile Asp
      35      40      45
Leu Ala Leu Ser Thr Ser Ser Val Pro Arg Met Leu Gly Ile Phe Trp
      50      55      60
Phe Asp Ala His Lys Ile Gly Phe Gly Ala Trp Val Ala Gln Met Phe
 65      70      75      80
Leu Ile His Thr Phe Thr Gly Met Glu Ser Thr Val Leu Leu Ala Met
      85      90      95
Ala Phe Asp Arg Tyr Val Ala Ile Cys Thr Ser Leu His Tyr Thr Ser
      100      105      110
Thr Leu Thr Pro Arg Val Leu Ala Gly Ile Gly Val Ser Ile Ile Met
      115      120      125
Arg Pro Val Leu Leu Met Leu Pro Ile Leu Tyr Leu Thr His Arg Leu
      130      135      140
Pro Phe Cys Glu Ala Arg Ile Ile Ala His Ser Tyr Cys Glu His Met
 145      150      155      160
Gly Ile Ala Lys Leu Ala Cys Ala Ser Ile His Ile Asn Ala Ile Tyr
      165      170      175

```

Gly Leu Phe Val Ala Ser Phe Leu Asp Val Ala Leu Val Gly Ile Ser
 180 185 190
 Tyr Thr Tyr Ile Leu Arg Ala Val Phe His Leu Pro Ser Gln Asp Ala
 195 200 205
 Arg His Lys Ala Leu Arg Thr Cys Gly Ser His Val Gly Val Met Cys
 210 215 220
 Val Phe Tyr Thr Pro Ser Leu Phe Ser Phe Leu Thr Tyr Arg Phe Ala
 225 230 235 240
 Lys Lys Ile Pro Arg Tyr Val His Ile Leu Val Ala Asn Leu Tyr Val
 245 250 255
 Val Ile Pro Pro Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys
 260 265 270
 Gln Ile His Glu His Val Val His Thr Phe Thr Ser Lys Xaa Gly Leu
 275 280 285
 Leu

<210> 1199

<211> 174

<212> PRT

<213> Unknown (H38g116 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(174)

<223> Xaa = Any Amino Acid

<400> 1199

Thr Cys Trp Val Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly
 1 5 10 15
 Leu Ser Gly Ala Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe
 20 25 30
 Cys Asp Asp Asn Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys
 35 40 45
 Leu Ile Xaa Asn Thr Ser Gly Asn Ser Lys Ile Ile Ile Val Ile Phe
 50 55 60
 Asp Ser Phe Leu Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr
 65 70 75 80
 Leu Leu Ile Ile Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Lys Ala
 85 90 95
 Lys Xaa Phe Tyr Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr
 100 105 110
 Phe Leu Trp Asp Pro His Leu Gln Tyr Met Xaa Ser Thr Ser Asp Lys
 115 120 125
 Ser Leu Thr Glu Asp Lys Leu Ala Ser Val Thr Cys Thr Ile Phe Ile
 130 135 140
 Pro Met Leu Glu Leu Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val
 145 150 155 160
 Ala Phe Lys Lys Ala Ile Gly Asn Phe Trp Val Phe Glu Arg
 165 170

<210> 1200

<211> 318

<212> PRT

<213> Unknown (H38g117 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1200

```

Ile Ser Thr Met Ser Val Phe Lys Ser Ser Ala Xaa Asn Pro Arg Phe
 1          5          10          15
Leu Gln Thr Gly Leu Ser Gly Leu Glu Ser Arg Tyr Asp Leu Ile Ser
          20          25          30
Leu Pro Ile Phe Leu Val Tyr Ala Thr Ser Ile Ala Gly Asn Ile Ser
          35          40          45
Ile Leu Phe Ile Ile Arg Thr Glu Ser Ser Leu His Gln Pro Met Tyr
          50          55          60
Tyr Phe Leu Ser Met Leu Ala Phe Thr Asp Leu Gly Leu Ser Asn Thr
65          70          75          80
Thr Leu Pro Thr Met Phe Ser Val Phe Trp Phe His Ala Arg Glu Ile
          85          90          95
Ser Phe Asn Ala Cys Leu Val Gln Met Tyr Phe Ile His Val Phe Ser
          100          105          110
Ile Ile Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Cys Phe Ile
          115          120          125
Ala Ile Xaa Glu Pro Leu Arg Tyr Ala Ala Ile Leu Thr Asn Asp Val
130          135          140
Ile Ile Gly Ile Gly Leu Ala Ile Ala Gly Arg Ala Leu Ala Leu Val
145          150          155          160
Phe Pro Ala Ser Phe Leu Leu Lys Arg Leu Gln Tyr His Asp Val Asn
          165          170          175
Ile Leu Ser Tyr Leu Phe Cys Leu His Gln Asp Leu Ile Lys Thr Thr
          180          185          190
Val Ser Asn Cys Arg Val Ser Ser Ile Tyr Gly Leu Met Val Val Ile
          195          200          205
Cys Ser Met Gly Leu Asp Ser Val Leu Leu Leu Leu Ser Tyr Val Leu
210          215          220
Ile Leu Gly Thr Ala Leu Ser Ile Ala Ser Lys Ala Glu Arg Val Arg
225          230          235          240
Ala Leu Asn Thr Cys Ile Ser His Ile Cys Ala Val Leu Thr Phe Tyr
          245          250          255
Thr Pro Met Ile Gly Leu Ser Met Ile His Arg Tyr Gly Gln Asn Ala
          260          265          270
Pro His Ile Val His Val Leu Met Ala Asn Val Tyr Leu Met Gly Pro
          275          280          285
Pro Leu Met Asn Pro Val Phe Tyr Ser Val Lys Thr Arg Gln Ile Arg
290          295          300
Asp Arg Ile Phe Gln Ile Lys Phe Arg Asn Met Lys Cys Arg
305          310          315

```

<210> 1201

<211> 315

<212> PRT

<213> Unknown (H38g118 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1201

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1          5          10          15

```

Phe Leu Cys Gln Gln Gly Phe Leu Trp Glu Ile Pro Leu Phe Leu Ala
 20 25 30
 Phe Leu Val Ile Asp Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile
 35 40 45
 Phe Leu Ile Trp Lys Asp Pro His Leu His Ile Ser Met Tyr Leu Phe
 50 55 60
 Leu Gly Ser Leu Ala Phe Val Asp Thr Trp Leu Ser Ser Thr Val Thr
 65 70 75 80
 Pro Lys Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu
 85 90 95
 Ser Glu Cys Met Val Gln Phe Phe Ser Leu Ala Ile Ser Val Thr Thr
 100 105 110
 Glu Cys Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Ala Asp Ile
 115 120 125
 Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile
 130 135 140
 Trp Leu Phe Val Leu Ser Phe Leu Gly Gly Leu Phe His Ala Leu Ile
 145 150 155 160
 His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Met Ile
 165 170 175
 Gln His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr
 180 185 190
 Asp Ser Cys Ile Asn Phe Leu Met Phe Phe Ile Phe Ser Gly Ser Ile
 195 200 205
 Gln Val Leu Thr Ile Gly Ile Val Phe Val Ser Tyr Met Phe Val Leu
 210 215 220
 Phe Thr Ile Leu Lys Lys Lys Ser Asn Lys Gly Ile Arg Glu Ala Phe
 225 230 235 240
 Ser Thr Cys Gly Ala His Tyr Ile Pro Leu Ser Leu Cys Tyr Gly Leu
 245 250 255
 Leu Leu Phe Met Tyr Val Gly Pro Ala Ala Pro Gln Ala Asp Asn Gln
 260 265 270
 Asp Met Met Glu Tyr Leu Phe Tyr Pro Ile Ile Val Arg Leu Leu Asn
 275 280 285
 Pro Tyr Tyr Tyr Ser Leu Arg Asn Lys Gln Val Ile Gly Ser Leu Thr
 290 295 300
 Lys Met Leu Lys Xaa Asn Ile Cys Ile Ala Tyr
 305 310 315

<210> 1202

<211> 313

<212> PRT

<213> Unknown (H38g119 protein)

<220>

<223> Synthetic construct

<400> 1202

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu
 1 5 10 15
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro
 20 25 30
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu
 35 40 45
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Gly Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
 65 70 75 80
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Thr Ser Ser
 85 90 95
 Ser Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu

```

      100      105      110
Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile
      115      120      125
His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala
      130      135      140
Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro
145      150      155      160
Phe Pro Phe Thr Leu Arg Ser Leu Arg Tyr Cys Lys Lys Asn Gln Leu
      165      170      175
Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser
      180      185      190
Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu
      195      200      205
Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys
210      215      220
Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Glu Leu Lys Ala Leu Asn
225      230      235      240
Thr Cys Val Ser His Ile Cys Ala Val Ile Ile Phe Tyr Leu Pro Ile
      245      250      255
Ile Asn Leu Ala Val Val His Arg Phe Ala Gly His Val Ser Pro Leu
      260      265      270
Ile Asn Val Leu Met Ala Asn Val Leu Leu Leu Val Pro Pro Leu Met
      275      280      285
Lys Pro Ile Val Tyr Cys Val Lys Thr Lys Gln Ile Arg Val Arg Val
290      295      300
Val Ala Lys Leu Cys Gln Trp Lys Ile
305      310

```

<210> 1203

<211> 314

<212> PRT

<213> Unknown (H38g120 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1203

```

Met Glu Glu Lys Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Leu
 1      5      10      15
Phe Leu Tyr Gln Pro His Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
      20      25      30
Val Ile Tyr Leu Ile Thr Ile Phe Gly Asn Leu Gly Leu Ile Ala Val
      35      40      45
Val Trp Lys Asp Pro His Leu His Ile Pro Ile Tyr Leu Phe Leu Glu
50      55      60
Asn Leu Ala Phe Val Asp Asp Leu Leu Ser Ser Thr Val Thr Leu Lys
65      70      75      80
Met Leu Ile Asn Phe Thr Lys Ser Lys Leu Ile Ser Leu Glu Cys
      85      90      95
Trp Ile His Phe Phe Ser Phe Ala Ile Gly Val Thr Thr Glu Cys Phe
      100      105      110
Ile Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro
      115      120      125
Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu Leu
130      135      140
Ile Leu Ser Phe Leu Gly Gly Leu Leu His Ala Leu Ile His Glu Ala
145      150      155      160

```

[illegible]

```
<210> 1204
<211> 171
<212> PRT
<213> Unknown (H38q121 protein)
```

<220>
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(171)
<223> Xaa = Any Amino Acid
```

<400> 1204															
Cys	Xaa	Val	Gln	Val	Ser	Xaa	Val	Ala	Glu	Lys	Tyr	Xaa	Xaa	Ile	Leu
1				5					10					15	
Phe	Val	Ala	Leu	Phe	Asn	Lys	Thr	Lys	Ser	Ile	Cys	Gln	Pro	Gln	Asn
			20					25					30		
Ile	Ala	Thr	Pro	Arg	Pro	Trp	Ala	Phe	Pro	Gln	His	Ser	Phe	Thr	Ser
		35					40					45			
Thr	Ser	Cys	Phe	Gly	Gly	Thr	Ser	Thr	Gly	Leu	Ser	Xaa	Ala	Val	Lys
	50				55					60					
Ser	Pro	Ile	Ser	Ser	Val	Cys	Pro	Leu	Leu	Gln	Leu	Leu	Leu	Gln	Tyr
65					70					75					80
Pro	Cys	Asn	Asn	Ile	Thr	Cys	Leu	Xaa	Asn	Ala	Ala	Asp	Arg	Glu	Phe
				85					90					95	
Leu	Ser	Phe	Xaa	Asp	Pro	Leu	Leu	Ala	Val	Gly	Ser	Phe	Thr	Ile	Ser
		100						105					110		
Ser	Cys	Leu	Leu	Met	Leu	Lys	Leu	Ile	Ser	Phe	Ser	Ser	Ser	Arg	Ile
		115				120						125			
Ile	Ala	Ser	Leu	Leu	Ser	Arg	Cys	Pro	Thr	Glu	Ser	His	Arg	Ser	Pro
	130					135					140				
Phe	Xaa	Tyr	Ser	Phe	Cys	His	Leu	Phe	Cys	Leu	Phe	Phe	Phe	Met	Thr
145					150					155					160
Glu	Asn	Pro	Trp	Xaa	Tyr	Leu	Xaa	Phe	Pro	Ser					
				165					170						

<210> 1205
<211> 308
<212> PRT
<213> Unknown (H38g122 protein)

<220>

<223> Synthetic construct

<400> 1205

```

Met Asn Thr Thr Leu Phe His Pro Tyr Ser Phe Leu Leu Leu Gly Ile
 1           5           10           15
Pro Gly Leu Glu Ser Met His Leu Trp Val Gly Phe Pro Phe Phe Ala
           20           25           30
Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile
 35           40           45
Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile
 50           55           60
Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met
 65           70           75           80
Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys
           85           90           95
Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala
           100          105          110
Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro
           115          120          125
Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala
 130          135          140
Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu
 145          150          155          160
Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr
           165          170          175
Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg
           180          185          190
Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp
 195          200          205
Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe
 210          215          220
Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly
 225          230          235          240
Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser
           245          250          255
Phe Met Thr His Arg Phe Gly Arg Asn Ile Pro His Phe Ile His Ile
           260          265          270
Leu Leu Ala Asn Phe Tyr Val Val Ile Pro Pro Ala Leu Asn Ser Val
           275          280          285
Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Ala Gln Val Leu Lys Met
 290          295          300
Phe Phe Asn Lys
305

```

<210> 1206

<211> 309

<212> PRT

<213> Unknown (H38g123 protein)

<220>

<223> Synthetic construct

<400> 1206

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15
Phe Leu His Gln Pro Asp Cys Lys Ile Pro Leu Phe Leu Ala Phe Leu
           20           25           30
Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Val Leu
 35           40           45

```

Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr Leu Phe Leu Gly
 50 55 60
 Ser Leu Ala Phe Val Asp Ala Ser Leu Ser Ser Thr Val Thr Pro Lys
 65 70 75 80
 Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu
 85 90 95
 Cys Met Val Gln Phe Phe Ser Leu Val Thr Thr Val Thr Thr Glu Cys
 100 105 110
 Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile Gln Leu
 130 135 140
 Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu
 145 150 155 160
 Ala Phe Ser Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His
 165 170 175
 Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser
 180 185 190
 Ser Ile Asn Phe Leu Met Val Phe Ile Phe Ala Gly Ser Val Gln Val
 195 200 205
 Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Ile Ile Leu Phe Thr
 210 215 220
 Ile Leu Glu Lys Lys Ser Ile Lys Gly Ile Arg Lys Ala Val Ser Thr
 225 230 235 240
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Thr
 245 250 255
 Phe Lys Tyr Leu Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
 260 265 270
 Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met
 290 295 300
 Phe Lys Ser Asn Val
 305

<210> 1207

<211> 308

<212> PRT

<213> Unknown (H38g124 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 1207

Met Ala Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Val Ile Tyr
 20 25 30
 Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Ile Thr Ala
 35 40 45
 Ser Pro Ser Leu Arg Ser Pro Met Xaa Phe Phe Leu Ala Tyr Leu Ser
 50 55 60
 Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Val Ser Lys Leu Ile Thr
 65 70 75 80
 Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met Thr
 85 90 95
 Gln Val Phe Gly Glu His Phe Phe Arg Gly Val Glu Val Ile Leu Leu

```

      100      105      110
Thr Val Met Ala Tyr Asp Cys Tyr Val Val Ile Cys Lys Pro Leu Arg
      115      120      125
Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly Val
      130      135      140
Ser Arg Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe Ile
145      150      155      160
Phe Gln Leu Pro Phe Cys Ser Ser Asn Val Ile Asp His Phe Ile Cys
      165      170      175
Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asn Thr His Thr Leu
      180      185      190
Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn Phe
      195      200      205
Leu Leu Leu Leu Val Ser Tyr Val Val Ile Leu Tyr Ser Leu Arg Thr
      210      215      220
His Ser Leu Glu Ala Arg His Lys Gly Leu Ser Thr Cys Val Ser His
225      230      235      240
Asn Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr Met
      245      250      255
Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe Tyr
      260      265      270
Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275      280      285
Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala Ile
      290      295      300
Ser Ser Val Lys
305

```

<210> 1208

<211> 321

<212> PRT

<213> Unknown (H38g125 protein)

<220>

<223> Synthetic construct

<400> 1208

```

Met Phe Leu Pro Asn Asp Thr Gln Phe His Pro Ser Ser Phe Leu Leu
 1      5      10      15
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
      20      25      30
Phe Cys Ala Val Tyr Met Ile Ala Leu Ile Gly Asn Phe Thr Ile Leu
      35      40      45
Leu Val Ile Lys Thr Asp Ser Ser Leu His Gln Pro Met Phe Tyr Phe
      50      55      60
Leu Ala Met Leu Ala Thr Thr Asp Val Gly Leu Ser Thr Ala Thr Ile
      65      70      75      80
Pro Lys Met Leu Gly Ile Phe Trp Ile Asn Leu Arg Gly Ile Ile Phe
      85      90      95
Glu Ala Cys Leu Thr Gln Met Phe Phe Ile His Asn Phe Thr Leu Met
      100      105      110
Glu Ser Ala Val Leu Val Ala Met Ala Tyr Asp Ser Tyr Val Ala Ile
      115      120      125
Cys Asn Pro Leu Gln Tyr Ser Ala Ile Leu Thr Asn Lys Val Val Ser
      130      135      140
Val Ile Gly Leu Gly Val Phe Val Arg Ala Leu Ile Phe Val Ile Pro
145      150      155      160
Ser Ile Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Asn His Val Ile
      165      170      175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ala
      180      185      190

```

```

Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Cys Ala Ile Cys Asn Leu
  195      200      205
Val Phe Asp Ile Thr Val Ile Ala Leu Ser Tyr Val His Ile Leu Cys
  210      215      220
Ala Val Phe Arg Leu Pro Thr His Glu Pro Arg Leu Lys Ser Leu Ser
  225      230      235      240
Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala
      245      250      255
Leu Phe Ser Phe Met Thr His Cys Phe Gly Arg Asn Val Pro Arg Tyr
      260      265      270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu
      275      280      285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Lys Cys Val
      290      295      300
Lys Lys Ile Leu Leu Gln Glu Gln Gly Met Glu Lys Glu Glu Tyr Leu
  305      310      315      320
Ile

```

<210> 1209

<211> 298

<212> PRT

<213> Unknown (H38g126 protein)

<220>

<223> Synthetic construct

<400> 1209

```

Met Arg Asn His Thr Met Val Thr Glu Phe Ile Leu Leu Gly Ile Pro
  1      5      10      15
Glu Thr Glu Gly Leu Glu Thr Ala Leu Leu Phe Leu Phe Ser Ser Phe
      20      25      30
Tyr Leu Cys Thr Leu Leu Gly Asn Val Leu Ile Leu Thr Ala Ile Ile
      35      40      45
Ser Ser Thr Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Leu
      50      55      60
Ser Ile Phe Asp Leu Gly Phe Ser Ser Thr Thr Val Pro Lys Met Leu
      65      70      75      80
Phe Tyr Leu Ser Gly Asn Ser His Ala Ile Ser Tyr Ala Gly Cys Val
      85      90      95
Ser Gln Leu Phe Phe Tyr His Phe Leu Gly Cys Thr Glu Cys Phe Leu
      100      105      110
Tyr Thr Val Met Ala Cys Asp Arg Phe Val Ala Ile Cys Phe Pro Leu
      115      120      125
Arg Tyr Thr Val Ile Met Asn His Arg Val Cys Phe Met Leu Ala Thr
      130      135      140
Gly Thr Trp Met Ile Gly Cys Val His Ala Met Ile Leu Thr Pro Leu
      145      150      155      160
Thr Phe Gln Leu Pro Tyr Cys Gly Pro Asn Lys Val Gly Tyr Tyr Phe
      165      170      175
Cys Asp Ile Pro Ala Val Leu Pro Leu Ala Cys Lys Asp Thr Ser Leu
      180      185      190
Ala Gln Arg Val Gly Phe Thr Asn Val Gly Leu Leu Ser Leu Ile Cys
      195      200      205
Phe Phe Leu Ile Leu Val Ser Tyr Thr Cys Ile Gly Ile Ser Ile Ser
      210      215      220
Lys Ile Arg Ser Ala Glu Gly Arg Gln Arg Ala Phe Ser Thr Cys Ser
      225      230      235      240
Ala His Leu Thr Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Val Ile
      245      250      255
Tyr Leu Gln Pro Asn Pro Ser Ala Leu Leu Gly Ser Ile Ile Gln Ile

```

260 265 270
 Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
 275 280 285
 Arg Asn Lys Asp Val Lys Ser Asp Gln Pro
 290 295

<210> 1210
 <211> 324
 <212> PRT
 <213> Unknown (H38g127 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 1210
 Met Glu Glu Glu Asn Thr Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1 5 10 15
 Phe Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
 20 25 30
 Val Ile Xaa Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Val Leu
 35 40 45
 Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr Leu Phe Arg Gly
 50 55 60
 Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Thr Val Thr Pro Lys
 65 70 75 80
 Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu
 85 90 95
 Cys Met Val Gln Phe Phe Ser Phe Val Ile Ser Val Thr Thr Glu Cys
 100 105 110
 Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Gln Leu
 130 135 140
 Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu
 145 150 155 160
 Ile Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His
 165 170 175
 Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser
 180 185 190
 Phe Ile Asn Phe Leu Met Val Phe Ile Phe Ala Asp Ser Ile Gln Val
 195 200 205
 Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Leu Val Leu Leu Ile
 210 215 220
 Ile Leu Lys Asn Lys Ser Val Lys Gly Ile Gln Lys Ala Val Ser Thr
 225 230 235 240
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Val
 245 250 255
 Phe Met Tyr Val Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
 260 265 270
 Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Ser Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met
 290 295 300
 Phe Lys Arg Asn Val Xaa Ile Ser Tyr Asn Leu Cys Ser Leu Phe Thr
 305 310 315 320
 Lys Ile Phe Pro

<210> 1211
 <211> 308
 <212> PRT
 <213> Unknown (H38g128 protein)

<220>
 <223> Synthetic construct

<400> 1211

```

Met Met Ser Asn Gln Thr Leu Val Thr Glu Phe Ile Leu Gln Gly Phe
 1          5          10          15
Ser Glu His Pro Glu Tyr Arg Val Phe Leu Phe Ser Cys Phe Leu Phe
          20          25          30
Leu Tyr Ser Gly Ala Leu Thr Gly Asn Val Leu Ile Thr Leu Ala Ile
          35          40          45
Thr Phe Asn Pro Gly Leu His Ala Pro Met Tyr Phe Phe Leu Leu Asn
 50          55          60
Leu Ala Thr Met Asp Ile Ile Cys Thr Ser Ser Ile Met Pro Lys Ala
65          70          75          80
Leu Ala Ser Leu Val Ser Glu Glu Ser Ser Ile Ser Tyr Gly Gly Cys
          85          90          95
Met Ala Gln Leu Tyr Phe Leu Thr Trp Ala Ala Ser Ser Glu Leu Leu
          100          105          110
Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro
          115          120          125
Leu His Tyr Ser Ser Met Met Ser Lys Val Phe Cys Ser Gly Leu Ala
          130          135          140
Thr Ala Val Trp Leu Leu Cys Ala Val Asn Thr Ala Ile His Thr Gly
          145          150          155          160
Leu Met Leu Arg Leu Asp Phe Cys Gly Pro Asn Val Ile Ile His Phe
          165          170          175
Phe Cys Glu Val Pro Pro Leu Leu Leu Ser Cys Ser Ser Thr Tyr
          180          185          190
Val Asn Gly Val Met Ile Val Leu Ala Asp Ala Phe Tyr Gly Ile Val
          195          200          205
Asn Phe Leu Met Thr Ile Ala Ser Tyr Gly Phe Ile Val Ser Ser Ile
          210          215          220
Leu Lys Val Lys Thr Ala Trp Gly Arg Gln Lys Ala Phe Ser Thr Cys
          225          230          235          240
Ser Ser His Leu Thr Val Val Cys Met Tyr Tyr Thr Ala Val Phe Tyr
          245          250          255
Ala Tyr Ile Ser Pro Val Ser Gly Tyr Ser Ala Gly Lys Ser Lys Leu
          260          265          270
Ala Gly Leu Leu Tyr Thr Val Leu Ser Pro Thr Leu Asn Pro Leu Ile
          275          280          285
Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Leu Arg Lys Leu Phe
          290          295          300
Pro Phe Phe Arg
305

```

<210> 1212
 <211> 319
 <212> PRT
 <213> Unknown (H38g129 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1212

```

Met Asp Asp Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
1          5          10          15
Leu Thr Tyr Gln Ser Glu Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
20          25          30
Val Ile Tyr Leu Ile Thr Ile Met Ala Asn Leu Gly Leu Ile Ala Val
35          40          45
Ile Trp Lys Asp Ser His Leu His Ile Pro Met Tyr Leu Phe Leu Gly
50          55          60
Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Ser Val Thr Pro Lys
65          70          75          80
Met Leu Ile Ser Phe Leu Ala Lys Ser Met Ile Ile Ser Val Ser Glu
85          90          95
Cys Lys Ile Gln Phe Phe Ser Phe Gly Ile Ser Gly Thr Thr Glu Cys
100         105         110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
115         120         125
Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu
130         135         140
Leu Val Leu Ser Phe Ile Gly Gly Phe Leu His Ala Leu Ile His Glu
145         150         155         160
Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile His His
165         170         175
Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Pro
180         185         190
Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser Gly Ser Ile Gln Val
195         200         205
Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Thr Phe Val Leu Phe Thr
210         215         220
Ile Leu Lys Lys Lys Ser Ala Lys Asp Ile Arg Lys Ala Phe Ser Thr
225         230         235         240
Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Leu
245         250         255
Phe Met Tyr Val His Pro Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
260         265         270
Val Glu Ser Leu Phe Tyr Thr Val Ile Ile Pro Phe Leu Asn Pro Ile
275         280         285
Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Leu Thr Lys Thr
290         295         300
Leu Lys Gly Asn Val Xaa Ile Ser Tyr Trp Asn Val Phe Ser Ile
305         310         315

```

<210> 1213

<211> 311

<212> PRT

<213> Unknown (H38g130 protein)

<220>

<223> Synthetic construct

<400> 1213

```

Met Val Glu Glu Asn His Thr Met Lys Asn Glu Phe Ile Leu Thr Gly
1          5          10          15
Phe Thr Asp His Pro Glu Leu Lys Thr Leu Leu Phe Val Val Phe Phe
20          25          30
Ala Ile Tyr Leu Ile Thr Val Val Gly Asn Ile Ser Leu Val Ala Leu
35          40          45
Ile Phe Thr His Arg Arg Leu His Thr Pro Met Tyr Ile Phe Leu Gly
50          55          60

```

```

Asn Leu Ala Leu Val Asp Ser Cys Cys Ala Cys Ala Ile Thr Pro Lys
65          70          75          80
Met Leu Glu Asn Phe Phe Ser Glu Gly Lys Arg Ile Ser Leu Tyr Glu
          85          90          95
Cys Ala Val Gln Phe Tyr Phe Leu Cys Thr Val Glu Thr Ala Asp Cys
          100          105          110
Phe Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Gln Tyr His Ile Met Met Ser Lys Lys Leu Cys Ile Gln Met
          130          135          140
Thr Thr Gly Ala Phe Ile Ala Gly Asn Leu His Ser Met Ile His Val
          145          150          155          160
Gly Leu Val Phe Arg Leu Val Phe Cys Gly Leu Asn His Ile Asn His
          165          170          175
Phe Tyr Cys Asp Thr Leu Pro Leu Tyr Arg Leu Ser Cys Val Asp Pro
          180          185          190
Phe Ile Asn Glu Leu Val Leu Phe Ile Phe Ser Gly Ser Val Gln Val
          195          200          205
Phe Thr Ile Gly Ser Val Leu Ile Ser Tyr Leu Tyr Ile Leu Leu Thr
          210          215          220
Ile Phe Arg Met Lys Ser Lys Glu Gly Arg Ala Lys Ala Phe Ser Thr
          225          230          235          240
Cys Ala Ser His Phe Ser Ser Val Ser Leu Phe Tyr Gly Ser Ile Phe
          245          250          255
Phe Leu Tyr Ile Arg Pro Asn Leu Leu Glu Glu Gly Gly Asn Asp Ile
          260          265          270
Pro Ala Ala Ile Leu Phe Thr Ile Val Val Pro Leu Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Ser Val Leu Arg Lys Ile
          290          295          300
Leu Leu Lys Ile Lys Ser Gln
          305          310

```

<210> 1214

<211> 328

<212> PRT

<213> Unknown (H38gl31 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1214

```

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu
1          5          10          15
Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys
          20          25          30
Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala
          35          40          45
Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys
          50          55          60
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys
          65          70          75          80
Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu
          100          105          110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys

```



```

      115      120      125
His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe
 130      135      140
Leu Val Leu Leu Ser Phe Phe Ser Val Phe Xaa His Ser Gln Leu
145      150      155      160
Gln Asn Leu Ile Ala Leu Gln Ile Thr Cys Ser Lys Asp Val Glu Ile
      165      170      175
Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys
      180      185      190
Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe
      195      200      205
Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val
      210      215      220
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Ser Tyr Lys Ala Phe
225      230      235      240
Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr
      245      250      255
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys
      260      265      270
Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
      275      280      285
Pro Leu Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu Trp
      290      295      300
Gln Pro Cys Ser Arg Thr Ala Ala Gln Ser Pro Ser Gln Tyr Leu His
305      310      315      320
Leu Phe His Ser Phe Cys Arg Met
      325

```

<210> 1215

<211> 328

<212> PRT

<213> Unknown (H38g132 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1215

```

Met Glu Pro Gln Phe Thr Thr Gln Gly Ser Met Phe Val Leu Leu Gly
 1      5      10      15
Xaa Ser Gln Thr Gln Glu Leu Gln Arg Val Met Phe Ile Leu Phe Leu
      20      25      30
Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Ile Met Val Thr
      35      40      45
Val Thr Phe Asp Cys Arg Leu His Pro Met Tyr Phe Leu Leu Arg Asn
      50      55      60
Leu Ala Leu Ile Asp Val Cys Tyr Ser Thr Val Thr Ser Pro Lys Met
65      70      75      80
Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly Cys
      85      90      95
Met Ala Gln Ile Phe Phe Phe His Leu Leu Gly Gly Gly Thr Val Phe
      100      105      110
Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln Pro
      115      120      125
Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu Val
      130      135      140
Val Ala Ala Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu Ala
145      150      155      160

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```
<221> VARIANT
<222> (1) ... (335)
```

<223> Xaa = Any Amino Acid

<400> 1217

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1           5           10           15
Gly Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe
      20           25           30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
      35           40           45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
      50           55           60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65           70           75           80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Phe Tyr Ala
      85           90           95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
      100          105          110
Glu Asn Thr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
      115          120          125
Cys His Pro Leu Cys His Ser Ala Ser Met Asn Pro Cys Phe Cys Gly
      130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Thr Gln
145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Asp
      165          170          175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
      180          185          190
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
      195          200          205
Phe Gly Phe Leu Gln Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
      210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Asn Tyr Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
      245          250          255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
      260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
      275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
      290          295          300
Arg Arg Pro Gln Gly Ser Lys Val Xaa Tyr Gln Tyr Leu Leu Ile Cys
305          310          315          320
Ser Ile Pro Phe Val Gly Trp Val Lys Lys Gly Ser Lys Val Lys
      325          330          335

```

<210> 1218

<211> 319

<212> PRT

<213> Unknown (H38gl35 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1218

```

Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr
 1           5           10           15

```

Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu
 20 25 30
 Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Leu Val Val Thr Ile Thr
 35 40 45
 Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu
 50 55 60
 Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ser Ala Pro Lys Leu Ile
 65 70 75 80
 Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met
 85 90 95
 Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu
 100 105 110
 Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val
 130 135 140
 Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe
 145 150 155 160
 Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
 165 170 175
 Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr
 180 185 190
 Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
 195 200 205
 Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys
 210 215 220
 Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser
 225 230 235 240
 His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
 245 250 255
 Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Val Phe
 260 265 270
 Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val
 290 295 300
 Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg
 305 310 315

<210> 1219

<211> 312

<212> PRT

<213> Unknown (H38g136 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1219

Met Glu Ile Gly Asn His Thr Thr Val Thr Glu Phe Ile Ile Leu Gly
 1 5 10 15
 Leu Thr Glu Asp Pro Thr Leu Cys Asp Ile Phe Phe Val Ile Phe Leu
 20 25 30
 Gly Ile Tyr Ile Val Thr Leu Ile Gly Asn Ile Ser Ile Ile Lys Lys
 35 40 45
 Arg Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser His Leu Ala
 50 55 60
 Phe Val Asp Ile Gly Leu Ala Thr Val Val Thr Pro Ile Met Leu Met

```

65      70      75      80
Gly Phe Leu Arg Arg Gly Thr Ala Leu Pro Val Thr Ser Cys Glu Ala
      85      90      95
Gln Leu Cys Ser Val Val Met Phe Gly Thr Ser Glu Cys Phe Leu Leu
      100      105      110
Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu Val
      115      120      125
Asn Ser Thr His Leu Ser Pro Ile Ile Cys Ile Leu Leu Val Gly Val
      130      135      140
Cys Tyr Leu Gly Gly Trp Val Asn Ala Ser Thr Phe Thr Ser Cys Leu
145      150      155      160
Leu Ser Leu Ser Phe Cys Gly Pro Asn Gln Ile Asp His Phe Phe Cys
      165      170      175
Asp Phe Ser Pro Leu Leu Lys Leu Ser Cys Ser Asn Ile Ser Ile Pro
      180      185      190
Glu Ile Ile Pro Ser Ile Ser Ser Gly Ser Ile Ile Val Val Thr Val
      195      200      205
Phe Ala Ile Ala Ile Ser Tyr Ile Tyr Ile Leu Ile Thr Ile Leu Lys
      210      215      220
Met Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr Cys Thr Ser
225      230      235      240
His Leu Ala Ala Val Thr Leu Tyr Tyr Gly Thr Ile Thr Phe Ile Tyr
      245      250      255
Val Met Pro Lys Ser Ser Tyr Ser Thr Ser Gln Asn Arg Leu Ile Ser
      260      265      270
Leu Ser Tyr Thr Val Val Ile Pro Ile Leu Asn Pro Phe Ile Tyr Ser
      275      280      285
Leu Arg Asn Arg Asp Val Lys Glu Ala Leu Arg Lys Ala Thr Val Arg
290      295      300
Ile Tyr Ser Xaa Asp Gln Phe Val
305      310

```

<210> 1220

<211> 324

<212> PRT

<213> Unknown (H38g137 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1220

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35      40      45
Ile Pro Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Thr Tyr Phe
50      55      60
Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65      70      75      80
Val Ser Lys Thr Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85      90      95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
100      105      110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
115      120      125

```

```

Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
          180          185          190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Gly Ser Thr Met
          195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
210          215          220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225          230          235          240
Phe Ser Thr Tyr Gly Ser His Leu Ala Val Phe Cys Xaa Phe Asp Gly
          245          250          255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg
          260          265          270
Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
          275          280          285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
290          295          300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
305          310          315          320
Phe Phe Trp Cys

```

<210> 1221

<211> 318

<212> PRT

<213> Unknown (H38g138 protein)

<220>

<223> Synthetic construct

<400> 1221

```

Met Ile Gln Pro Met Ala Ser Pro Ser Asn Ser Ser Thr Val Pro Val
 1          5          10          15
Ser Glu Phe Leu Leu Thr Cys Phe Pro Asn Phe Gln Ser Trp Gln His
          20          25          30
Trp Leu Ser Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala
          35          40          45
Asn Thr Thr Leu Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln
50          55          60
Pro Leu Tyr Tyr Leu Leu Ser Leu Leu Ser Leu Asp Ile Val Leu
65          70          75          80
Cys Leu Thr Val Ile Pro Lys Val Leu Ala Ile Phe Trp Tyr Asp Leu
          85          90          95
Arg Ser Ile Ser Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn
          100          105          110
Ser Phe Leu Pro Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp
          115          120          125
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr
130          135          140
Asn Gln Phe Val Ala Lys Ala Ser Val Phe Ile Val Val Arg Asn Ala
145          150          155          160
Leu Leu Thr Ala Pro Ile Pro Ile Leu Thr Ser Leu Leu His Tyr Cys
          165          170          175
Gly Glu Asn Val Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser
          180          185          190
Arg Leu Ser Cys Asp Asn Phe Thr Leu Asn Arg Ile Tyr Gln Phe Val

```

```

      195              200              205
Ala Gly Trp Thr Leu Leu Gly Ser Asp Leu Phe Leu Ile Phe Leu Ser
  210              215              220
Tyr Thr Phe Ile Leu Arg Ala Val Leu Arg Phe Lys Ala Glu Gly Ala
  225              230              235              240
Ala Val Lys Ala Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu
      245              250              255
Phe Phe Ser Thr Ile Leu Leu Val Val Val Leu Thr Asn Val Ala Arg
      260              265              270
Lys Lys Val Pro Met Asp Ile Leu Ile Leu Leu Asn Val Leu His His
      275              280              285
Leu Ile Pro Pro Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys
      290              295              300
Glu Ile Lys Gln Gly Ile Gln Lys Leu Leu Gln Arg Gly Arg
  305              310              315

```

<210> 1222

<211> 236

<212> PRT

<213> Unknown (H38g139 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(236)

<223> Xaa = Any Amino Acid

<400> 1222

```

Pro Lys Val Pro Asp Phe Phe Val Phe Gly Leu Arg Ala Ile Ser Phe
  1              5              10              15
Pro Ala Gly Phe Leu Gln Lys Tyr Ile Lys Asn Cys Phe Gln Ala Met
      20              25              30
Glu Phe Trp Pro Phe Lys Val Arg Ala Met Asp Arg Xaa Gly Thr Leu
      35              40              45
Cys His Pro Leu Lys Tyr Pro Ser Ile Ile Thr Asp Pro Phe Gly Val
      50              55              60
Lys Ala Ala Arg Phe Ile Leu Pro Arg Asn Val Leu Met Thr Leu Pro
      65              70              75              80
Ile Pro Ile Leu Ser Ala Gln Leu Arg Tyr Cys Gly Arg Asn Val Ile
      85              90              95
Glu Asn Cys Ile Cys Ala Asn Met Ser Val Ser Arg Leu Ser Cys Asp
      100              105              110
Asp Val Thr Ile Asn His Leu Tyr Gln Phe Ala Gly Gly Trp Thr Leu
      115              120              125
Leu Gly Ser Asp Leu Ile Leu Ile Phe Leu Ser Tyr Thr Phe Ile Leu
      130              135              140
Arg Ala Val Leu Arg Leu Lys Ala Glu Gly Ala Val Ala Lys Ala Leu
      145              150              155              160
Ser Thr Cys Gly Ser His Phe Met Leu Ile Leu Phe Phe Ser Thr Ile
      165              170              175
Leu Leu Val Phe Val Leu Thr His Val Ala Lys Lys Lys Val Ser Pro
      180              185              190
Asp Val Pro Val Leu Leu Asn Val Leu His His Val Ile Pro Ala Ala
      195              200              205
Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Gln Glu Ile Lys Gln Gly
      210              215              220
Met Gln Arg Leu Leu Lys Lys Gly Cys Xaa Gln Gly
  225              230              235

```

<210> 1223

<211> 308
 <212> PRT
 <213> Unknown (H38g140 protein)

<220>
 <223> Synthetic construct

<400> 1223
 Met Asn Ser Leu Lys Asp Gly Asn His Thr Ala Leu Thr Gly Phe Ile
 1 5 10 15
 Leu Leu Gly Leu Thr Asp Asp Pro Ile Leu Arg Val Ile Leu Phe Met
 20 25 30
 Ile Ile Leu Ser Gly Asn Leu Ser Ile Ile Leu Ile Arg Ile Ser
 35 40 45
 Ser Gln Leu His His Pro Met Tyr Phe Phe Leu Ser His Leu Ala Phe
 50 55 60
 Ala Asp Met Ala Tyr Ser Ser Ser Val Thr Pro Asn Met Leu Val Asn
 65 70 75 80
 Phe Leu Val Glu Arg Asn Thr Val Ser Tyr Leu Gly Cys Ala Ile Gln
 85 90 95
 Leu Gly Ser Ala Ala Phe Phe Ala Thr Val Glu Cys Val Leu Leu Ala
 100 105 110
 Ala Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Ser Pro Leu Leu Tyr
 115 120 125
 Ser Thr Lys Met Ser Thr Gln Val Ser Val Gln Leu Leu Val Val
 130 135 140
 Tyr Ile Ala Gly Phe Leu Ile Ala Val Ser Tyr Thr Thr Ser Phe Tyr
 145 150 155 160
 Phe Leu Leu Phe Cys Gly Pro Asn Gln Val Asn His Phe Phe Cys Asp
 165 170 175
 Phe Ala Pro Leu Leu Glu Leu Ser Cys Ser Asp Ile Ser Val Ser Thr
 180 185 190
 Val Val Leu Ser Phe Ser Ser Gly Ser Ile Ile Val Val Thr Val Cys
 195 200 205
 Val Ile Ala Val Cys Tyr Ile Tyr Ile Leu Ile Thr Ile Leu Lys Met
 210 215 220
 Arg Ser Thr Glu Gly His His Lys Ala Phe Ser Thr Cys Thr Ser His
 225 230 235 240
 Leu Thr Val Val Thr Leu Phe Tyr Gly Thr Ile Thr Phe Ile Tyr Val
 245 250 255
 Met Pro Asn Phe Ser Tyr Ser Thr Asp Gln Asn Lys Val Val Ser Val
 260 265 270
 Leu Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
 275 280 285
 Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu Leu Val Arg Lys
 290 295 300
 Ile Leu Ser His
 305

<210> 1224
 <211> 335
 <212> PRT
 <213> Unknown (H38g141 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(335)
 <223> Xaa = Any Amino Acid

<400> 1224

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
 20          25          30
Leu Ser Met Cys Leu Val Met Val Leu Glu Asn Leu Leu Ile Ile Leu
 35          40          45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly
 85          90          95
Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu
 100          105          110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115          120          125
His Pro Leu Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe
 130          135          140
Leu Asp Leu Leu Ser Phe Phe Phe Phe Pro Arg Leu Leu Asp Ser Gln
 145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
 165          170          175
Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys
 180          185          190
Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala Val
 195          200          205
Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Met
 210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Lys Tyr Lys Ala
 225          230          235          240
Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
 245          250          255
Thr Gly Val Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg
 260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
 275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
 290          295          300
Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile Cys
 305          310          315          320
Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys
 325          330          335

```

<210> 1225

<211> 311

<212> PRT

<213> Unknown (H38g142 protein)

<220>

<223> Synthetic construct

<400> 1225

```

Met Gly Thr Gly Asn Asp Thr Thr Val Val Glu Phe Thr Leu Leu Gly
 1          5          10          15
Leu Ser Glu Asp Thr Thr Val Cys Ala Ile Leu Phe Leu Val Phe Leu
 20          25          30
Gly Ile Tyr Val Val Thr Leu Met Gly Asn Ile Ser Ile Ile Val Leu
 35          40          45
Ile Arg Arg Ser His His Leu His Thr Pro Met Tyr Ile Phe Leu Cys
 50          55          60

```

His Leu Ala Phe Val Asp Ile Gly Tyr Ser Ser Ser Val Thr Pro Val
 65 70 75 80
 Met Leu Met Ser Phe Leu Arg Lys Glu Thr Ser Leu Pro Val Ala Gly
 85 90 95
 Cys Val Ala Gln Leu Cys Ser Val Val Thr Phe Gly Thr Ala Glu Cys
 100 105 110
 Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser
 115 120 125
 Pro Leu Leu Tyr Ser Thr Cys Met Ser Pro Gly Val Cys Ile Ile Leu
 130 135 140
 Val Gly Met Ser Tyr Leu Gly Gly Trp Val Asn Ala Trp Thr Phe Ile
 145 150 155 160
 Gly Cys Leu Leu Arg Leu Ser Phe Cys Gly Pro Asn Lys Val Asn His
 165 170 175
 Phe Phe Cys Asp Tyr Ser Pro Leu Leu Lys Leu Ala Cys Ser His Asp
 180 185 190
 Phe Thr Phe Glu Ile Ile Pro Ala Ile Ser Ser Gly Ser Ile Ile Val
 195 200 205
 Ala Thr Val Cys Val Ile Ala Ile Ser Tyr Ile Tyr Ile Leu Ile Thr
 210 215 220
 Ile Leu Lys Met His Ser Thr Lys Gly Arg His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Thr Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Thr Ile Thr
 245 250 255
 Phe Ile Tyr Val Met Pro Lys Ser Ser Tyr Ser Thr Asp Gln Asn Lys
 260 265 270
 Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu
 290 295 300
 Leu Arg Ile Lys Ile Phe Ser
 305 310

<210> 1226

<211> 314

<212> PRT

<213> Unknown (H38g143 protein)

<220>

<223> Synthetic construct

<400> 1226

Met Leu Leu Ser Asn Ser Ser Trp Arg Leu Ser Gln Pro Ser Phe Leu
 1 5 10 15
 Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu
 20 25 30
 Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
 35 40 45
 Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
 50 55 60
 Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr
 65 70 75 80
 Ala Pro Lys Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly
 85 90 95
 Tyr Ile Val Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser
 100 105 110
 Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
 130 135 140
 Gly Arg Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile

```

145          150          155          160
Pro Phe Pro Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile
          165          170          175
Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
          180          185          190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu
          195          200          205
Val Ile Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
          210          215          220
Leu Gln Ala Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Val
          245          250          255
Pro Gly Ile Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
          260          265          270
His His Val His Val Leu Leu Ala Thr Arg Tyr Leu Leu Met Pro Pro
          275          280          285
Ala Leu Asn Pro Leu Val Tyr Gly Val Lys Thr Gln Gln Ile Arg Gln
          290          295          300
Arg Val Leu Arg Val Phe Thr Gln Lys Asp
305          310

```

<210> 1227

<211> 315

<212> PRT

<213> Unknown (H38g144 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1227

```

Met Thr Lys Gly Asn Arg Thr Thr Val Thr Glu Phe Val Leu Met Gly
 1          5          10          15
Phe Thr Asp Arg Pro Glu Leu Gln Leu Pro Leu Phe Val Val Phe Leu
          20          25          30
Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Met Ile Leu Leu
          35          40          45
Ile Arg Ala Asp Ser Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
          50          55          60
His Leu Ala Phe Ile Asp Leu Cys Tyr Ser Ser Ile Gly Pro Lys
65          70          75          80
Met Leu Gln Asn Val Leu Val Lys Lys Lys Thr Ile Ser Phe Ser Gly
          85          90          95
Cys Phe Ala Gln Leu Tyr Phe Ser Gly Ala Phe Ala Thr Thr Glu Xaa
          100          105          110
Phe Leu Leu Ala Thr Met Pro Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Ile Tyr Thr Ala Ile Met Thr Gln Arg Val Cys Arg Glu Leu
          130          135          140
Val Ile Gly Val Tyr Thr Tyr Gly Phe Arg Asn Ser Val Ile Gln Thr
145          150          155          160
Ala Leu Thr Phe Gln Leu Ser Phe Cys Asn Ser Asp Val Ile His His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
          180          185          190
His Asn Lys Glu Lys Gln Leu Met Ile Phe Ser Ala Val Asn Leu Thr
          195          200          205

```

Gly Ser Leu Leu Thr Ile Phe Ile Ser Tyr Ile Cys Ile Leu Phe Ser
 210 215 220
 Ile Ile Lys Ile Gln Ser Ser Glu Gly Lys Cys Arg Ala Phe Ser Thr
 225 230 235 240
 Arg Ala Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Thr Leu Phe
 245 250 255
 Phe Met Tyr Leu Gln Gln Pro Lys Ala Gly Asn Ser Trp Lys Pro Asn
 260 265 270
 Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Arg Leu Arg Asn Thr Glu Val Lys Asp Ala Leu Lys Lys
 290 295 300
 Met Leu Glu Gly Lys Glu Leu Xaa Xaa Val Ser
 305 310 315

<210> 1228

<211> 202

<212> PRT

<213> Unknown (H38g145 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(202)

<223> Xaa = Any Amino Acid

<400> 1228

Met Thr Thr His Arg Asn Asp Thr Leu Ser Thr Glu Ala Ser Asp Phe
 1 5 10 15
 Leu Leu Asn Cys Phe Val Arg Ser Pro Ser Trp Gln His Trp Leu Ser
 20 25 30
 Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Val Gly Ala Asn Thr Thr
 35 40 45
 Leu Leu Met Thr Ile Trp Leu Glu Ala Ser Leu His Gln Pro Leu Tyr
 50 55 60
 Tyr Leu Leu Ser Leu Leu Ser Lys Leu Asp Ile Val Leu Cys Leu Thr
 65 70 75 80
 Val Ile Pro Lys Val Leu Thr Ile Phe Trp Phe Asp Leu Arg Pro Ile
 85 90 95
 Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Ile Met Asn Cys Phe Leu
 100 105 110
 Ala Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp His Phe
 130 135 140
 Val Val Lys Ala Ala Met Phe Ile Leu Thr Arg Asn Val Leu Met Thr
 145 150 155 160
 Leu Ala Ile Pro Ile Leu Ser Ala Gln Leu Leu Gly Thr Met Phe
 165 170 175
 Leu Lys Pro Phe Cys Gly Lys Cys Phe Val His Asn Phe Cys Gly Asp
 180 185 190
 Ala Pro Xaa Xaa Pro Tyr Thr Phe Leu Lys
 195 200

<210> 1229

<211> 203

<212> PRT

<213> Unknown (H38g146 protein)

<220>

<223> Synthetic construct

<400> 1229

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
 1           5           10           15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
      20           25           30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
      35           40           45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
      50           55           60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
      65           70           75           80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
      85           90           95
His Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
      100          105          110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
      115          120          125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
      130          135          140
Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
      145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
      165          170          175
Phe Phe Cys Asp Leu Pro Leu Ala Ser Lys Leu Ala Cys Ile Asp Thr
      180          185          190
Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser
      195          200

```

<210> 1230

<211> 304

<212> PRT

<213> Unknown (H38g147 protein)

<220>

<223> Synthetic construct

<400> 1230

```

Met Ala Leu Ser Asn Ser Ser Trp Arg Leu Pro Gln Pro Ser Phe Phe
 1           5           10           15
Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu
      20           25           30
Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
      35           40           45
Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
      50           55           60
Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Val Ala Ser Ser Thr
      65           70           75           80
Ala Pro Lys Ala Leu Ala Val Leu Leu Val Arg Ala Gln Glu Ile Gly
      85           90           95
Tyr Thr Val Cys Leu Ile Gln Met Phe Phe Thr His Ala Phe Ser Ser
      100          105          110
Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
      115          120          125
Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
      130          135          140
Gly His Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile
      145          150          155          160
Pro Phe Leu Ile Leu Leu Arg Lys Leu Ile Phe Cys Gln Ala Thr Ile
      165          170          175

```

```

Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
      180      185      190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Val Ala Leu Leu
      195      200      205
Val Val Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
      210      215      220
Leu Gln Ala Val Leu Lys Val Pro Gly Asn Glu Ala Arg Leu Lys Ala
      225      230      235      240
Phe Ser Thr Cys Gly Ser His Val Cys Val Ile Leu Val Phe Tyr Ile
      245      250      255
Pro Gly Met Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
      260      265      270
His His Val His Val Leu Leu Ala Ile Leu Tyr Arg Leu Val Pro Pro
      275      280      285
Ala Leu Asn Pro Leu Val Tyr Arg Val Lys Thr Gln Lys Ile His Gln
      290      295      300

```

<210> 1231
 <211> 110
 <212> PRT
 <213> Unknown (H38g148 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(110)
 <223> Xaa = Any Amino Acid

```

<400> 1231
Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
  1      5      10      15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Trp Leu
      20      25      30
Ser Leu Ser Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile
      35      40      45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Ile Tyr Phe Phe
      50      55      60
Leu Phe Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Ala Met Val
      65      70      75      80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr
      85      90      95
Ala Gly Cys Leu Thr Xaa Met Ser Phe Phe Val Leu Phe Phe
      100      105      110

```

<210> 1232
 <211> 327
 <212> PRT
 <213> Unknown (H38g149 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(327)
 <223> Xaa = Any Amino Acid

```

<400> 1232
Phe Phe Ser Asn Asn Ser Val Leu Phe Pro His Thr Phe Phe Leu Ala
  1      5      10      15
Gly Ile Pro Gly Leu Thr Ala Thr His Ile Trp Ile Leu Leu Pro Phe

```

```

      20      25      30
Cys Phe Met Phe Phe Leu Ser Leu Thr Gly Asn Gly Val Leu Leu Phe
      35      40      45
Leu Ile Arg Thr Glu Cys Ser Leu Arg Gln Pro Met Phe Leu Phe Leu
      50      55      60
Ala Met Leu Ser Phe Val Asp Leu Val Leu Ser Leu Ser Thr Leu Pro
      65      70      75      80
Lys Met Leu Ala Ile Phe Trp Phe Gly Ala Thr Ala Ile Ser Ser His
      85      90      95
Ser Cys Leu Ser Gln Met Phe Phe Ile His Ala Phe Ser Ala Met Glu
      100      105      110
Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Ser Val Ala Ile Cys
      115      120      125
Asn Pro Leu Arg Tyr Ala Thr Ile Leu Pro Pro Val Val Val Ala Lys
      130      135      140
Ile Gly Gly Leu Val Val Leu Xaa Gly Val Gly Leu Thr Ile Ser Phe
      145      150      155      160
Pro Ser Leu Ala His Arg Leu His Tyr His Gly Ser His Met Ile Ala
      165      170      175
Tyr Thr Phe Cys Glu His Met Ala Val Val Lys Leu Ala Cys Glu Ala
      180      185      190
Thr Thr Val Asp Asn Leu Tyr Ala Phe Val Val Ala Ile Phe Leu Gly
      195      200      205
Gly Gly Asp Val Val Cys Ile Ala Tyr Ser Tyr Gly Leu Ile Val Arg
      210      215      220
Thr Val Met His Phe Pro Ser Pro Glu Glu Arg Ala Lys Ala Gly Ser
      225      230      235      240
Thr Cys Thr Ala His Val Cys Val Ile Leu Phe Phe Tyr Gly Leu Gly
      245      250      255
Phe Leu Ser Val Val Met Gln Arg Phe Gly Ala Pro Thr Ala Ser Thr
      260      265      270
Ala Lys Val Ile Leu Ala Asn Leu Tyr Leu Leu Phe Pro Pro Ala Leu
      275      280      285
Asp Pro Ile Val Tyr Gly Met Glu Thr Lys Gln Ile Xaa Glu Arg Leu
      290      295      300
Leu Met Ile Leu Ser Pro Lys Gln Ile Glu Leu Thr Xaa Val Xaa Leu
      305      310      315      320
Ser Pro Ala Gly Leu Gln Gly
      325

```

<210> 1233

<211> 241

<212> PRT

<213> Unknown (H38g150 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(241)

<223> Xaa = Any Amino Acid

<400> 1233

```

Leu Arg Gln Leu His Asn Leu Phe Leu Pro Val Gly Phe Phe Leu Ser
  1          5          10          15
Ser Tyr Ser Phe Xaa Val Ile Trp His Asn Leu Asn Ser Val Thr Lys
      20      25      30
Phe Ser Ser Lys Thr Asp Glu Ser Lys Leu Lys Ser Xaa Cys Lys Val
      35      40      45
Lys Ser Leu Phe Phe Thr Tyr Ala Gly Cys Cys Glu Lys Leu Leu Leu
      50      55      60

```

Ala Val Glu Lys Arg Asp Arg Ser Phe Leu Phe Ile His Phe Leu Leu
 65 70 75 80
 His Xaa Ser Thr Ala Val Ser Asp His Ala Lys Val Glu Pro Gly Val
 85 90 95
 Gly Arg Arg Glu Arg Gly Xaa Gly Lys Ser His Xaa Leu Thr Leu Lys
 100 105 110
 Xaa Asp Gly Phe Thr Phe Ser Gly Pro Gly Gln Cys Leu Leu Phe Leu
 115 120 125
 Thr His Ile Lys Pro Leu Xaa Met His Leu Thr Met Gly Ala Ser Pro
 130 135 140
 Leu Pro Glu Val Arg Pro Pro Asp Phe Phe Gln Phe Pro Val Val Pro
 145 150 155 160
 His Asn Pro His Ser Trp Thr Phe Thr Gln Tyr Val Arg Leu Pro Ser
 165 170 175
 Trp Val Gln Ser Leu Ser Lys Gln Leu Thr His Phe Ser Phe His Gly
 180 185 190
 Gln Ser Phe Lys Ser Ala Tyr Ile Xaa Leu Ala Ile Ser Gly Ala Val
 195 200 205
 Thr Pro Ile Leu Leu Gln Arg Pro Arg Gly Gln Ser Ser Val Ala Val
 210 215 220
 Xaa His Ile Pro Asp Asp Arg Ile His Thr Leu Lys Pro Leu Ser Gly
 225 230 235 240
 Pro

<210> 1234

<211> 313

<212> PRT

<213> Unknown (H38g151 protein)

<220>

<223> Synthetic construct

<400> 1234

Met Ala Ser Pro Asn Asn Asp Ser Thr Ala Pro Val Ser Glu Phe Leu
 1 5 10 15
 Leu Ile Cys Phe Pro Asn Phe Gln Ser Trp Gln His Trp Leu Ser Leu
 20 25 30
 Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala Asn Thr Thr Leu
 35 40 45
 Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln Pro Leu Tyr Tyr
 50 55 60
 Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr Val
 65 70 75 80
 Ile Pro Lys Val Leu Ala Ile Phe Trp Phe Asp Leu Arg Ser Ile Ser
 85 90 95
 Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn Ser Phe Leu Thr
 100 105 110
 Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp Gln Phe Val
 130 135 140
 Ala Arg Ala Val Val Phe Val Ile Ala Arg Asn Ala Phe Val Ser Leu
 145 150 155 160
 Pro Val Pro Met Leu Ser Ala Arg Leu Arg Tyr Cys Ala Gly Asn Ile
 165 170 175
 Ile Lys Asn Cys Ile Cys Ser Asn Leu Ser Val Ser Lys Leu Ser Cys
 180 185 190
 Asp Asp Ile Thr Phe Asn Gln Leu Tyr Gln Phe Val Ala Gly Trp Thr
 195 200 205
 Leu Leu Gly Ser Asp Leu Ile Leu Ile Val Ile Ser Tyr Ser Phe Ile


```

      210              215              220
Leu Lys Val Val Leu Arg Ile Lys Ala Glu Gly Ala Val Ala Lys Ala
225              230              235              240
Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu Phe Phe Ser Thr
      245              250              255
Val Leu Leu Val Leu Val Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro
      260              265              270
Pro Asp Val Pro Ile Leu Leu Asn Ile Leu His His Leu Ile Pro Pro
      275              280              285
Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln
      290              295              300
Gly Ile Gln Asn Leu Leu Lys Arg Leu
305              310

```

<210> 1235
 <211> 135
 <212> PRT
 <213> Unknown (H38g152 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(135)
 <223> Xaa = Any Amino Acid

```

<400> 1235
Lys Asp Leu Xaa Arg Arg Ser Asn Ile Asn Phe Arg Ile Glu Arg Leu
 1              5              10              15
Tyr Phe Phe Ile Xaa Gly Trp Glu Met Lys Met Gly Leu Xaa Asn Xaa
      20              25              30
Leu Leu Met Phe Cys Glu Ser Phe Xaa Xaa Xaa Lys Thr Val Leu Arg
      35              40              45
Ile Lys Gly Glu Gly Asp Met Ala Lys Ala Leu Gly Thr Cys Gly Ser
      50              55              60
His Phe Ile Leu Ile Leu Phe Phe Thr Thr Val Leu Leu Val Leu Val
      65              70              75              80
Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro Pro Asp Val Pro Ile Leu
      85              90              95
Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val
      100             105             110
Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu
      115             120             125
Arg Arg Leu Xaa Lys Ile Lys
      130             135

```

<210> 1236
 <211> 319
 <212> PRT
 <213> Unknown (H38g153 protein)

<220>
 <223> Synthetic construct

```

<400> 1236
Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1              5              10              15
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys
      20              25              30
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala
      35              40              45

```

```

Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu
 50          55          60
Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro
 65          70          75          80
Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln
      85          90          95
Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu
      100          105          110
Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys
      115          120          125
Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser
      130          135          140
Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His
      145          150          155          160
Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg
      165          170          175
Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp
      180          185          190
Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val
      195          200          205
Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val
      210          215          220
Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly
      225          230          235          240
Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser
      245          250          255
Val Leu Ser Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr
      260          265          270
Asp Arg Leu Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn
      275          280          285
Pro Phe Ile Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys
      290          295          300
Arg Gly Leu Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala
      305          310          315

```

<210> 1237

<211> 325

<212> PRT

<213> Unknown (H38g154 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1237

```

Met Phe Leu Pro Asn Asn Thr Gln Phe His Pro Ser Ser Phe Leu Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
      20          25          30
Phe Cys Ala Val Tyr Ile Ile Ala Leu Ile Gly Arg Phe Thr Ile Leu
      35          40          45
Leu Val Ile Lys Thr Asp Ser Ser Leu Tyr Gln Pro Met Phe Tyr Phe
      50          55          60
Leu Ala Met Leu Ala Thr Ile Asp Leu Gly Leu Ser Thr Ala Thr Ile
      65          70          75          80
Pro Lys Met Leu Gly Ile Phe Trp Phe Ser Leu Arg Glu Ile Ile Cys
      85          90          95
Asp Ala Cys Leu Ile Gln Met Phe Phe Ile His Asn Phe Thr Gly Met

```

```

      100      105      110
Glu Ser Ala Ala Leu Val Gly Met Ala Tyr Asp His Phe Val Ala Ile
      115      120      125
Cys Asn Pro Leu Arg Tyr Ser Ile Ile Leu Thr Lys Lys Ala Val Ser
      130      135      140
Val Ile Gly Leu Gly Val Leu Val Arg Ser Phe Met Ser Val Ile Pro
      145      150      155      160
Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly Asp His Val Ile
      165      170      175
Pro His Thr Asn Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ser
      180      185      190
Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Gly Ala Ile Ser Ile Leu
      195      200      205
Val Phe Asp Ile Ile Ala Ile Ala Leu Ser Tyr Val Gln Ile Leu His
      210      215      220
Ala Val Phe His Leu Pro Ser Cys Lys Ala Xaa Leu Lys Ser Leu Ser
      225      230      235      240
Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala
      245      250      255
Leu Phe Ser Phe Val Thr His Arg Phe Gly Gln Asn Val Pro Arg Tyr
      260      265      270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu
      275      280      285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Val Cys Val
      290      295      300
Lys Asn Ile Phe Leu Gln Lys Xaa Glu Ile Glu Lys Lys Ser His Leu
      305      310      315      320
Ile His Ile Arg Arg
      325

```

<210> 1238

<211> 319

<212> PRT

<213> Unknown (H38g155 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1238

```

Met Ser Pro Leu Asn Asp Thr Lys Met Glu Val Leu Arg Phe Leu Leu
  1          5          10          15
Ile Gly Ile Thr Gly Leu Glu Lys Ser Arg Thr Trp Ile Ser Ile Pro
      20      25      30
Phe Leu Ser Val Tyr Leu Leu Ser Trp Met Gly Asn Phe Thr Val Leu
      35      40      45
Phe Phe Ile Lys Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Leu
      50      55      60
Leu Ser Met Leu Ser Ile Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
      65      70      75      80
Pro Ile Thr Leu Gly Leu Phe Leu Phe Asp Val His Glu Ile His Ala
      85      90      95
Ala Pro Cys Phe Ala Xaa Glu Phe Phe Ile His Leu Phe Thr Val Ser
      100      105      110
Glu Ala Ser Val Leu Ser Val Met Ala Phe Asp Trp Tyr Val Ala Ile
      115      120      125
His Ser Pro Leu Arg Tyr Ser Thr Ile Leu Thr Ser Pro Arg Ala Ile
      130      135      140

```

Lys Thr Gly Val Leu Leu Thr Ser Lys Asn Val Leu Leu Ile Leu Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Gln Arg Leu Arg Tyr Cys His Gln Asn Leu Leu
 165 170 175
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Met Cys Ser
 180 185 190
 Asp Asn Thr Val Asn Val Val Tyr Gly Leu Cys Ala Gly Leu Ser Thr
 195 200 205
 Met Leu Asp Leu Val Leu Ile Thr Phe Ser Xaa Ile Met Ile Leu Arg
 210 215 220
 Ala Val Leu Gly Ile Ala Thr Pro Arg Gln Gln Phe Lys Ala Leu Asn
 225 230 235 240
 Thr Cys Ile Ser His Ile Cys Ala Val Leu Ile Phe Tyr Val Pro Thr
 245 250 255
 Leu Ser Ala Ala Met Leu His Gln Phe Ala Arg Asp Val Ser Pro Met
 260 265 270
 Ile His Val Leu Met Ala Asp Ile Phe Leu Leu Val Pro Pro Leu Leu
 275 280 285
 Asn Pro Ile Val Tyr Cys Val Lys Thr His Gln Ile Arg Glu Lys Val
 290 295 300
 Val Gly Lys Leu Cys Pro Lys Val Ser Xaa Ser Lys Glu Xaa Glu
 305 310 315

<210> 1239

<211> 313

<212> PRT

<213> Unknown (H38g156 protein)

<220>

<223> Synthetic construct

<400> 1239

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu
 1 5 10 15
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro
 20 25 30
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu
 35 40 45
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
 65 70 75 80
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Ile Ser Ser
 85 90 95
 Asn Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu
 100 105 110
 Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile
 115 120 125
 His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala
 130 135 140
 Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro
 145 150 155 160
 Phe Pro Phe Thr Leu Arg Asn Leu Arg Tyr Cys Lys Lys Asn Gln Leu
 165 170 175
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser
 180 185 190
 Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu
 195 200 205
 Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys
 210 215 220
 Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Gln Leu Lys Ala Leu Asn

```

225          230          235          240
Thr Cys Val Ser His Ile Cys Ala Val Ile Ile Phe Tyr Leu Pro Ile
          245          250          255
Ile Asn Leu Ala Val Val His Arg Phe Ala Arg His Val Ser Pro Leu
          260          265          270
Ile Asn Val Leu Met Ala Asn Val Leu Leu Leu Val Pro Pro Leu Thr
          275          280          285
Asn Pro Ile Val Tyr Cys Val Lys Thr Lys Gln Ile Arg Val Arg Val
          290          295          300
Val Ala Lys Leu Cys Gln Arg Lys Ile
305          310

```

<210> 1240

<211> 308

<212> PRT

<213> Unknown (H38g157 protein)

<220>

<223> Synthetic construct

<400> 1240

```

Met Val Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Ile
1          5          10          15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Val Ile Tyr
          20          25          30
Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Val Thr Ala
          35          40          45
Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Tyr Leu Ala Tyr Leu Ser
50          55          60
Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Ala Pro Lys Leu Ile Thr
65          70          75          80
Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met Thr
          85          90          95
Gln Val Phe Gly Glu His Phe Phe Gly Gly Val Glu Val Ile Leu Leu
          100          105          110
Thr Val Met Ala Tyr Asp Arg Tyr Val Val Ile Cys Lys Pro Leu His
          115          120          125
Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly Val
130          135          140
Ser Trp Val Gly Gly Phe Leu His Ala Thr Val Gln Ile Leu Phe Ile
145          150          155          160
Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met Trp
          165          170          175
Asp Leu Asn Pro Leu Leu Asn Leu Val Cys Thr Asn Thr His Thr Leu
          180          185          190
Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn Phe
          195          200          205
Leu Leu Leu Leu Val Ser Tyr Met Val Ile Leu Tyr Ser Leu Arg Thr
210          215          220
His Ser Leu Glu Ala Arg Cys Lys Ala Leu Ser Thr Cys Val Ser His
225          230          235          240
Ile Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr Met
          245          250          255
Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe Tyr
          260          265          270
Thr Met Ile Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
275          280          285
Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala Ile
290          295          300
Ser Ser Val Lys
305

```

<210> 1241
 <211> 321
 <212> PRT
 <213> Unknown (H38g158 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(321)
 <223> Xaa = Any Amino Acid

<400> 1241
 Met Ala Tyr His Gly Asn Arg Gly Thr Phe His Pro Ala Thr Phe Phe
 1 5 10 15
 Leu Ile Gly Ile Pro Gly Leu Glu Asp Val His Met Xaa Ile Ser Leu
 20 25 30
 His Phe Cys Ser Val Tyr Leu Leu Ala Leu Leu Gly Asn Ala Thr Ile
 35 40 45
 Leu Leu Val Ile Lys Ala Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr
 50 55 60
 Phe Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Thr Thr Ser
 65 70 75 80
 Val Pro Arg Thr Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn
 85 90 95
 Phe Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly
 100 105 110
 Met Glu Ala Glu Val Leu Val Ala Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys Asn Pro Leu His Tyr Thr Asn Ile Leu Thr Ser Arg Val Leu
 130 135 140
 Val Gly Ile Thr Met Cys Ile Val Ile Arg Pro Val Leu Phe Thr Leu
 145 150 155 160
 Pro Ile Ile Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Gly His Ile
 165 170 175
 Ile Ala His Ser Tyr Tyr Glu His Met Gly Ile Ala Lys Leu Ser Cys
 180 185 190
 Gly Asn Ile Arg Val Asn Ala Ile Tyr Gly Leu Phe Val Val Ser Phe
 195 200 205
 Tyr Leu Leu Asn Leu Val Leu Ile Val Ile Ser Tyr Val Tyr Ile Leu
 210 215 220
 Cys Ala Val Phe Cys Leu Ala Ser His Asp Ala Arg Leu Lys Ala Leu
 225 230 235 240
 Ser Thr Cys Gly Ser His Val Gly Val Ile Cys Val Phe Tyr Ile Pro
 245 250 255
 Ser Asp Phe Ser Phe Leu Thr His Xaa Phe Gly His Asn Ile Pro His
 260 265 270
 Tyr Met His Ile Leu Val Ala Thr Leu Tyr Leu Val Ile Pro Pro Ser
 275 280 285
 Leu Asn Pro Ile Ile Cys Gly Val Arg Thr Lys Trp Lys Arg Glu Arg
 290 295 300
 Val Leu Tyr Val Leu Thr Lys Lys Xaa Asp Ser Asp His Val Leu Leu
 305 310 315 320
 Leu

<210> 1242
 <211> 162
 <212> PRT
 <213> Unknown (H38g159 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(162)

<223> Xaa = Any Amino Acid

<400> 1242

```

Gly Thr Val Xaa Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr Asp Pro
 1           5           10           15
Asn Val Ile Ala His Phe Met Cys Asp Leu Asn Thr Leu Leu Lys Leu
      20           25           30
Leu Cys Met Gly Thr Thr Asn Thr Leu Gly Phe Phe Val Ala Ala Asn
      35           40           45
Gly Gly Phe Asn Tyr Leu Leu Asn Ile Ile Phe Leu Met Val Ser Xaa
 50           55           60
Val Ala Ile Leu Cys Thr Leu Lys Thr His Ser Leu Glu Glu Arg Cys
65           70           75           80
Lys Ala Leu Ser Thr Cys Ile Ser His Thr Thr Val Val Ile Leu Phe
      85           90           95
Phe Gly Phe Cys Ile Ser Val Tyr Leu Cys Pro Val Thr Leu Leu Pro
      100           105           110
Ile Asn Lys Ala Val Ala Val Phe Tyr Thr Met Ile Asn Pro Met Leu
      115           120           125
Lys Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser Ala Leu
      130           135           140
Arg Lys Leu Trp Val Lys Arg Xaa Thr Glu Glu Arg Asn Asn Pro Asn
145           150           155           160
Ile Arg

```

<210> 1243

<211> 311

<212> PRT

<213> Unknown (H38g160 protein)

<220>

<223> Synthetic construct

<400> 1243

```

Met Phe Tyr His Asn Lys Ser Ile Phe His Pro Val Thr Phe Phe Leu
 1           5           10           15
Ile Gly Ile Pro Gly Leu Glu Asp Phe His Met Trp Ile Ser Gly Pro
      20           25           30
Phe Cys Ser Val Tyr Leu Val Ala Leu Leu Gly Asn Ala Thr Ile Leu
      35           40           45
Leu Val Ile Lys Val Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr Phe
 50           55           60
Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Ala Thr Ser Val
65           70           75           80
Pro Arg Met Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn Tyr
      85           90           95
Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly Met
      100           105           110
Glu Ala Glu Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
      115           120           125
Cys Ala Pro Leu His Tyr Ala Thr Ile Leu Thr Ser Leu Val Leu Val
      130           135           140
Gly Ile Ser Met Cys Ile Val Ile Arg Pro Val Leu Leu Thr Leu Pro
145           150           155           160

```

Met Val Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Ala His Ile Ile
 165 170 175
 Ala His Ser Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ser Cys Gly
 180 185 190
 Asn Ile Arg Ile Asn Gly Ile Tyr Gly Leu Phe Val Val Ser Phe Phe
 195 200 205
 Val Leu Asn Leu Val Leu Ile Gly Ile Ser Tyr Val Tyr Ile Leu Arg
 210 215 220
 Ala Val Phe Arg Leu Pro Ser His Asp Ala Gln Leu Lys Ala Leu Ser
 225 230 235 240
 Thr Cys Gly Ala His Val Gly Val Ile Cys Val Phe Tyr Ile Pro Ser
 245 250 255
 Val Phe Ser Phe Leu Thr His Arg Phe Gly His Gln Ile Pro Gly Tyr
 260 265 270
 Ile His Ile Leu Val Ala Asn Leu Tyr Leu Ile Ile Pro Pro Ser Leu
 275 280 285
 Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Arg Val
 290 295 300
 Leu Tyr Val Phe Thr Lys Lys
 305 310

<210> 1244

<211> 315

<212> PRT

<213> Unknown (H38g161 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1244

Met Glu Asn Arg Asn Asn Val Thr Glu Phe Val Leu Leu Gly Leu Thr
 1 5 10 15
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val Ile
 20 25 30
 Tyr Ile Ile Thr Val Val Gly Asn Ala Leu Ile Val Val Thr Ile Thr
 35 40 45
 Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Leu Phe Leu Ala Tyr Leu
 50 55 60
 Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu Ile
 65 70 75 80
 Thr Asp Ser Leu Tyr Gly Lys Asn Thr Ile Leu Phe Asn Gly Cys Met
 85 90 95
 Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Ala Glu Gly Ile Leu
 100 105 110
 Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Met Thr Ile Met Asn Gln Cys Val Tyr Ala Leu Leu Met Gly
 130 135 140
 Val Val Trp Met Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe
 145 150 155 160
 Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
 165 170 175
 Cys Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asp Thr His Met
 180 185 190
 Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
 195 200 205
 Phe Val Leu Leu Leu Val Ser Tyr Val Val Ile Leu Arg Ser Leu Arg

210	215	220
Thr His Ser Leu Glu	Ala Arg His Lys Ala Leu Ser Thr Cys Val Ser	
225	230	235
His Ile Thr Val Val	Ile Leu Phe Phe Val Pro Cys Ile Phe Val Tyr	240
	245	250
Met Arg Pro Ala Ala	Thr Leu Pro Ile Asp Lys Ala Val Ala Ile Phe	255
	260	265
Tyr Thr Met Ile Thr	Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg	270
	275	280
Asn Ala Gln Met Lys	Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Asp	285
	290	295
Ile Ser Gly Asn Lys	Xaa Met Xaa Leu Glu Leu	300
305	310	315

<210> 1245

<211> 322

<212> PRT

<213> Unknown (H38g162 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1245

Ser Asn Thr Gly Met	Ser Ile Leu Asn Thr	Ser Glu Met Glu Ile Ser
1	5	10
Ile Phe Tyr Leu Val	Gly Ile Pro Gly Leu Glu His Ala Asn Ile Trp	15
	20	25
Ile Ser Ile Pro Ile	Cys Leu Met Tyr Thr Val Ala Ile Leu Gly Asn	30
	35	40
Cys Thr Ile Leu Phe	Phe Ile Lys Thr Glu Pro Ser Leu His Glu Pro	45
	50	55
Met Tyr Tyr Phe Leu	Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser	60
	65	70
Leu Ser Ser Leu Pro	Thr Met Leu Arg Ile Phe Leu Phe Asn Ala Pro	75
	85	90
Gly Ile Ser Pro Asp	Ala Cys Ile Ala Gln Glu Phe Phe Ile His Gly	95
	100	105
Phe Ser Ala Met Glu	Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg	110
	115	120
Phe Ile Ala Ile Cys	Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Ser	125
	130	135
Ala Arg Val Ile Gln	Ile Gly Leu Ala Phe Ser Leu Lys Asn Val Leu	140
	145	150
Leu Ile Leu Pro Phe	Pro Phe Thr Leu Lys His Leu Lys Tyr Cys Lys	155
	165	170
Lys Asn Leu Leu Ser	Gln Ser Tyr Cys Leu His Gln Asp Val Met Lys	175
	180	185
Leu Ala Cys Thr Asp	Asn Lys Val Asn Ile Ile Tyr Gly Leu Phe Val	190
	195	200
Ala Leu Thr Gly Ile	Leu Asp Leu Thr Phe Ile Phe Met Ser Tyr Met	205
	210	215
Leu Ile Leu Lys Ala	Val Leu Ser Ile Ala Ser Xaa Lys Lys Arg Leu	220
	225	230
Lys Val Leu Asn Thr	Cys Val Ser His Ile Cys Ala Val Leu Ile Phe	235
	245	250
Tyr Val Pro Ile Ile	Ser Leu Ala Val Ile Tyr Arg Phe Ala Lys His	255
	260	265
		270

Ser Phe Pro Ile Thr Arg Ile Leu Ile Ala Asp Ala Phe Leu Leu Val
 275 280 285
 Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val Lys Ser Gln Gln Ile
 290 295 300
 Arg Asn Leu Val Leu Glu Lys Leu Cys Gln Lys Gln Ser Xaa Ser Gly
 305 310 315 320
 Cys Leu

<210> 1246

<211> 319

<212> PRT

<213> Unknown (H38g163 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1246

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
 1 5 10 15
 Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu
 20 25 30
 Phe Leu Ser Met Cys Leu Val Thr Met Leu Arg Glu Leu Leu Ile Ile
 35 40 45
 Leu Ala Val Thr Ser Asp Ser His Leu His Ile Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Val Leu Gly His Asp Ile Gly Phe Thr Xaa Ala Thr
 65 70 75 80
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Ala Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys
 100 105 110
 Ile Asp Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala
 115 120 125
 Ile Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys
 130 135 140
 Val Phe Leu Val Leu Met Phe Phe Leu Ser Leu Leu Asp Ser Xaa Leu
 145 150 155 160
 His Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
 180 185 190
 Val Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser
 210 215 220
 Ile Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val
 260 265 270
 Val Ala Ser Val Leu Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu
 290 295 300
 Cys Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser

305

310

315

<210> 1247

<211> 320

<212> PRT

<213> Unknown (H38g164 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1247

Met	Arg	Leu	Ile	Xaa	Asp	Glu	Glu	Met	Ser	Arg	Arg	Asn	Tyr	Thr	Glu
1				5					10					15	
Leu	Thr	Glu	Phe	Val	Leu	Leu	Gly	Leu	Thr	Ser	Arg	Pro	Glu	Leu	Arg
			20				25						30		
Val	Ala	Phe	Leu	Ala	Leu	Phe	Leu	Phe	Val	Tyr	Ile	Ala	Thr	Val	Val
			35				40					45			
Gly	Asn	Leu	Gly	Met	Ile	Ile	Leu	Ile	Lys	Val	Asp	Ser	Arg	Leu	His
	50				55					60					
Thr	Pro	Met	Xaa	Phe	Phe	Leu	Ser	Ser	Leu	Ser	Ile	Leu	Asp	Leu	Cys
65				70					75					80	
Phe	Ser	Thr	Asn	Phe	Thr	Pro	Lys	Met	Leu	Glu	Asn	Phe	Leu	Ser	Glu
			85					90					95		
Lys	Lys	Thr	Ile	Ser	Tyr	Ala	Gly	Cys	Leu	Met	Gln	Cys	Tyr	Val	Val
			100				105					110			
Ile	Ala	Val	Val	Leu	Ala	Glu	His	Cys	Met	Leu	Ala	Val	Met	Ala	Tyr
			115				120					125			
Asp	Arg	Tyr	Met	Ala	Ile	Cys	Asn	Pro	Leu	Leu	Tyr	Ser	Ser	Lys	Met
	130				135					140					
Ser	Gln	Gly	Val	Cys	Val	His	Leu	Val	Ile	Val	Pro	Tyr	Val	Tyr	Gly
145				150					155					160	
Phe	Leu	Leu	Ser	Val	Met	Glu	Thr	Leu	Arg	Thr	Tyr	Asn	Leu	Ser	Phe
			165					170					175		
Cys	Gly	Thr	Asn	Glu	Ile	Asn	His	Phe	Tyr	Cys	Ala	Asp	Pro	Pro	Leu
			180				185					190			
Ile	Lys	Leu	Ala	Cys	Ser	Asp	Thr	Tyr	Ser	Lys	Glu	Leu	Ser	Met	Tyr
		195				200					205				
Ile	Val	Ala	Gly	Tyr	Ser	Asn	Val	Gln	Ser	Leu	Leu	Ile	Ile	Leu	Thr
	210				215					220					
Ser	Tyr	Met	Phe	Ile	Leu	Val	Ala	Ile	Leu	Arg	Ser	His	Ser	Ala	Glu
225				230					235					240	
Gly	Arg	Lys	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Thr	Val	Val
			245					250					255		
Thr	Ile	Phe	Tyr	Gly	Thr	Leu	Phe	Cys	Met	His	Leu	Arg	Arg	Pro	Thr
			260				265					270			
Asp	Glu	Ser	Val	Glu	Gln	Gly	Lys	Met	Val	Ala	Val	Phe	Tyr	Thr	Thr
		275				280					285				
Val	Ile	Leu	Met	Leu	Asn	Ser	Met	Ile	Tyr	Gly	Leu	Arg	Asn	Lys	Asp
	290				295				300						
Val	Lys	Glu	Ala	Leu	Lys	Lys	Ala	Ile	Gly	Lys	Gln	Thr	Leu	Gly	Lys
305				310					315					320	

<210> 1248

<211> 316

<212> PRT

<213> Unknown (H38g165 protein)

<220>

<223> Synthetic construct

<400> 1248

```

Arg Arg Met Gly Asn His Thr Ala Val Ser Leu Phe Leu Leu Trp Gly
1      5      10      15
Phe Ser Ser Phe Ser Asp Leu Gln Ser Leu Leu Phe Val Val Ile Leu
20      25      30
Leu Leu His Val Thr Ile Leu Ala Ala Asn Val Ser Ile Met Gly Ala
35      40      45
Ile Lys Leu Ser His Asn Leu His Thr Pro Met Tyr Phe Phe Leu Cys
50      55      60
Gly Leu Ser Phe Ser Glu Thr Cys Thr Thr Val Val Val Ile Pro Arg
65      70      75      80
Met Leu Val Asp Phe Leu Ser Glu Ser Lys Thr Ile Ser Leu Pro Glu
85      90      95
Cys Ala Thr Gln Met Phe Phe Phe Leu Gly Phe Ala Ser Asn Asn Cys
100     105     110
Phe Ile Met Ala Ala Met Ser Tyr Asp Arg Tyr Thr Ala Ile His Asn
115     120     125
Pro Leu Gln Tyr His Thr Leu Met Thr Arg Lys Ile Cys Leu Gln Met
130     135     140
Met Met Ala Ser Trp Met Val Gly Phe Leu Phe Ser Leu Cys Ile Ile
145     150     155     160
Val Thr Val Phe Asn Leu Ser Leu Cys Asp Leu Asn Thr Ile Gln His
165     170     175
Tyr Phe Cys Asp Ile Ser Pro Val Val Ser Leu Ala Cys Asn Tyr Thr
180     185     190
Phe Tyr His Glu Met Ala Ile Phe Val Leu Ser Ala Phe Val Leu Val
195     200     205
Gly Ser Cys Ile Leu Ile Met Ile Ser Tyr Val Phe Ile Val Phe Ile
210     215     220
Val Ile Lys Met Pro Ser Ala Lys Gly Arg Ser Lys Ala Phe Ser Thr
225     230     235     240
Cys Ser Ser His Leu Thr Val Val Ser Ile His Tyr Gly Phe Ala Cys
245     250     255
Phe Val Tyr Leu Arg Pro Lys Asn Ser Asn Ser Phe Asp Glu Asp Met
260     265     270
Leu Thr Ala Met Ile Tyr Thr Ile Leu Met Pro Leu Leu Asn Pro Ile
275     280     285
Val Tyr Ser Leu Arg Asn Lys Glu Met Gln Ile Ala Leu Arg Lys Thr
290     295     300
Leu Gly Ser Val Phe Gly Val Phe Pro Gln Lys Thr
305     310     315

```

<210> 1249

<211> 319

<212> PRT

<213> Unknown (H38g166 protein)

<220>

<223> Synthetic construct

<400> 1249

```

Met Ser Ala Tyr Asn Asn Thr Asn Ala Arg Pro Ser Thr Phe Ile Leu
1      5      10      15
Ile Gly Ile Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Ile Pro
20      25      30
Phe Cys Val Val Tyr Leu Leu Ala Leu Leu Gly Asn Gly Ser Leu Leu
35      40      45
Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Leu Phe

```

50	55	60
Leu Cys Met Leu Ala Val Val Asp Leu Val Val Cys Ser Thr Ala Val		
65	70	75
Pro Lys Leu Leu Ser Leu Phe Trp Phe His Asp Gly Glu Ile Arg Phe		
	85	90
Glu Thr Cys Leu Thr Gln Met Phe Leu Ile His Ser Cys Ser Thr Met		
	100	105
Glu Ser Gly Phe Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile		
	115	120
Cys Asn Pro Leu Arg His Ser Ala Ile Leu Thr Arg Ala Val Ile Gly		
	130	135
Arg Val Gly Leu Ala Ile Val Leu Arg Gly Ile Ala Leu Leu Ser Pro		
145	150	155
His Ser Phe Leu Leu Arg Trp Leu Pro Tyr Cys Arg Thr His Ile Ile		
	165	170
Ser His Thr Tyr Cys Glu Phe Met Ala Leu Ile Arg Ile Ala Cys Ala		
	180	185
Glu Thr Lys Phe Arg Arg Ala Tyr Ser Leu Ile Val Ala Phe Leu Thr		
	195	200
Gly Val Val Asp Phe Ile Leu Ile Ile Tyr Ser Tyr Val Leu Ile Leu		
	210	215
His Thr Val Phe Gln Leu Pro Ser Lys Asp Ala Arg Leu Lys Ser Leu		
225	230	235
Gly Thr Cys Gly Ser His Val Cys Val Ile Leu Val Ser Tyr Thr Pro		
	245	250
Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Ala Pro		
	260	265
His Phe His Ile Phe Val Ala Asn Ile Tyr Leu Leu Val Pro Pro Met		
	275	280
Val Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Arg Ile Trp Asp Arg		
	290	295
Phe Leu Lys Val Phe Ser Phe Ser Lys Pro Leu Ser Lys Ser Phe		
305	310	315

<210> 1250

<211> 307

<212> PRT

<213> Unknown (H38g167 protein)

<220>

<223> Synthetic construct

<400> 1250

Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu Thr		
1	5	10
Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Ile Phe Leu Val Val		
	20	25
Tyr Ile Ile Thr Met Val Gly Asn Ile Gly Met Met Val Leu Ile Lys		
	35	40
Val Ser Pro Gln Leu Asn Asn Pro Met Tyr Phe Phe Leu Ser His Leu		
	50	55
Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met Leu		
65	70	75
Glu Asn Leu Leu Ser Asp Lys Lys Thr Ile Thr Tyr Ala Gly Cys Leu		
	85	90
Val Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile Phe Ile		
	100	105
Leu Ala Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Gly Asn Pro Leu		
	115	120
Leu Tyr Gly Ser Lys Met Ser Arg Val Val Cys Ile Arg Leu Ile Thr		
	130	135
		140

Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Ala Ala Thr Leu Trp
 145 150 155 160
 Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His Phe Tyr
 165 170 175
 Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr Phe Val
 180 185 190
 Lys Glu Tyr Thr Met Ile Ile Leu Ala Gly Ile Asn Phe Thr Tyr Ser
 195 200 205
 Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala Ile Leu
 210 215 220
 Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile Phe Met
 245 250 255
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val
 260 265 270
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val Ile Ser
 290 295 300
 Arg Ser Cys
 305

<210> 1251

<211> 322

<212> PRT

<213> Unknown (H38g168 protein)

<220>

<223> Synthetic construct

<400> 1251

Met Thr Met Thr Thr Glu Asn Pro Asn Gln Thr Val Val Ser His Phe
 1 5 10 15
 Phe Leu Glu Gly Leu Arg Tyr Thr Ala Lys His Ser Ser Leu Phe Phe
 20 25 30
 Leu Leu Phe Leu Leu Ile Tyr Ser Ile Thr Val Ala Gly Asn Leu Leu
 35 40 45
 Ile Leu Leu Thr Val Gly Ser Asp Ser His Leu Ser Leu Pro Met Tyr
 50 55 60
 His Phe Leu Gly His Leu Ser Phe Leu Asp Ala Trp Leu Ser Thr Val
 65 70 75 80
 Thr Val Pro Lys Val Met Ala Gly Leu Leu Thr Leu Asp Gly Lys Val
 85 90 95
 Ile Ser Phe Glu Gly Cys Ala Val Gln Leu Tyr Cys Phe His Phe Leu
 100 105 110
 Ala Ser Thr Glu Cys Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Tyr
 115 120 125
 Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Ala Met Asn Arg Arg
 130 135 140
 Met Cys Ala Glu Met Ala Gly Ile Thr Trp Ala Ile Gly Ala Thr His
 145 150 155 160
 Ala Ala Ile His Thr Ser Leu Thr Phe Arg Leu Leu Tyr Cys Gly Pro
 165 170 175
 Cys His Ile Ala Tyr Phe Phe Cys Asp Ile Pro Pro Val Leu Lys Leu
 180 185 190
 Ala Cys Thr Asp Thr Thr Ile Asn Glu Leu Val Met Leu Ala Ser Ile
 195 200 205
 Gly Ile Val Ala Ala Gly Cys Leu Ile Leu Ile Val Ile Ser Tyr Ile
 210 215 220
 Phe Ile Val Ala Ala Val Leu Arg Ile Arg Thr Ala Gln Gly Arg Gln

```

225          230          235          240
Arg Ala Phe Ser Pro Cys Thr Ala Gln Leu Thr Gly Val Leu Leu Tyr
          245          250          255
Tyr Val Pro Pro Val Cys Ile Tyr Leu Gln Pro Arg Ser Ser Glu Ala
          260          265          270
Gly Ala Gly Ala Pro Ala Val Phe Tyr Thr Ile Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys His Ala Leu
          290          295          300
Gln Arg Leu Leu Cys Ser Ser Phe Arg Glu Ser Thr Ala Gly Ser Pro
305          310          315          320
Pro Pro

```

<210> 1252

<211> 322

<212> PRT

<213> Unknown (H38g169 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1252

```

Lys Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu
 1          5          10          15
Thr Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Val Phe Leu Val
          20          25          30
Val Tyr Ile Ile Thr Val Val Gly Asn Ile Gly Met Met Leu Leu Ile
          35          40          45
Lys Val Ser Pro Gln Leu Asn Ser Pro Met Tyr Phe Phe Leu Ser His
          50          55          60
Leu Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met
65          70          75          80
Leu Glu Asn Leu Leu Ser Asp Lys Lys Lys Thr Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Ala Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile
          100          105          110
Phe Ile Leu Ala Ala Ile Ala Phe Asp Arg Tyr Thr Val Ile Gly Asn
          115          120          125
Pro Leu Leu Tyr Gly Ser Lys Met Ser Arg Asp Val Cys Ile Arg Leu
          130          135          140
Ile Thr Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Thr Ala Thr
145          150          155          160
Leu Trp Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr
          180          185          190
Phe Val Lys Glu Tyr Thr Met Leu Ile Leu Ala Gly Ile Asn Phe Thr
          195          200          205
Tyr Ser Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala
          210          215          220
Ile Leu Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile
          245          250          255
Phe Met Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys
          260          265          270

```

Met Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val
 290 295 300
 Ile Ser Arg Ser Cys Xaa Thr Lys Xaa Asn Gln Val Xaa Ile Asn Phe
 305 310 315 320
 Val Phe

<210> 1253

<211> 311

<212> PRT

<213> Unknown (H38g170 protein)

<220>

<223> Synthetic construct

<400> 1253

Met Ser Asn Ala Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1 5 10 15
 His Ala Pro Gly Leu Asp Ala Leu Leu Phe Gly Ile Phe Leu Val Val
 20 25 30
 Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
 35 40 45
 Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
 50 55 60
 Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
 65 70 75 80
 Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
 85 90 95
 Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe
 100 105 110
 Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
 115 120 125
 Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala
 130 135 140
 Thr Gly Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile
 145 150 155 160
 Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr
 165 170 175
 Phe Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
 180 185 190
 Ala Asn Val Met Val Ile Phe Val Asp Ile Gly Ile Val Ala Ser Gly
 195 200 205
 Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
 210 215 220
 Leu Arg Ile Arg Thr Ser Asp Gly Arg Arg Arg Ala Phe Gln Thr Cys
 225 230 235 240
 Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Val
 245 250 255
 Ile Tyr Leu Arg Pro Gly Ser Met Asp Ala Met Asp Gly Val Val Ala
 260 265 270
 Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys
 290 295 300
 Val Ala His Pro Gln Arg Lys
 305 310

<210> 1254

<211> 320

<212> PRT
 <213> Unknown (H38g171 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

<400> 1254
 Gly Val Gly Leu Xaa Lys Leu Xaa Trp Gln Ile Ile Phe Ser Gly Asp
 1 5 10 15
 Ser Phe Ser Thr Trp Glu Met Phe Ser Leu Ser Ile Leu Gln Leu Pro
 20 25 30
 Xaa Met Tyr Thr Val Ala Leu Ser Gly Thr Ser Ile Leu Ile Phe Leu
 35 40 45
 Ile Xaa Thr Asp Phe Xaa Val His Thr Ser Leu Tyr Ser Phe Xaa Val
 50 55 60
 Leu Ile Asp Ile Ala Ile Ser Val Val Lys Ile Gly Ile Glu Val Phe
 65 70 75 80
 Ser Gly Lys Ile Asn Phe Ser His Thr Gly Cys Gly Thr Gln Ile Phe
 85 90 95
 Phe Phe Leu Thr Ala Gly Ile Phe Lys Tyr Val Leu Leu Thr Tyr Met
 100 105 110
 Ala Tyr Asp His Asn Val Ala Ile Cys Asp Leu Arg Xaa Pro Thr Phe
 115 120 125
 Met Ser Asp Gln Val Phe Xaa Gln Trp Ala Val Glu Ser Trp Ile Gly
 130 135 140
 Gly Lys Leu Ser Ser Leu Ala His Thr Ile Tyr Ile Phe His Leu Phe
 145 150 155 160
 Ser Tyr Lys Ala Lys Glu Ile Ser His Leu Trp Pro Lys Leu Phe Xaa
 165 170 175
 Ser Ser Ser Val Gly Ile Pro Tyr Ile Gln Asn Asp Val Phe Phe Thr
 180 185 190
 Ile Ile Thr Phe Leu Phe Thr Leu Leu Pro Leu Thr Leu Thr Leu Ser
 195 200 205
 Ser Lys Leu Ile Val Phe Thr Ile Leu His Met Asn Ser Ser Asn Gly
 210 215 220
 Gly Ala Lys Ser Trp His Thr Tyr Cys Phe His Leu Ser Val Leu Ile
 225 230 235 240
 Pro Cys Cys Gly Gln Ala Ile Phe Val Tyr Met Thr Ser Ser Ser Phe
 245 250 255
 Xaa Thr Val Asn Lys Tyr Gln Thr Met Ser Val Leu Thr Ala Xaa Leu
 260 265 270
 Tyr Pro Leu Leu Lys Pro Leu Ile Asp Ile Leu Lys Asn Ala Glu Val
 275 280 285
 Ala Gly Ala Trp Ser Lys Phe Leu Xaa Lys Lys Ala Leu Lys Ser Gln
 290 295 300
 His Leu Ile Thr Arg Ser Cys Glu Asn Lys Xaa Thr Thr Glu Gln Ser
 305 310 315 320

<210> 1255
 <211> 320
 <212> PRT
 <213> Unknown (H38g172 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1255

```

Met Leu Val Pro Lys Lys Met Val Arg Gly Asn Ser Thr Leu Val Thr
 1              5              10              15
Glu Phe Ile Leu Leu Gly Leu Lys Asp Leu Pro Glu Leu Gln Pro Ile
      20              25              30
Leu Phe Val Leu Phe Leu Leu Ile Tyr Leu Ile Thr Val Gly Gly Asn
      35              40              45
Leu Gly Met Leu Val Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro
      50              55              60
Met Tyr Phe Phe Leu Ala Ser Leu Ser Cys Leu Asp Leu Tyr Tyr Ser
65              70              75              80
Thr Asn Val Thr Pro Lys Met Leu Val Asn Phe Phe Ser Asp Lys Lys
      85              90              95
Ala Ile Ser Tyr Ala Ala Cys Leu Val Gln Cys Tyr Phe Phe Ile Ala
      100              105              110
Val Val Ile Thr Glu Tyr Tyr Met Leu Ala Val Met Ala Tyr Asp Arg
      115              120              125
Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Ser Ser Lys Met Ser Lys
      130              135              140
Gly Leu Cys Ile Arg Leu Ile Ala Gly Pro Tyr Val Tyr Gly Phe Leu
145              150              155              160
Ser Gly Leu Met Glu Thr Met Trp Thr Tyr His Leu Thr Phe Cys Gly
      165              170              175
Ser Asn Ile Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Ile Arg
      180              185              190
Leu Ser Cys Ser Asp Thr Phe Ile Lys Glu Thr Ser Met Phe Val Val
      195              200              205
Ala Xaa Phe Asn Leu Ser Ser Ser Leu Ile Ile Ile Leu Ile Ser Tyr
      210              215              220
Ile Phe Ile Leu Ile Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg
225              230              235              240
Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Ala Val Thr Val
      245              250              255
Phe Tyr Gly Thr Leu Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg
      260              265              270
Ser Val Glu Gln Ser Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser
      275              280              285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290              295              300
Gln Ala Phe Trp Lys Leu Ile Arg Arg Asn Val Leu Leu Lys Xaa Asn
305              310              315              320

```

<210> 1256

<211> 235

<212> PRT

<213> Unknown (H38g173 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(235)

<223> Xaa = Any Amino Acid

<400> 1256

```

Met Leu Phe Ile Ser Gln Trp Gly Glu Arg Xaa Arg Val Arg Arg Asn
 1              5              10              15
Val Gln Leu Met Thr Ala Phe Ile Leu Met Asp Leu Pro His Val Pro

```

```

      20      25      30
Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val Tyr Val Leu
  35      40      45
Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg Val Tyr Ser
  50      55      60
His Leu His Thr Pro Lys Tyr Tyr Phe Leu Thr Asn Leu Ser Phe Ile
  65      70      75      80
Asp Leu Trp Phe Phe Thr Val Met Val Pro Lys Met Pro Arg Thr Leu
      85      90      95
Leu Ser Leu Cys Gly Lys Ala Val Ser Phe His Ser Cys Met Thr Gln
      100      105      110
Leu Tyr Phe Phe Tyr Phe Leu Gly Ser Thr Glu Cys Leu Leu Tyr Thr
      115      120      125
Val Met Ser Tyr Asp Arg Tyr Arg Gly Asn Thr Gln His Phe Pro Gly
      130      135      140
Ser Glu Asn Leu Pro Thr Lys Xaa Ala Lys Cys Xaa Trp Pro Gly Gly
      145      150      155      160
His Thr Gly Leu Pro Leu Ile Ile Leu Ala Asp Leu Ser Gly Xaa Leu
      165      170      175
Arg Val Asp Ser Ser Xaa Trp Ala Ile Gln Asn Xaa Xaa Tyr Asn Leu
      180      185      190
Val Ile Gln Val Lys Phe Ile Thr Cys Ile Gly Leu Ser Ile Lys His
      195      200      205
Tyr Ser Lys Gln Leu Ala Gln Leu Xaa Phe Phe His Arg Leu Ser Lys
      210      215      220
Thr Phe Leu Asn Ser Gln Leu Asp Phe Tyr Leu
      225      230      235

```

<210> 1257

<211> 307

<212> PRT

<213> Unknown (H38g174 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(307)

<223> Xaa = Any Amino Acid

<400> 1257

```

Met Ile Thr Glu Phe Ile Leu Ile Gly Phe Ser Asn Leu Gly Asp Leu
  1      5      10      15
Gln Ile Leu Leu Phe Phe Ile Phe Leu Leu Val Tyr Leu Thr Thr Leu
      20      25      30
Met Ala Asn Thr Thr Ile Met Thr Val Ile His Leu Asp Arg Ala Leu
      35      40      45
His Thr Pro Met Tyr Phe Phe Leu Phe Val Leu Ser Cys Ser Glu Thr
      50      55      60
Cys Tyr Thr Leu Val Ile Val Pro Lys Met Leu Thr Asn Leu Leu Ser
      65      70      75      80
Ala Ile Pro Thr Ile Ser Phe Ser Gly Cys Val Val Gln Leu Tyr Leu
      85      90      95
Phe Val Gly Leu Ala Cys Thr Asn Cys Phe Leu Ile Ala Val Met Gly
      100      105      110
Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Asn Tyr Thr Leu Ile
      115      120      125
Val Ser Xaa Ala Thr Cys Met Gln Leu Val Leu Ala Ser Ser Phe Cys
      130      135      140
Gly Phe Leu Thr Ser Val Ile Val Asn Ile Leu Val Phe Ser Val Leu
      145      150      155      160

```

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1259

```

Gly Thr Lys Ser Ile Lys Leu Thr Ser Leu Ser Glu Phe Leu Leu Leu
 1          5          10          15
Glu Phe Ser Ser Leu Glu Glu Ile Gln Ile Leu Phe Leu Val Cys
          20          25          30
Leu Trp Leu Tyr Leu Ile Val Leu Ser Gly Asn Ile Thr Thr Val Thr
          35          40          45
Val Ile Arg Leu Asp Gln Ser Leu His Ile Pro Val Tyr Leu Phe Leu
          50          55          60
Gly Ile Leu Ser Ile Ser Gly Thr Cys Tyr Thr Phe Val Ile Leu Pro
65          70          75          80
Lys Met Leu Ile Asp Leu Leu Ser Leu Leu Arg Thr Ile Ser Phe Ile
          85          90          95
Asn Cys Ala Leu Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn
          100          105          110
Phe Met Phe Leu Gly Met Thr Val Tyr Asp Ser Tyr Val Ala Ile Cys
          115          120          125
His Pro Leu His Tyr Pro Val Leu Thr Ser Trp Gln Ile Cys Lys Gln
          130          135          140
Leu Ala Ala Thr Cys Ala Val Ile Val Phe Phe Cys Leu Phe Val Phe
145          150          155          160
Thr Asp Arg Leu Leu Leu Arg Phe Ser Leu Leu Phe Cys Gly Pro Asn
          165          170          175
Lys Ile Asn His Tyr Phe Cys Asp Ile Ser Leu Leu Ile Gln Leu Ala
          180          185          190
Cys Thr Asp Thr Tyr Ile Arg Glu Leu Val Ile Phe Ile Gly Gly Ile
          195          200          205
Leu Ala Leu Thr Val Pro Leu Met Phe Ile Cys Ile Ser Tyr Gly Phe
          210          215          220
Ile Val His Thr Ile Leu Arg Ile Pro Ser Cys Glu Ser Lys Gln Lys
225          230          235          240
Ala Ile Ser Thr Cys Ala Ser His Leu Ile Met Val Val Val His Tyr
          245          250          255
Gly Cys Ala Ser Phe Val Asn Leu Xaa Pro Ser Ala Lys Xaa Ser Ser
          260          265          270
Ser Lys Xaa Pro Ser Ser Lys Asn Arg Leu Val Thr Val Thr Tyr Thr
          275          280          285
Val Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Phe Lys Asn Lys
          290          295          300
Asn Val Gln Met Ala Ile Trp Lys Val Ile Cys Gln Gly Gly Phe Pro
305          310          315          320
Pro

```

<210> 1260

<211> 317

<212> PRT

<213> Unknown (H38g177 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1260

```

Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
 1              5              10              15
Ala Asn His Arg Glu Leu Gln Ile Phe Leu Phe Thr Leu Phe Leu Thr
      20              25              30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Ala Leu Ile
      35              40              45
Gln Ala Asn Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 50              55              60
Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Arg Met
65              70              75              80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Arg
      85              90              95
Leu Val Gln Cys Tyr Leu Phe Ile Thr Leu Val His Val Glu Leu Tyr
      100             105             110
Ile Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Ile Cys Asn Pro
      115             120             125
Leu Leu Tyr Gly Ser Arg Met Ser Lys Ser Val Cys Ser Phe Leu Ile
      130             135             140
Thr Val Leu Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met
145             150             155             160
Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Ser Glu Ile Asn His Phe
      165             170             175
Tyr Cys Val Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr
      180             185             190
Asn Lys Glu Val Ser Met Phe Val Val Ala Gly Phe Asn Phe Thr Tyr
      195             200             205
Pro Leu Leu Ile Ile Leu Ile Ser Tyr Leu Tyr Ile Phe Pro Ala Thr
      210             215             220
Leu Arg Ile Cys Ser Thr Glu Gly Arg His Lys Ala Phe Ser Thr Cys
225             230             235             240
Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ser Ala Leu Phe Phe
      245             250             255
Met Tyr Leu Arg Arg Pro Ser Glu Glu Ser Met Glu Gln Gly Lys Met
      260             265             270
Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile
      275             280             285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Cys Lys Glu Leu
      290             295             300
Phe Lys Arg Lys Leu Phe Ser Lys Xaa Thr Leu Leu Leu
305             310             315

```

<210> 1261

<211> 317

<212> PRT

<213> Unknown (H38g178 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1261

```

Thr Asp Val Xaa Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Glu
 1              5              10              15
Leu Gln Pro Val Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu
      20              25              30
Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val Ser Ser Asp

```

```

      35      40      45
Ser Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp
  50      55      60
Pro Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met Ile Val Asp
  65      70      75      80
Thr Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr Gln
      85      90      95
Met Ser Phe Leu Leu Leu Val Ala Cys Ile Glu Gly Met Leu Leu Thr
      100      105      110
Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro Leu His Tyr
      115      120      125
Pro Ile Ile Val Asn Pro His Leu Cys Val Phe Phe Val Leu Val Ser
      130      135      140
Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu
  145      150      155      160
Gln Leu Thr Ile Ile Lys Asn Val Glu Ile Ser Asn Leu Val Cys Asp
      165      170      175
Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Asn
      180      185      190
Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu Pro Ile Ser
      195      200      205
Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg Ile
      210      215      220
Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Cys His
  225      230      235      240
Leu Ala Val Val Cys Trp Phe Tyr Gly Thr Gly Ile Gly Leu Tyr Leu
      245      250      255
Thr Ser Ala Gly Ser Pro Pro Pro Arg Asn Gly Val Val Ala Ser Val
      260      265      270
Met Tyr Ala Val Val Thr Pro Met Leu Asn Leu Phe Ile Cys Ser Leu
      275      280      285
Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu Arg Ser Arg Ala
      290      295      300
Val Glu Tyr Pro Xaa Ser Val Pro Ser Phe Phe Leu Cys
  305      310      315

```

<210> 1262

<211> 314

<212> PRT

<213> Unknown (H38g179 protein)

<220>

<223> Synthetic construct

<400> 1262

```

Met Arg Gly Phe Asn Lys Thr Thr Val Val Thr Gln Phe Ile Leu Val
  1      5      10      15
Gly Phe Ser Ser Leu Gly Glu Leu Gln Leu Leu Leu Phe Val Ile Phe
      20      25      30
Leu Leu Leu Tyr Leu Thr Ile Leu Val Ala Asn Val Thr Ile Met Ala
      35      40      45
Val Ile Arg Phe Ser Trp Thr Leu His Thr Pro Met Tyr Gly Phe Leu
      50      55      60
Phe Ile Leu Ser Phe Ser Glu Ser Cys Tyr Thr Phe Val Ile Ile Pro
  65      70      75      80
Gln Leu Leu Val His Leu Leu Ser Asp Thr Lys Thr Ile Ser Phe Met
      85      90      95
Ala Cys Ala Thr Gln Leu Phe Phe Phe Leu Gly Phe Ala Cys Thr Asn
      100      105      110
Cys Leu Leu Ile Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
      115      120      125

```

His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly Leu Glu
 130 135 140
 Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu Val Ala
 145 150 155 160
 Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg Val Asn
 165 170 175
 His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys Thr Asp
 180 185 190
 Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu Val Ile
 195 200 205
 Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile Val Asn
 210 215 220
 Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe Val Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys Ala Ser
 245 250 255
 Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys Asp Gln
 260 265 270
 Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu
 275 280 285
 Val Tyr Ser Leu Arg Asn Lys Glu Val Lys Thr Ala Leu Lys Arg Val
 290 295 300
 Leu Gly Met Pro Val Ala Thr Lys Met Ser
 305 310

<210> 1263

<211> 314

<212> PRT

<213> Unknown (H38g180 protein)

<220>

<223> Synthetic construct

<400> 1263

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser


```

      210              215              220
Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
225              230              235              240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
      245              250              255
Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
      260              265              270
Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val
      290              295              300
Ile His Gln Lys Lys Thr Phe Phe Ser Leu
305              310

```

<210> 1264
 <211> 275
 <212> PRT
 <213> Unknown (H38g181 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(275)
 <223> Xaa = Any Amino Acid

```

<400> 1264
Thr Ile Ile Asn Val Asn Ile Ser Pro Glu Phe Val Leu Val Gly Phe
  1              5              10              15
Ser Ser Asp Ala Glu Ile Gln Ile Met Leu Phe Val Leu Ile Leu Val
      20              25              30
Ile His Leu Leu Thr Leu Thr Gly Lys Leu Val Met Ile Leu Glu Ile
      35              40              45
Arg Ala Asp Ser His Leu Gln Arg Pro Met Tyr Phe Phe Leu Xaa His
      50              55              60
Leu Ser Phe Leu Asp Leu Ser Tyr Ser Ser Val Thr Val Pro Arg Met
      65              70              75              80
Leu Gln Asn Phe Leu Ser Gly Arg Lys Ala Ser Gln Cys Gly Ala Ala
      85              90              95
Ser Pro Ser Phe Phe Phe Thr Leu Ser Gly Gly Thr Glu Ala Cys Leu
      100             105             110
Phe Ser Ala Met Ala Tyr Asp His Tyr Ala Thr Ile Arg His Pro Val
      115             120             125
Val Tyr Thr Met Val Met Asn Arg Ser Leu Cys Met Val Ile Leu Arg
      130             135             140
Ile Ala Trp Ala Ala Gly Phe Leu Ile Ser Leu Met Asp Ser Leu Phe
      145             150             155             160
Thr His Lys Leu His Phe Cys Gly Pro Asp Ile Ile Pro Tyr Phe Arg
      165             170             175
Cys Lys Leu Pro Pro Phe Phe Pro Leu Ser Tyr Ile Asp Pro Thr Val
      180             185             190
Asn Glu Ile Leu Leu Ala Val Ser Gln Ala Phe Trp Gly Leu Leu Thr
      195             200             205
Leu Ser Leu Ile Phe Phe Ser Tyr Ser Arg Ile Thr Ser Val Ile Leu
      210             215             220
Ser Ile Cys Ser Ser Glu Gly Gln Gly Lys Ala Phe Ser Ala Cys Pro
      225             230             235             240
Ser His Leu Ala Val Val Leu Ser Phe Tyr Gly Thr Ala Phe Phe Arg
      245             250             255
Tyr Pro Gly Ser Thr Ser Gly Ser Val Leu Gly Gln Val Val Ser Val
      260             265             270

```

Gln Tyr Ser
275

<210> 1265
<211> 312
<212> PRT
<213> Unknown (H38g182 protein)

<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(312)
<223> Xaa = Any Amino Acid

<400> 1265
Met Arg Arg Asn Phe Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
1 5 10 15
Thr Asn His Gln Glu Leu Gln Ile Leu Leu Phe Met Leu Phe Leu Ala
20 25 30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Ser Met Ile Ala Leu Ile
35 40 45
Gln Ala Asn Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
50 55 60
Leu Ser Phe Leu Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Lys Met
65 70 75 80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Cys
85 90 95
Leu Val Gln Cys Tyr Leu Tyr Ile Ile Leu Val His Val Glu Ile Tyr
100 105 110
Ile Leu Ala Val Met Ala Phe Asp Xaa Tyr Met Ala Ile Xaa Asn Pro
115 120 125
Leu Leu Tyr Gly Ser Lys Met Ser Lys Ser Val Cys Ser Phe Leu Ile
130 135 140
Thr Val Pro Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met
145 150 155 160
Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Asn Glu Ile Asn His Phe
165 170 175
Tyr Cys Ala Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr
180 185 190
Asn Lys Glu Leu Ser Met Phe Val Val Ala Gly Trp Asn Leu Ser Phe
195 200 205
Ser Leu Phe Ile Ile Phe Ile Ser Tyr Phe Tyr Ile Phe Pro Ala Ile
210 215 220
Leu Arg Ile Arg Ser Thr Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys
225 230 235 240
Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ala Thr Leu Phe Phe
245 250 255
Met Cys Leu Arg Pro Pro Ser Glu Glu Ser Met Glu Gln Gly Gln Met
260 265 270
Val Ala Val Leu Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile
275 280 285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ser Lys Glu Leu
290 295 300
Phe Lys Arg Lys Leu Phe Pro Lys
305 310

<210> 1266
<211> 315
<212> PRT
<213> Unknown (H38g183 protein)

<220>

<223> Synthetic construct

<400> 1266

```

Met Glu Pro Glu Ala Gly Thr Asn Arg Thr Ala Val Ala Glu Phe Ile
 1           5           10           15
Leu Leu Gly Leu Val Gln Thr Glu Glu Met Gln Pro Val Val Phe Val
           20           25           30
Leu Leu Leu Phe Ala Tyr Leu Val Thr Ile Gly Gly Asn Leu Ser Ile
           35           40           45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ala Pro Met Tyr Phe
           50           55           60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Thr Val Thr
65           70           75           80
Val Pro Ala Met Leu Gly Arg Leu Leu Ser His Lys Ser Thr Ile Ser
           85           90           95
Tyr Asp Ala Cys Leu Ser Gln Leu Phe Phe Phe His Leu Leu Ala Gly
           100          105          110
Met Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala
115          120          125
Ile Cys Gln Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
130          135          140
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu
145          150          155          160
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu
           165          170          175
Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
           180          185          190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Val Ala Ala Ala Phe
195          200          205
Met Ala Val Ala Pro Leu Val Phe Ile Ser Val Ser Tyr Ala His Val
210          215          220
Val Ala Ala Val Leu Gln Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
           245          250          255
Thr Gly Val Phe Ser Tyr Met Arg Leu Gly Ser Val Glu Ser Ser Asp
           260          265          270
Lys Asp Lys Gly Val Gly Val Phe Met Thr Val Ile Asn Pro Met Leu
275          280          285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Thr Asp Val Gln Gly Ala Leu
290          295          300
Trp Gln Leu Leu Val Gly Glu Arg Ser Leu Thr
305          310          315

```

<210> 1267

<211> 317

<212> PRT

<213> Unknown (H38g184 protein)

<220>

<223> Synthetic construct

<400> 1267

```

Met Leu Arg Asn Gly Ser Ile Val Thr Glu Phe Ile Leu Val Gly Phe
 1           5           10           15
Gln Gln Ser Ser Thr Ser Thr Arg Ala Leu Leu Phe Ala Leu Phe Leu
           20           25           30
Ala Leu Tyr Ser Leu Thr Met Ala Met Asn Gly Leu Ile Ile Phe Ile
           35           40           45

```

Thr Ser Trp Thr Asp Pro Lys Leu Asn Ser Pro Met Tyr Phe Phe Leu
 50 55 60
 Gly His Leu Ser Leu Leu Asp Val Cys Phe Ile Thr Thr Thr Ile Pro
 65 70 75 80
 Gln Met Leu Ile His Leu Val Val Arg Asp His Ile Val Ser Phe Val
 85 90 95
 Cys Cys Met Thr Gln Thr Tyr Phe Val Phe Cys Val Gly Val Ala Glu
 100 105 110
 Cys Ile Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Tyr Pro Leu Asn Tyr Val Pro Ile Ile Ser Gln Lys Val Cys Val Arg
 130 135 140
 Leu Val Gly Thr Ala Trp Phe Phe Gly Leu Ile Asn Gly Ile Phe Leu
 145 150 155 160
 Glu Tyr Ile Ser Phe Arg Glu Pro Phe Arg Arg Asp Asn His Ile Glu
 165 170 175
 Ser Phe Phe Cys Glu Ala Pro Ile Val Ile Gly Leu Ser Cys Gly Asp
 180 185 190
 Pro Gln Phe Ser Leu Trp Ala Ile Phe Ala Asp Ala Ile Val Val Ile
 195 200 205
 Leu Ser Pro Met Val Leu Thr Val Thr Ser Tyr Val His Ile Leu Ala
 210 215 220
 Thr Ile Leu Ser Lys Ala Ser Ser Ser Gly Arg Gly Lys Thr Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Val Val Ile Phe Leu Tyr Thr Ser Ala
 245 250 255
 Met Phe Ser Tyr Met Asn Pro His Ser Thr His Gly Pro Asp Lys Asp
 260 265 270
 Lys Pro Phe Ser Leu Leu Tyr Thr Ile Ile Thr Pro Met Cys Asn Pro
 275 280 285
 Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Glu Ala Met Val Arg
 290 295 300
 Ala Leu Gly Arg Thr Arg Leu Ala Gln Pro Gln Ser Val
 305 310 315

<210> 1268

<211> 324

<212> PRT

<213> Unknown (H38g185 protein)

<220>

<223> Synthetic construct

<400> 1268

Met Phe Tyr Phe Phe Pro Pro Leu Gln Ile Leu Ala Glu Asn Leu Thr
 1 5 10 15
 Met Val Thr Glu Phe Leu Leu Leu Gly Phe Ser Ser Leu Gly Glu Ile
 20 25 30
 Gln Leu Ala Leu Phe Val Val Phe Leu Phe Leu Tyr Leu Val Ile Leu
 35 40 45
 Ser Gly Asn Val Thr Ile Ile Ser Val Ile His Leu Asp Lys Ser Leu
 50 55 60
 His Thr Pro Met Tyr Phe Phe Leu Gly Ile Leu Ser Thr Ser Glu Thr
 65 70 75 80
 Phe Tyr Thr Phe Val Ile Leu Pro Lys Met Leu Ile Asn Leu Leu Ser
 85 90 95
 Val Ala Arg Thr Ile Ser Phe Asn Cys Cys Ala Leu Gln Met Phe Phe
 100 105 110
 Phe Leu Gly Phe Ala Ile Thr Asn Cys Leu Leu Leu Gly Val Met Gly
 115 120 125
 Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu His Tyr Pro Thr Leu

```

      130              135              140
Met Ser Trp Gln Val Cys Gly Lys Leu Ala Ala Ala Cys Ala Ile Gly
145              150              155              160
Gly Phe Leu Ala Ser Leu Thr Val Val Asn Leu Val Phe Ser Leu Pro
      165              170              175
Phe Cys Ser Ala Asn Lys Val Asn His Tyr Phe Cys Asp Ile Ser Ala
      180              185              190
Val Ile Leu Leu Ala Cys Thr Asn Thr Asp Val Asn Glu Phe Val Ile
      195              200              205
Phe Ile Cys Gly Val Leu Val Leu Val Val Pro Phe Leu Phe Ile Cys
      210              215              220
Val Ser Tyr Leu Cys Ile Leu Arg Thr Ile Leu Lys Ile Pro Ser Ala
225              230              235              240
Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser Val
      245              250              255
Val Ile Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr
      260              265              270
Ala Asn Tyr Val Ser Asn Lys Asp Arg Leu Val Thr Val Thr Tyr Thr
      275              280              285
Ile Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Leu Arg Asn Lys
      290              295              300
Asp Val Gln Leu Ala Ile Arg Lys Val Leu Gly Lys Lys Gly Ser Leu
305              310              315              320
Lys Leu Tyr Asn

```

<210> 1269

<211> 327

<212> PRT

<213> Unknown (H38g186 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1269

```

Lys Leu Gln Leu Asn Asn Phe Thr Glu Val Thr Met Phe Ile Leu Ile
 1              5              10              15
Ser Phe Thr Glu Phe Asp Val Gln Val Phe Leu Phe Leu Leu Phe
      20              25              30
Leu Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val
      35              40              45
Pro Ile Ile Gly Asp Phe Trp Leu His Ser Pro Met Tyr Tyr Phe Leu
      50              55              60
Gly Val Leu Ser Phe Leu Asp Val Cys Tyr Ser Thr Val Val Thr Pro
65              70              75              80
Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Leu
      85              90              95
Gly Cys Ala Thr Gln Met Phe Leu Ala Cys Thr Phe Gly Thr Thr Glu
      100              105              110
Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr
      115              120              125
Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro
130              135              140
Leu Ile Thr Ala Ser Tyr Val Ala Ser Ile Leu His Ala Thr Ile His
145              150              155              160
Thr Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg
      165              170              175

```

```

His Val Phe Cys Asn Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp
      180      185      190
Thr His Val Ile Gln Leu Leu Phe Phe Tyr Phe Val Gly Ser Ile Glu
      195      200      205
Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu
      210      215      220
Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser
      225      230      235      240
Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile
      245      250      255
Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp
      260      265      270
Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro
      275      280      285
Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg
      290      295      300
Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu Xaa Phe Xaa Asn Xaa
      305      310      315      320
Val Lys Leu Gln Ile Ile Leu
      325

```

<210> 1270

<211> 319

<212> PRT

<213> Unknown (H38g187 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1270

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
  1      5      10      15
Leu Ser Lys Pro Pro Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe
      20      25      30
Ser Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe
      35      40      45
Thr Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu
      50      55      60
Ala Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe
      65      70      75      80
Phe Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Ile Ile Gln Ile
      85      90      95
Phe Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr
      100      105      110
Met Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu
      115      120      125
Thr Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp
      130      135      140
Ile Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn
      145      150      155      160
Leu Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe
      165      170      175
Pro Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val
      180      185      190
Val Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu
      195      200      205
Leu Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser

```

210	215	220
Ser Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr		
225	230	235
Val Gly Ile Leu Phe Phe Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro		240
	245	250
Leu Pro Lys Thr Thr His Asp Xaa Tyr Leu Phe Ile Val Pro Leu Leu		255
	260	265
Ser Pro Leu Ser Arg Ile Tyr Thr Leu Arg Asn Lys Asp Met Asn Val		270
	275	280
Ser Met Glu Arg Leu Gly Lys Trp Ile Ala Gly Ser Ser Arg Met Ser		285
	290	300
Xaa Xaa Met Val Leu Ser Arg Val Gln Asp Asp Ser Val Ser Pro		
305	310	315

<210> 1271

<211> 324

<212> PRT

<213> Unknown (H38g188 protein)

<220>

<223> Synthetic construct

<400> 1271

Met Thr Thr Ile Ile Leu Glu Val Asp Asn His Thr Val Thr Thr Arg		
1	5	10
Phe Ile Leu Leu Gly Phe Pro Thr Arg Pro Ala Phe Gln Leu Leu Phe		15
	20	25
Phe Ser Ile Phe Leu Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu		30
	35	40
Leu Ile Ile Leu Ala Ile His Ser Asp Gly Gln Leu His Lys Pro Met		45
	50	55
Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr		60
	65	70
Val Ile Ser Pro Lys Met Leu Val Asp Phe Leu Ser His Asp Lys Ser		75
	80	85
Ile Ser Phe Asn Gly Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe		90
	95	100
Val Cys Thr Glu Tyr Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr		105
	110	115
Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln		120
	125	130
Leu Cys Gly Thr Leu Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr		135
	140	145
Ala Met Ile Lys Met Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met		150
	155	160
Pro Gln Ile Asn His Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val		165
	170	175
Ser Cys Glu Asp Ala Ser Gln Ala Glu Met Val Asp Phe Phe Leu Ala		180
	185	190
Leu Met Val Ile Ala Ile Pro Leu Cys Val Val Val Ala Ser Tyr Ala		195
	200	205
Ala Ile Leu Ala Thr Ile Leu Arg Ile Pro Ser Ala Gln Gly Arg Gln		210
	215	220
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Leu Phe		225
	230	235
Tyr Ser Met Thr Leu Phe Thr Tyr Ala Arg Pro Lys Leu Met Tyr Ala		240
	245	250
Tyr Asn Ser Asn Lys Val Val Ser Val Leu Tyr Thr Val Ile Val Pro		255
	260	265
Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn His Glu Val Lys Ala		270
	275	280
	285	290
	295	300

Ala Leu Arg Lys Thr Ile His Cys Arg Gly Ser Gly Pro Gln Gly Asn
 305 310 315 320
 Gly Ala Phe Ser

<210> 1272

<211> 323

<212> PRT

<213> Unknown (H38g189 protein)

<220>

<223> Synthetic construct

<400> 1272

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile
 130 135 140
 Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu
 145 150 155 160
 Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys
 165 170 175
 Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala
 180 185 190
 Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile
 195 200 205
 Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu
 210 215 220
 Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser
 225 230 235 240
 Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val
 245 250 255
 Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser
 260 265 270
 Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr
 275 280 285
 Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg
 290 295 300
 Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro
 305 310 315 320
 Phe Leu Leu

<210> 1273

<211> 311

<212> PRT

<213> Unknown (H38g190 protein)

<220>

<223> Synthetic construct

<400> 1273

```

Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly
 1          5          10          15
Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu
          20          25          30
Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile
          35          40          45
Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr
          50          55          60
His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys
65          70          75          80
Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys
          85          90          95
Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe
          100          105          110
Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro
          115          120          125
Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val
          130          135          140
Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val
145          150          155          160
Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe
          165          170          175
Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr
          180          185          190
Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val
          195          200          205
Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile
          210          215          220
Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys
225          230          235          240
Ala Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile Phe
          245          250          255
Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln Val
          260          265          270
Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Leu Ile Arg Val Met
          290          295          300
Gln Arg Arg Gln Asp Ser Arg
305          310

```

<210> 1274

<211> 305

<212> PRT

<213> Unknown (H38g191 protein)

<220>

<223> Synthetic construct

<400> 1274

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Glu Leu
 1          5          10          15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
          20          25          30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
          35          40          45

```

His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu
 50 55 60
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser
 65 70 75 80
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
 85 90 95
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
 100 105 110
 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile
 115 120 125
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Thr Trp Gly Ile
 130 135 140
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Leu
 145 150 155 160
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
 165 170 175
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
 180 185 190
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile
 195 200 205
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp
 210 215 220
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
 225 230 235 240
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
 245 250 255
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
 260 265 270
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
 275 280 285
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
 290 295 300
 Phe
 305

<210> 1275

<211> 312

<212> PRT

<213> Unknown (H38g192 protein)

<220>

<223> Synthetic construct

<400> 1275

Met Glu Arg Val Asn Glu Thr Val Val Arg Glu Val Ile Phe Leu Gly
 1 5 10 15
 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu
 20 25 30
 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ile Ser Thr
 35 40 45
 Ile Val Leu Asp Arg Ala Leu His Ile Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Ile Ile Val Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly
 85 90 95
 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Leu Gly Cys Ser His Ser
 100 105 110
 Phe Leu Leu Ala Val Met Gly Tyr Asp Arg Tyr Ile Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu

```

      130              135              140
Val Ala Ala Ala Cys Ala Cys Gly Phe Thr Val Ala Gln Ile Ile Thr
145              150              155              160
Ser Leu Val Phe His Leu Pro Phe Tyr Ser Ser Asn Gln Leu His His
      165              170              175
Phe Phe Cys Asp Ile Ala Pro Val Leu Lys Leu Ala Ser His His Asn
      180              185              190
His Phe Ser Gln Ile Val Ile Phe Met Leu Cys Thr Leu Val Leu Ala
      195              200              205
Ile Pro Leu Leu Leu Ile Leu Val Ser Tyr Val His Ile Leu Ser Ala
      210              215              220
Ile Leu Gln Phe Pro Ser Thr Leu Gly Arg Cys Lys Ala Phe Ser Thr
225              230              235              240
Cys Val Ser His Leu Ile Ile Val Thr Val His Tyr Gly Cys Ala Ser
      245              250              255
Phe Ile Tyr Leu Arg Pro Gln Ser Asn Tyr Ser Ser Ser Gln Asp Ala
      260              265              270
Leu Ile Ser Val Ser Tyr Thr Ile Ile Thr Pro Leu Phe Asn Pro Met
      275              280              285
Ile Tyr Ser Leu Arg Asn Lys Glu Phe Lys Ser Ala Leu Cys Lys Ile
      290              295              300
Val Arg Arg Thr Ile Ser Leu Leu
305              310

```

<210> 1276

<211> 244

<212> PRT

<213> Unknown (H38g193 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(244)

<223> Xaa = Any Amino Acid

<400> 1276

```

Met Met Ile Ser Ser Asp Glu Glu Asn Asp Thr Asn Met Met Glu Phe
 1              5              10              15
Ile Leu Val Gly Leu Ser Arg Gln Pro Ala Ser Gln Leu Leu Phe Phe
      20              25              30
Xaa Ala Ile Leu Phe Ile Tyr Ser Val Thr Leu Val Gly Asn Ile Leu
      35              40              45
Ile Ile Val Ile Ile Gln Ile Asp Ser His Leu Gln Thr Pro Met Tyr
      50              55              60
Phe Phe Leu Ile Gln Val Ser Phe Leu Asp Ile Cys Ser Thr Pro Thr
65              70              75              80
Val Leu Val Asn Cys Xaa Lys Asp Phe Pro Ser Val Ser Tyr Ser Gly
      85              90              95
Cys Leu Phe Xaa Met Thr Ile Phe Leu Tyr Leu Gly Val Thr Glu Cys
      100              105              110
Val Phe Phe Leu Phe Cys Phe Glu Cys Phe Leu Ile Ala Val Met Ala
      115              120              125
Tyr Asp Arg Phe Val Ala Ile Ser Lys Pro Leu Cys Tyr Pro Phe Ile
      130              135              140
Ile Asn Ser Asn Val Cys Ile Trp Met Val Ala Gly Val Trp Ala His
145              150              155              160
Pro Gly Arg Thr Asn Pro Ile Leu Trp Pro Gln Cys Ser Gln His Phe
      165              170              175
Thr Cys Glu Leu Gln Val Ile Phe Lys Leu Thr Cys Ser Pro Val Leu
      180              185              190

```

Val Lys Glu Ile Gln Xaa Phe Met Ile Pro Gly Cys Thr Leu Xaa Ala
 195 200 205
 Leu Tyr Gln His Xaa Val Cys Ser Tyr Ser Xaa Ala Arg Gln Gln Thr
 210 215 220
 His Pro Arg Ser Xaa Glu Ala Tyr Asn Xaa Gly Ile Arg Xaa Gly Ile
 225 230 235 240
 Ile Gly Val His

<210> 1277

<211> 306

<212> PRT

<213> Unknown (H38g194 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(306)

<223> Xaa = Any Amino Acid

<400> 1277

Thr Ala Gly Ser Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly
 1 5 10 15
 Tyr Ala Asn His Pro Glu Leu Gln Val Ser Phe Phe Leu Met Phe Leu
 20 25 30
 Phe Ile Tyr Leu Phe Thr Ile Leu Gly Asn Leu Gly Leu Ile Met Leu
 35 40 45
 Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Val Thr Pro Lys
 65 70 75 80
 Thr Leu Ala Asn Phe Gln Ser Asn Gln Arg Ser Ile Ser Phe Val Gly
 85 90 95
 Cys Phe Val Gln Met Tyr Phe Ser Val Gly Leu Val Cys Thr Glu Cys
 100 105 110
 Phe Leu Leu Gly Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Trp Asn
 115 120 125
 Pro Tyr Ser Val Val Ile Ser Xaa Lys Ala Cys Asn Trp Leu Gly Val
 130 135 140
 Met Ser Tyr Thr Ile Gly Phe Thr Asn Ser Leu Val Ser Val Trp Val
 145 150 155 160
 Ile Ser Gly Leu Phe Cys Asp Ser Ser Ile Asn Phe Phe Phe Cys Asp
 165 170 175
 Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Ala Phe Ser Thr Glu
 180 185 190
 Met Val Ser Phe Ala Leu Ala Gly Phe Thr Leu Leu Gly Ser Ile Leu
 195 200 205
 Ile Ile Thr Val Thr Tyr Ile Ala Ile Thr Ser Ala Ile Leu Lys Asn
 210 215 220
 Gln Trp Ala Ala Gly Trp Gln Lys Ala Phe Ser Thr Cys Ala Phe His
 225 230 235 240
 Leu Met Ala Leu Thr Ile Phe Tyr Gly Ser Leu Ile Phe Thr Tyr Leu
 245 250 255
 Gln Leu Asp Lys Thr Ser Ser Leu Ile His Ala Gln Leu Ala Phe Val
 260 265 270
 Phe Tyr Met Thr Val Ile Pro Met Leu Asn Pro Leu Ile Xaa Ser Leu
 275 280 285
 Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Val Ile His Arg Lys
 290 295 300
 Leu Phe

305

<210> 1278

<211> 251

<212> PRT

<213> Unknown (H38g195 protein)

<220>

<223> Synthetic construct

<400> 1278

```

Met Ala Asn Ser Ser Ser Val Thr Glu Phe Leu Val Leu Gly Phe Ser
 1           5           10           15
Ser Leu Gly Glu Leu Gln Leu Val Leu Phe Ala Val Phe Leu Cys Leu
           20           25           30
Tyr Leu Ile Ile Leu Ser Gly Asn Ile Ile Ile Ser Val Ile His
           35           40           45
Leu Asp His Ser Leu His Thr Pro Met Tyr Phe Phe Leu Gly Ile Leu
 50           55           60
Ser Ile Ser Glu Ile Phe Tyr Thr Thr Val Ile Leu Pro Lys Met Leu
 65           70           75           80
Ile Asn Leu Phe Ser Val Phe Arg Thr Leu Ser Phe Val Ser Cys Ala
           85           90           95
Thr Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn Cys Leu Leu
           100          105          110
Leu Gly Val Met Gly Tyr Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu
           115          120          125
Gln Tyr Ala Val Leu Met Ser Trp Arg Val Cys Gly Gln Leu Ile Ala
 130          135          140
Thr Cys Ile Ile Ser Gly Phe Leu Ile Ser Leu Val Gly Thr Thr Phe
 145          150          155          160
Val Phe Ser Leu Pro Phe Cys Gly Ser Asn Lys Val Asn His Tyr Phe
           165          170          175
Cys Asp Ile Ser Pro Val Ile Arg Leu Ala Cys Ala Asp Ser Tyr Ile
           180          185          190
Ser Glu Leu Val Ile Phe Ile Phe Gly Val Leu Val Leu Val Val Pro
           195          200          205
Leu Ile Phe Ile Cys Ile Ser Tyr Gly Phe Ile Val Arg Thr Ile Leu
 210          215          220
Lys Ile Pro Ser Ala Glu Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala
 225          230          235          240
Ser His Leu Ile Val Val Ile Val His Tyr Gly
           245          250

```

<210> 1279

<211> 315

<212> PRT

<213> Unknown (H38g196 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1279

```

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1           5           10           15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
           20           25           30

```

Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
 35 40 45
 Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe
 50 55 60
 Phe Phe Leu Ser Thr Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser
 65 70 75 80
 Trp Glu Leu Xaa Val Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile
 85 90 95
 Ser Tyr Asn Ser Cys Ser Val Gln Met Ile Thr His Leu Phe Leu Gly
 100 105 110
 Thr Ala Gln Cys Leu Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val
 115 120 125
 Glu Ile Ser Tyr Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val
 130 135 140
 Cys Ile Gln Leu Ala Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala
 145 150 155 160
 Val Thr Leu Ile Ile Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val
 165 170 175
 Ile Asn His Phe Thr Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys
 180 185 190
 Ser Asp Thr Leu Val Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe
 195 200 205
 Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile
 210 215 220
 Phe Val Arg Ala Val Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Gly Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met
 245 250 255
 Tyr Leu Lys Pro Gln Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val
 260 265 270
 Ser Lys Leu Tyr Gly Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr
 275 280 285
 Ile Gln Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys
 290 295 300
 Gly Asn Glu Lys Ser Xaa Gln Phe Ser Leu Asn
 305 310 315

<210> 1280

<211> 319

<212> PRT

<213> Unknown (H38g197 protein)

<220>

<223> Synthetic construct

<400> 1280

Met Asn His Val Val Lys His Asn His Thr Ala Val Thr Lys Val Thr
 1 5 10 15
 Glu Phe Ile Leu Met Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro
 20 25 30
 Leu Phe Gly Leu Phe Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn
 35 40 45
 Leu Gly Met Val Ile Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Arg His Leu Ser Ile Thr Asp Leu Gly Tyr Ser
 65 70 75 80
 Thr Val Ile Ala Pro Lys Met Leu Val Asn Phe Ile Val His Lys Asn
 85 90 95
 Thr Ile Ser Tyr Asn Trp Tyr Ala Thr Gln Leu Ala Phe Phe Glu Ile
 100 105 110
 Phe Ile Ile Ser Glu Leu Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg

```

      115              120              125
Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Val Ile Ile Met Ala Glu
 130              135              140
Lys Val Leu Trp Val Leu Val Ile Val Pro Tyr Leu Tyr Ser Thr Phe
 145              150              155              160
Val Ser Leu Phe Leu Thr Ile Lys Leu Phe Lys Leu Ser Phe Cys Gly
      165              170              175
Ser Asn Ile Ile Ser Tyr Phe Tyr Cys Asp Cys Ile Pro Leu Met Ser
      180              185              190
Ile Leu Cys Ser Asp Thr Asn Glu Leu Glu Leu Ile Ile Leu Ile Phe
      195              200              205
Ser Gly Cys Asn Leu Leu Phe Ser Leu Ser Ile Val Leu Ile Ser Tyr
 210              215              220
Met Phe Ile Leu Val Ala Ile Leu Arg Met Asn Ser Arg Lys Gly Arg
 225              230              235              240
Tyr Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Met
      245              250              255
Phe Tyr Gly Thr Leu Leu Phe Ile Tyr Leu Gln Pro Lys Ser Ser His
      260              265              270
Thr Leu Ala Ile Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Leu Ile
      275              280              285
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
 290              295              300
Asp Ala Leu Lys Arg Thr Leu Thr Asn Arg Phe Lys Ile Pro Ile
 305              310              315

```

<210> 1281

<211> 157

<212> PRT

<213> Unknown (H38g198 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1281

```

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
 1      5      10      15
Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
      20      25      30
Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
      35      40      45
Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
      50      55      60
Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu
 65      70      75      80
Cys Thr Cys Leu Asp Thr Phe Thr Lys Ser Tyr Ile Thr Xaa Ile Arg
      85      90      95
Gly Leu Lys Gly Phe Asn His Leu Cys Phe Leu Leu His Tyr Cys His
      100      105      110
Cys Ala Arg Ala Gln Val Ser Xaa Asn Ala Pro Trp Ser Leu Ala Gln
      115      120      125
Arg Cys Gln Pro Asn Met Leu Ile Arg Xaa Leu Phe Cys Leu Lys Leu
      130      135      140
Val Val His Asp Arg Leu Xaa His Val Leu Ser Leu Leu
 145      150      155

```

<210> 1282

<211> 317
 <212> PRT
 <213> Unknown (H38g199 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(317)
 <223> Xaa = Any Amino Acid

<400> 1282

```

Met Gly Gln Lys Asn Leu Thr Val Leu Thr Glu Leu Ile Leu Met Glu
 1      5      10      15
Ile Thr Arg Arg Leu Glu Leu Gln Leu Ser Leu Phe Trp Val Phe Leu
 20      25      30
Ile Ile Cys Thr Phe Thr Val Val Ser Lys Glu Cys Ile Ile Ile Leu
 35      40      45
Asn Asn Val Asp Leu Gly Leu Gln Thr Phe Val Tyr Phe Leu Ile Arg
 50      55      60
Tyr Leu Asn Phe Ile Asn Leu Gly Asn Ser Met Val Ile Tyr Pro Lys
 65      70      75      80
Ile Leu Val Asn Phe Val Val Ala Gln Asn Ala Ile Pro Cys Tyr Ala
 85      90      95
Cys Thr Met Gln Met Ala Phe Phe Ile Met Phe Ile Ile Cys Glu Leu
100      105      110
Phe Val Ser Ser Ala Met Ala Tyr Asp His Tyr Val Asp Ile His Ser
115      120      125
Leu Leu Pro Xaa Asn Val Met Ser Gln Glu Leu Cys His Val Leu Val
130      135      140
Ala Ile Pro Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Val Thr Ile
145      150      155      160
Lys Ile Phe Ile Leu Ala Phe Tyr Gly Ser Asn Val Ile Ser Tyr Phe
165      170      175
Tyr Cys Xaa Asp Val Ser Leu Leu Ala Met Val Asp Ser Asn Ala Xaa
180      185      190
Gly Ile Glu Met Leu Ile Thr Leu Phe Ser Val Leu Asn Leu Ile Phe
195      200      205
Phe Leu Leu Val Val Leu Met Ser Ser Met Leu Ile Leu Leu Thr Val
210      215      220
Cys Xaa Met His Ser Ala Gly Glu Gln Xaa Lys Thr Phe Phe Thr Tyr
225      230      235      240
Val Ser Cys Leu Ile Val Val Val Val Phe Cys Gly Phe Leu Tyr Phe
245      250      255
Met Tyr Leu Gln Leu Lys Phe Ser Ser Phe Phe Phe Asp Asn Asn Lys
260      265      270
Met Thr Ser Met Phe Ser Ser Leu Val Ile Thr Met Leu Tyr His Leu
275      280      285
Val Cys Ser Val Lys Asn Lys Gly Ser Lys Lys Asn Ala Phe Tyr Ser
290      295      300
Phe Phe Met Lys Gln Xaa Lys Leu Cys Asn Leu Met Val
305      310      315

```

<210> 1283
 <211> 302
 <212> PRT
 <213> Unknown (H38g200 protein)

<220>
 <223> Synthetic construct

<400> 1283

```

Met Thr Asn Leu Asn Ala Ser Gln Ala Asn His Arg Asn Phe Ile Leu
 1           5           10           15
Thr Gly Ile Pro Gly Thr Pro Asp Lys Asn Pro Trp Leu Ala Phe Pro
          20           25           30
Leu Gly Phe Leu Tyr Thr Leu Thr Leu Gly Asn Gly Thr Ile Leu
 35           40           45
Ala Val Ile Lys Val Glu Pro Ser Leu His Glu Pro Thr Tyr Tyr Phe
 50           55           60
Leu Ser Ile Leu Ala Leu Thr Asp Val Ser Leu Ser Met Ser Thr Leu
 65           70           75           80
Pro Ser Met Leu Ser Ile Tyr Trp Phe Asn Ala Pro Gln Ile Val Phe
          85           90           95
Asp Ala Cys Ile Met Gln Met Phe Phe Ile His Val Phe Gly Ile Val
          100          105          110
Glu Ser Gly Val Leu Val Ser Met Ala Phe Asp Arg Phe Val Ala Ile
          115          120          125
Arg Asn Pro Leu His Tyr Val Ser Ile Leu Thr His Asp Val Ile Arg
          130          135          140
Lys Thr Gly Ile Ser Val Leu Thr Arg Ala Val Cys Val Val Phe Pro
          145          150          155          160
Val Pro Phe Leu Ile Lys Cys Leu Pro Phe Cys His Ser Asn Val Leu
          165          170          175
Ser His Ser Tyr Cys Leu His Gln Asn Met Met Arg Leu Ala Cys Ala
          180          185          190
Ser Thr Arg Ile Asn Ser Leu Tyr Gly Leu Ile Val Val Ile Phe Thr
          195          200          205
Leu Gly Leu Asp Val Leu Leu Thr Leu Leu Ser Tyr Val Leu Thr Leu
          210          215          220
Lys Thr Val Leu Gly Ile Val Ser Arg Gly Glu Arg Leu Lys Thr Leu
          225          230          235          240
Ser Thr Cys Leu Ser His Met Ser Thr Val Leu Leu Phe Tyr Val Pro
          245          250          255
Phe Met Gly Ala Ala Ser Met Ile His Arg Phe Trp Glu His Leu Ser
          260          265          270
Pro Val Val His Met Val Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro
          275          280          285
Val Leu Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
          290          295          300

```

<210> 1284

<211> 324

<212> PRT

<213> Unknown (H38g201 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1284

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Pro Ala Val Ser Ser Asp Ser His Leu His Thr Pro Thr Tyr Phe
          50           55           60

```

```

Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65          70          75          80
Val Pro Lys Met Ile Val Asp Met Gln Trp Tyr Ser Arg Val Ile Ser
          85          90          95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
          100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
          115          120          125
Ile Tyr Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
          145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Ser
          180          185          190
Tyr Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
          195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Ser Ser Tyr Tyr Lys Ile
          210          215          220
Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Thr
          225          230          235          240
Phe Ser Thr Tyr Gly Ser His Leu Ala Phe Val Cys Xaa Phe Tyr Gly
          245          250          255
Thr Gly Ile Asp Met Tyr Leu Ala Ser Ala Met Ser Pro Thr Pro Arg
          260          265          270
Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
          275          280          285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
          290          295          300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
          305          310          315          320
Phe Phe Trp Cys

```

<210> 1285

<211> 144

<212> PRT

<213> Unknown (H38g202 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(144)

<223> Xaa = Any Amino Acid

<400> 1285

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Phe Ser Val Thr Gly Ile Ser Val Val Asp Cys Cys Phe Xaa Ser Thr
1          5          10          15
Val Ile Pro Glu Met Leu Phe Ser Cys Gln Val Gln His Leu Val His
          20          25          30
Asn Pro Lys Gly Ile Leu Leu Leu Leu Leu Leu Leu Leu Leu
          35          40          45
Leu Leu Thr Phe Phe Xaa Lys Ile Ser Phe His Arg Met His Phe Cys
          50          55          60
Ile Arg Asp Ser Ser Ser Gly Lys Ile Thr Val Tyr Tyr Leu Xaa Phe
          65          70          75          80
Tyr Ile Cys Gly Gln Ile Val Leu Glu Gln Val Lys His Ile Xaa Glu
          85          90          95
Xaa Ser Leu Ser Leu Glu Phe Val Ile Phe Xaa Tyr Phe Tyr Lys Gly

```

	100		105		110										
Asp	Leu	Ala	Leu	Lys	Gln	Asn	Phe	Ala	Ile	Leu	Arg	Ser	Ile	Pro	Ser
	115		120		125										
Phe	Ser	Xaa	Asp	Leu	Glu	Ile	His	Asn	Val	Arg	Tyr	Gln	His	Phe	
	130		135		140										

<210> 1286

<211> 314

<212> PRT

<213> Unknown (H38g203 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1286

Thr	His	Gly	Tyr	Thr	Phe	Ser	Leu	Arg	Leu	Phe	Leu	His	Cys	Leu	Thr
1				5					10					15	
Tyr	Val	Xaa	Val	Ser	His	Cys	Leu	Leu	Ile	Trp	Leu	Ile	Thr	Phe	Ser
			20					25					30		
Pro	Phe	Asn	Leu	Leu	Phe	Lys	Xaa	Asn	Leu	Xaa	Phe	Thr	Ile	Xaa	Leu
		35					40					45			
Ile	Thr	Xaa	Ile	Glu	Ser	Arg	Tyr	Ser	Lys	His	Trp	Pro	Phe	Phe	Leu
	50				55					60					
Leu	Xaa	Cys	Phe	Cys	Asn	Val	Leu	Phe	His	Leu	Asp	Cys	Asp	Ser	Pro
65				70					75					80	
Val	Cys	Asn	Thr	Lys	Arg	Ile	Arg	Ser	Phe	Phe	Val	Leu	Glu	Arg	Xaa
			85					90					95		
Lys	Ser	Ser	Xaa	Lys	Ser	Glu	Lys	Ile	His	Phe	Xaa	Thr	Arg	Asn	Lys
			100					105					110		
Val	Ser	Cys	Phe	Xaa	Asp	Phe	Gly	Ile	Lys	Tyr	Thr	Val	Tyr	Leu	Leu
		115					120					125			
Leu	Leu	Lys	His	Phe	Leu	Leu	Ile	His	Ser	Ile	Leu	Arg	Tyr	Leu	Xaa
	130					135					140				
Val	Ala	Gly	Tyr	Gly	Thr	Ser	Xaa	Phe	Leu	Ser	Arg	Ile	Ser	Ser	Ile
145					150					155				160	
Thr	Leu	Lys	Thr	Ile	Ile	Cys	Ile	Leu	Lys	Lys	Ser	Tyr	His	Phe	Phe
			165					170					175		
Ser	Val	Gln	Tyr	Thr	Ile	Ser	Tyr	Ile	Asp	Pro	Phe	Ile	Asn	Ser	Leu
		180						185				190			
Val	Met	Phe	Val	Val	Phe	Thr	Ala	Phe	Ile	Gln	Ala	Phe	Ala	Phe	Met
	195					200					205				
Ile	Ile	Ile	Val	Ser	Tyr	Thr	Gln	Val	Leu	Phe	Ala	Leu	Leu	Lys	Lys
	210					215				220					
Asn	Ser	Glu	Lys	Gly	Arg	Ser	Lys	Ser	Phe	Leu	Met	Cys	Ser	Ala	His
225					230					235				240	
Leu	Leu	Ser	Val	Ser	Leu	Phe	Tyr	Ser	Ser	Val	Phe	Phe	Met	Tyr	Gly
			245					250					255		
Cys	Pro	Arg	Ser	Gly	Pro	Asp	Xaa	Gln	Trp	Asn	Glu	Met	Tyr	Phe	Pro
			260					265					270		
Phe	Tyr	Met	Ile	Ile	Ile	Pro	Leu	Gln	Thr	Pro	Phe	Ile	Tyr	Ser	Met
	275					280					285				
Lys	Asn	Lys	Glu	Val	Leu	Gly	Thr	Leu	Arg	Thr	Met	Ile	Lys	Lys	Tyr
	290					295					300				
Phe	Trp	Arg	Thr	Leu	Ser	Xaa	Phe	Phe	Pro						
305					310										

<210> 1287

<211> 253
 <212> PRT
 <213> Unknown (H38g204 protein)

<220>
 <223> Synthetic construct

<400> 1287
 Met Cys Leu Phe Leu Cys His Leu Ser Phe Leu Asp Met Thr Ile Ser
 1 5 10 15
 Cys Ala Ile Val Pro Lys Met Leu Ala Gly Phe Leu Leu Gly Ser Arg
 20 25 30
 Ile Ile Ser Phe Gly Gly Cys Val Ile Gln Leu Phe Ser Phe His Phe
 35 40 45
 Leu Gly Cys Thr Glu Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg
 50 55 60
 Phe Leu Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Thr His
 65 70 75 80
 Arg Val Cys Asn Ser Leu Ala Leu Gly Thr Trp Leu Gly Gly Thr Ile
 85 90 95
 His Ser Leu Phe Gln Thr Ser Phe Val Phe Arg Leu Pro Phe Cys Gly
 100 105 110
 Pro Asn Arg Val Asp Tyr Ile Phe Cys Asp Ile Pro Ala Met Leu Arg
 115 120 125
 Leu Ala Cys Ala Asp Thr Ala Ile Asn Glu Leu Val Thr Phe Ala Asp
 130 135 140
 Ile Gly Phe Leu Ala Leu Thr Cys Phe Met Leu Ile Leu Thr Ser Tyr
 145 150 155 160
 Gly Tyr Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Asp Gly Arg
 165 170 175
 Arg Asn Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ile Val
 180 185 190
 Tyr Tyr Val Pro Cys Thr Phe Ile Tyr Leu Arg Pro Cys Ser Gln Glu
 195 200 205
 Pro Leu Asp Gly Val Val Ala Val Phe Tyr Thr Val Ile Thr Pro Leu
 210 215 220
 Leu Asn Ser Ile Ile Tyr Thr Leu Cys Asn Lys Glu Met Lys Ala Ala
 225 230 235 240
 Leu Gln Arg Leu Gly Gly His Lys Glu Val Gln Pro His
 245 250

<210> 1288
 <211> 311
 <212> PRT
 <213> Unknown (H38g205 protein)

<220>
 <223> Synthetic construct

<400> 1288
 Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly
 1 5 10 15
 Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe
 20 25 30
 Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu
 35 40 45
 Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln
 65 70 75 80
 Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly

```
<210> 1289
<211> 311
<212> PRT
<213> Unknown (H38g206 protein)
```

<220>
<223> Synthetic construct

<400> 1289																
Met	Lys	Ile	Lys	Asn	His	Thr	Pro	Val	Thr	Glu	Val	Pro	Leu	Met	Gly	
1				5					10					15		
Ile	Pro	His	Thr	Lys	Gly	Met	Glu	Asn	Val	Leu	Phe	Val	Leu	Phe	Leu	
			20					25					30			
Ala	Phe	Tyr	Leu	Phe	Thr	Leu	Leu	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Ala	
		35					40					45				
Val	Leu	Thr	Phe	Ser	Asn	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly	
	50					55					60					
Asn	Leu	Ser	Val	Phe	Asp	Ile	Phe	Phe	Pro	Ser	Val	Ser	Ser	Pro	Lys	
65					70					75					80	
Met	Met	Leu	Cys	Leu	Val	Gly	Gln	Ser	Cys	Thr	Ile	Ser	Phe	Gln	Gly	
			85						90					95		
Cys	Ala	Ser	Gln	Leu	Phe	Phe	His	His	Phe	Leu	Gly	Cys	Thr	Glu	Cys	
			100					105					110			
Phe	Leu	Tyr	Thr	Val	Met	Ala	Tyr	Asp	Arg	Phe	Ala	Ala	Ile	Cys	His	
		115					120					125				
Pro	Leu	Pro	Tyr	Thr	Val	Ile	Met	Lys	Arg	Arg	Val	Cys	Ala	Leu	Leu	
		130				135					140					
Thr	Leu	Gly	Thr	Trp	Thr	Gly	Ser	Cys	Leu	His	Ala	Ser	Val	Leu	Thr	
145					150					155					160	
Leu	Leu	Ile	Phe	Lys	Leu	Ser	Tyr	Cys	Gly	Pro	Asn	Glu	Val	Asp	Asn	
				165					170					175		

Phe Phe Cys Asp Ile Pro Val Val Leu Pro Leu Ala Cys Ala Asp Thr
 180 185 190
 Ser Leu Ala Arg Thr Val Ser Phe Ile Asn Val Gly Val Val Ala Leu
 195 200 205
 Met Cys Phe Leu Leu Ile Leu Thr Ser Tyr Ala Cys Ile Val Ile Ser
 210 215 220
 Ile Leu Lys Ile Ser Ser Ser Glu Gly Arg Arg Arg Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Ser Ile Leu Leu Phe Tyr Gly Pro Ile Val
 245 250 255
 Leu Ile Tyr Leu Arg Pro Ala Ser Ser Pro Trp Leu Asp Ser Val Val
 260 265 270
 Gln Val Leu Asn Asn Ile Val Ile Pro Ser Leu Asn Pro Leu Ile Tyr
 275 280 285
 Thr Leu Arg Asn Lys Gly Val Lys Leu Ala Leu Arg Lys Val Leu Ile
 290 295 300
 Gln Gly Val His Asn Cys Gly
 305 310

<210> 1290

<211> 298

<212> PRT

<213> Unknown (H38g207 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(298)

<223> Xaa = Any Amino Acid

<400> 1290

Val Arg Gly Ser Lys Gln Leu Arg Asn Gly Thr Leu Val Ser Gln Phe
 1 5 10 15
 Leu Leu Lys Gly Leu Arg Asp Ser Lys Ala Trp Arg Pro Leu Leu Phe
 20 25 30
 Thr Thr Phe Leu Leu Ile Tyr Ile Val Val Val Val Gly Ser His Met
 35 40 45
 Phe Thr Val Asp Tyr Arg Arg His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Gly His Ser Leu Met Asp Ala Ala Cys Ile Ser Asn Met Val Thr Gln
 65 70 75 80
 Val Leu Val His Leu Leu Ala Pro Val Gly Pro Val Leu Tyr Cys Ala
 85 90 95
 Cys Leu Ile Gln Ile Cys Phe Leu His Phe Leu Ala Pro Xaa Glu Ser
 100 105 110
 Phe Leu Leu Thr Ala Val Ala Tyr Asp Ser Met Leu Ala Ile Cys Gln
 115 120 125
 Pro Leu His Tyr Phe Val Leu Val Gly Arg Leu Thr His Thr Gly Leu
 130 135 140
 Thr Ser Ile Ser Cys Leu Leu Ala Leu Ala Asn Ala Phe Thr Tyr Ser
 145 150 155 160
 Ile Leu Thr Ala Leu Pro Lys Phe Cys Arg Pro Cys Leu Ile Thr His
 165 170 175
 Phe Phe Cys Asp Leu Pro Ser Leu Leu Arg Leu Ser Cys Phe Ser Thr
 180 185 190
 Arg Thr Asn Glu Leu Ala Leu Phe Phe Ser Phe Leu Val Ala Leu Ala
 195 200 205
 His Cys Val Leu Val Val Val Ser Tyr Gly His Val Val Ala Ala Val
 210 215 220
 Gln Ile His Ser Thr Gln Gly Xaa Arg Lys Ala Phe Ser Thr Cys Val

225					230					235					240	
Ala	His	Leu	Ala	Met	Ile	Gly	Leu	Phe	Tyr	Val	Thr	Ser	Val	Pro	Cys	
				245					250					255		
Tyr	Ile	Leu	Pro	Asn	Ser	Ala	Tyr	Ser	Gly	Leu	Gly	Asp	Trp	Val	Leu	
				260					265					270		
Ser	Val	Leu	Cys	Val	Val	Leu	Thr	His	Met	Leu	Asn	Pro	Ile	Phe	Pro	
				275					280					285		
Ser	Met	Leu	Gly	Xaa	Gln	Cys	Met	Ser	His							
				290					295							

<210> 1291

<211> 312

<212> PRT

<213> Unknown (H38g208 protein)

<220>

<223> Synthetic construct

<400> 1291

[illegible]

<210> 1292

<211> 251
 <212> PRT
 <213> Unknown (H38g209 protein)

<220>
 <223> Synthetic construct

<400> 1292
 Met Tyr Tyr Phe Leu Ser His Leu Ala Phe Val Asp Leu Cys Tyr Ser
 1 5 10 15
 Ser Ala Ile Thr Pro Lys Met Met Val Asn Phe Val Val Glu Arg Asn
 20 25 30
 Thr Ile Pro Phe His Ala Cys Ala Thr Gln Leu Gly Cys Phe Leu Thr
 35 40 45
 Phe Met Ile Thr Glu Cys Phe Leu Leu Ala Ser Met Ala Tyr Asp Cys
 50 55 60
 Tyr Val Ala Ile Cys Ser Pro Leu His Tyr Ser Thr Leu Met Ser Arg
 65 70 75 80
 Arg Val Cys Ile Gln Leu Val Ala Val Pro Tyr Ile Tyr Ser Phe Leu
 85 90 95
 Val Ala Leu Phe His Thr Val Ile Thr Phe Arg Leu Thr Tyr Cys Gly
 100 105 110
 Pro Asn Leu Ile Asn His Phe Tyr Cys Asp Asp Leu Pro Phe Leu Ala
 115 120 125
 Leu Ser Cys Ser Asp Thr His Met Lys Glu Ile Leu Ile Phe Ala Phe
 130 135 140
 Ala Gly Phe Asp Met Ile Ser Ser Ser Ser Ile Val Leu Thr Ser Tyr
 145 150 155 160
 Ile Phe Ile Ile Ala Ala Ile Leu Arg Ile Arg Ser Thr Gln Gly Gln
 165 170 175
 His Lys Ala Ile Ser Thr Cys Gly Ser His Met Val Thr Val Thr Ile
 180 185 190
 Phe Tyr Gly Thr Leu Ile Phe Met Tyr Leu Gln Pro Lys Ser Asn His
 195 200 205
 Ser Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile
 210 215 220
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
 225 230 235 240
 Asp Ala Ser Lys Lys Ala Leu Asp Lys Gly Cys
 245 250

<210> 1293
 <211> 311
 <212> PRT
 <213> Unknown (H38g210 protein)

<220>
 <223> Synthetic construct

<400> 1293
 Met Ser Asn Ala Thr Leu Leu Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1 5 10 15
 His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
 20 25 30
 Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
 35 40 45
 Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
 50 55 60
 Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
 65 70 75 80
 Met Thr Leu Val Ser Pro Ser Gly Arg Thr Ile Ser Phe His Ser Cys


```

<400> 1294
His Ser Ser Leu Leu Phe Ala Val Phe Leu Leu Thr Tyr Ser Val Thr
 1          5          10          15
Leu Val Gly Asn Leu Gly Met Thr Asp Leu Ile Cys Gln Ser Arg Thr
 20          25          30
Ser Ser Ala Leu His Thr Pro Met Cys Phe Leu Leu Ser Val Phe Ser
 35          40          45
Phe Leu Asp Ile Cys Ser Ser Ser Ile Val His Pro Arg Leu Leu Ile
 50          55          60
His Phe Leu Thr Thr Arg Pro Ser Ile Ser Phe Ala Gly Gly Ile Ile
 65          70          75          80
Gln Met Ala Leu Met Thr Phe Tyr Gly Thr Gly Glu Cys Leu Leu Leu
 85          90          95
Ala Ile Val Ala Tyr Asp Xaa Val Val Ala Ile Cys His Pro Phe Pro
 100          105          110
Xaa His Ile Ile Met Ser Lys Gly Leu Cys Ala Gln Leu Val Val Val
 115          120          125
Thr Ser Ala Val Gly Val Leu Ile Ser Ala His Arg Gln Asp Ala Phe
 130          135          140

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Ile Ser Pro Tyr Arg Gly Leu Asn Ile Ile Asp His Tyr Tyr Cys Ser
145          150          155          160
Val Thr Phe Pro Thr Pro Met Leu Gln Leu Ala Cys Ser Asp Ala Thr
          165          170          175
Val Ala Asn Met Ile Leu Phe Val Ser Ser Ala Leu Ile Thr Ile Pro
          180          185          190
Thr Ile Ser Val Ile Leu Val Ser Tyr Thr Tyr Ile Leu Val Asn Leu
          195          200          205
Val Arg Met Arg Ser Leu Asp Ala Gln Cys Lys Ala Phe Ser Thr Arg
          210          215          220
Ala Ser His Leu Thr Ala His Cys Leu Phe Tyr Gly Phe Val Phe Leu
225          230          235          240
Val Tyr Ile Pro Pro Asn Pro Glu Met Ala Ser Ala Tyr Asn Lys Ile
          245          250          255
Leu Phe Thr Val Val Ile Pro Met Leu Asn Leu Leu Val Xaa Gly Leu
          260          265          270
Arg Asn Lys Asp Val Lys
          275

```

<210> 1295

<211> 312

<212> PRT

<213> Unknown (H38g212 protein)

<220>

<223> Synthetic construct

<400> 1295

```

Ser Val Ala Lys Gly Asn His Ser Thr Val Tyr Glu Phe Ile Leu Leu
1      5      10      15
Gly Leu Thr Asp Asn Ala Glu Leu Gln Val Thr Leu Phe Gly Ile Phe
          20      25      30
Leu Val Val Tyr Leu Ala Ser Phe Met Gly Asn Phe Gly Leu Ile Met
          35      40      45
Leu Ile Gln Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu
          50      55      60
Ser His Leu Ala Phe Val Asp Phe Ser Phe Thr Ser Ser Val Ala Pro
65      70      75      80
Asn Thr Leu Val Asn Phe Leu Cys Glu Val Lys Ser Ile Thr Phe Tyr
          85      90      95
Ala Cys Ala Ile Gln Val Cys Cys Phe Ile Thr Phe Val Val Cys Glu
          100     105     110
Leu Tyr Leu Leu Ser Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          115     120     125
Asn Pro Leu Leu Tyr Val Ile Leu Ile Pro Arg Lys Cys Ile Lys Leu
130     135     140
Ile Ala Ser Thr Tyr Val Tyr Gly Phe Thr Val Gly Leu Val Gln Thr
145     150     155     160
Val Ala Thr Ser Tyr Leu Ser Phe Cys Asp Ser Asn Val Ile Asn His
          165     170     175
Phe Tyr His Asp Asp Val Pro Leu Val Ala Leu Ala Cys Ser Asp Thr
          180     185     190
His Val Lys Glu Leu Met Leu Leu Ile Ala Gly Phe Asn Thr Leu
          195     200     205
Cys Ser Leu Val Ile Val Leu Ile Ser Tyr Gly Phe Ile Phe Phe Ala
210     215     220
Ile Leu Arg Ile His Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr
225     230     235     240
Ser Ala Ser His Leu Thr Ser Ile Thr Ile Phe Tyr Gly Thr Ile Ile
          245     250     255
Phe Met Tyr Pro Gln Pro Lys Ser Ser His Ser Leu Asn Met Asp Lys

```

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                260                265                270
Val Ala Ser Val Phe Asn Val Val Val Ile Pro Thr Leu Asn Pro Leu
                275                280                285
Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Asn Ala Leu Lys Arg Ile
                290                295                300
Ile Glu Lys Leu Cys Leu Ala Val
305                310

```

<210> 1296
 <211> 232
 <212> PRT
 <213> Unknown (H38g213 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(232)
 <223> Xaa = Any Amino Acid

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<400> 1296
Ser Gly Leu Val Pro Lys Ser Phe Pro Gly Cys Leu Thr Gln Leu Phe
  1                5                10                15
Phe Leu His Tyr Ser Phe Val Leu Asp Ser Ala Ile Leu Leu Ala Met
                20                25                30
Ala Phe Asp Arg Tyr Met Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr
                35                40                45
Ile Leu Thr Pro Lys Thr Ile Val Lys Ile Ala Val Gly Ile Cys Phe
                50                55                60
Arg Ser Phe Cys Val Phe Val Pro Cys Val Phe Leu Val Asn Arg Leu
                65                70                75                80
Pro Phe Cys Arg Thr His Ile Ile Ser His Thr Tyr Cys Glu His Ile
                85                90                95
Gly Val Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Ile Trp Cys
                100                105                110
Gly Phe Cys Val Pro Ile Met Thr Val Met Thr Asp Val Ile Leu Ile
                115                120                125
Ala Val Ser Tyr Thr Leu Ile Leu Cys Ala Val Phe Cys Leu Pro Ser
                130                135                140
Gln Asp Ala Arg Gln Lys Ala Leu Cys Ser Cys Gly Ser His Val Cys
                145                150                155                160
Val Ile Leu Ile Phe Tyr Ile Pro Ala Phe Phe Ser Ile Leu Ala His
                165                170                175
Cys Phe Gly His Asn Val Pro His Thr Phe His Ile Met Phe Ala Asn
                180                185                190
Leu Tyr Val Ile Ile Pro Pro Ala Leu Asn Ser Ile Val Tyr Arg Ile
                195                200                205
Lys Thr Lys Gln Ile Gln Asn Arg Ile Leu Leu Leu Phe Pro Lys Gly
                210                215                220
Ser Gln Xaa Xaa Val Pro Glu Leu
225                230

```

<210> 1297
 <211> 310
 <212> PRT
 <213> Unknown (H38g214 protein)

<220>
 <223> Synthetic construct

<400> 1297

```

Met Ser Asn Ala Ser Leu Leu Thr Ala Phe Ile Leu Met Gly Leu Pro
 1          5          10          15
His Ala Pro Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val
          20          25          30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
          35          40          45
Val Asp Ser His Leu His Thr Thr Met Tyr Tyr Phe Leu Thr Asn Leu
 50          55          60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Leu Leu
 65          70          75          80
Met Thr Leu Val Phe Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
          85          90          95
Met Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Gly Thr Glu Cys Phe
          100          105          110
Leu Tyr Arg Val Met Ser Cys Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
          115          120          125
Leu Arg Tyr Thr Ser Met Met Thr Gly Arg Ser Cys Thr Leu Leu Ala
 130          135          140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Ala Ile
 145          150          155          160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Trp Ile Gln His Tyr
          165          170          175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
          180          185          190
Ala Ile Glu Thr Val Ile Phe Val Thr Val Gly Ile Val Ala Ser Gly
          195          200          205
Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
 210          215          220
Leu Arg Ile Arg Thr Ser Glu Gly Lys His Arg Ala Phe Gln Thr Cys
 225          230          235          240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Gly Pro Gly Leu Phe
          245          250          255
Ile Tyr Leu Arg Pro Gly Ser Arg Lys Ala Val Asp Gly Val Val Ala
          260          265          270
Val Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
          275          280          285
Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Leu Lys Leu Lys Asp Lys
 290          295          300
Val Ala His Ser Gln Ser
305          310

```

<210> 1298

<211> 311

<212> PRT

<213> Unknown (H38g215 protein)

<220>

<223> Synthetic construct

<400> 1298

```

Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
 1          5          10          15
Thr Ser Arg Arg Glu Leu Gln Ile Leu Leu Phe Thr Leu Phe Leu Ala
          20          25          30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Val Leu Ile
          35          40          45
Gln Ala Asn Ala Trp Leu His Met Pro Met Tyr Phe Phe Leu Ser His
 50          55          60
Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Lys Met
 65          70          75          80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Cys

```

```
<210> 1299
<211> 315
<212> PRT
<213> Unknown (H38g216 protein)
```

<220>
<223> Synthetic construct

<400> 1299																
Met	Leu	Leu	Ser	Asn	Ile	Thr	Gln	Phe	Ser	Pro	Ile	Phe	Tyr	Leu	Thr	
1				5					10					15		
Ser	Phe	Pro	Gly	Leu	Glu	Gly	Ile	Lys	His	Trp	Ile	Phe	Ile	Pro	Phe	
			20					25					30			
Phe	Phe	Met	Tyr	Met	Val	Ala	Ile	Ser	Gly	Asn	Cys	Phe	Ile	Leu	Ile	
		35					40					45				
Ile	Ile	Lys	Thr	Asn	Pro	Arg	Leu	His	Thr	Pro	Met	Tyr	Tyr	Leu	Leu	
	50					55					60					
Ser	Leu	Leu	Ala	Leu	Thr	Asp	Leu	Gly	Leu	Cys	Val	Ser	Thr	Leu	Pro	
65					70					75					80	
Thr	Thr	Met	Gly	Ile	Phe	Trp	Phe	Asn	Ser	Gln	Ser	Ile	Tyr	Phe	Gly	
				85					90					95		
Ala	Cys	Gln	Ile	Gln	Met	Phe	Cys	Ile	His	Ser	Phe	Ser	Phe	Met	Glu	
			100					105						110		
Ser	Ser	Val	Leu	Leu	Met	Met	Ser	Phe	Asp	Arg	Phe	Val	Ala	Ile	Cys	
		115					120					125				
His	Pro	Leu	Arg	Tyr	Ser	Val	Ile	Ile	Thr	Gly	Gln	Gln	Val	Val	Arg	
	130					135					140					
Ala	Gly	Leu	Ile	Val	Ile	Phe	Arg	Gly	Pro	Val	Ala	Thr	Ile	Pro	Ile	
145					150					155					160	
Val	Leu	Leu	Leu	Lys	Ala	Phe	Pro	Tyr	Cys	Gly	Ser	Val	Val	Leu	Ser	
				165					170						175	

```

His Ser Phe Cys Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp
      180                      185                      190
Thr Thr Phe Asn Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val
      195                      200                      205
Met Leu Asp Leu Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His
      210                      215                      220
Thr Val Ala Gly Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln
      225                      230                      235                      240
Thr Cys Thr Ala His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met
      245                      250                      255
Met Gly Leu Ser Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala
      260                      265                      270
Ile His Leu Leu Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu
      275                      280                      285
Asn Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile
      290                      295                      300
Ile Lys Leu Leu Gly Leu Lys Lys Ala Ser Lys
      305                      310                      315

```

<210> 1300

<211> 323

<212> PRT

<213> Unknown (H38g217 protein)

<220>

<223> Synthetic construct

<400> 1300

```

Met Asn Pro Glu Asn Trp Thr Gln Val Thr Ser Phe Val Leu Leu Gly
  1                      5                      10                      15
Phe Pro Ser Ser His Leu Ile Gln Phe Leu Val Phe Leu Gly Leu Met
      20                      25                      30
Val Thr Tyr Ile Val Thr Ala Thr Gly Lys Leu Leu Ile Ile Val Leu
      35                      40                      45
Ser Trp Ile Asp Gln Arg Leu His Ile Gln Met Tyr Phe Phe Leu Arg
      50                      55                      60
Asn Phe Ser Phe Leu Glu Leu Leu Leu Val Thr Val Val Val Pro Lys
      65                      70                      75                      80
Met Leu Val Val Ile Leu Thr Gly Asp His Thr Ile Ser Phe Val Ser
      85                      90                      95
Cys Ile Ile Gln Ser Tyr Leu Tyr Phe Phe Leu Gly Thr Thr Asp Phe
      100                      105                      110
Phe Leu Leu Ala Val Met Ser Leu Asp Arg Tyr Leu Ala Ile Cys Arg
      115                      120                      125
Pro Leu Arg Tyr Glu Thr Leu Met Asn Gly His Val Cys Ser Gln Leu
      130                      135                      140
Val Leu Ala Ser Trp Leu Ala Gly Phe Leu Trp Val Leu Cys Pro Thr
      145                      150                      155                      160
Val Leu Met Ala Ser Leu Pro Phe Cys Gly Pro Asn Gly Ile Asp His
      165                      170                      175
Phe Phe Arg Asp Ser Trp Pro Leu Leu Arg Leu Ser Cys Gly Asp Thr
      180                      185                      190
His Leu Leu Lys Leu Val Ala Phe Met Leu Ser Thr Leu Val Leu Leu
      195                      200                      205
Gly Ser Leu Ala Leu Thr Ser Val Ser Tyr Ala Cys Ile Leu Ala Thr
      210                      215                      220
Val Leu Arg Ala Pro Thr Ala Ala Glu Arg Arg Lys Ala Phe Ser Thr
      225                      230                      235                      240
Cys Ala Ser His Leu Thr Val Val Val Ile Ile Tyr Gly Ser Ser Ile
      245                      250                      255
Phe Leu Tyr Ile Arg Met Ser Glu Ala Gln Ser Lys Leu Leu Asn Lys

```

<400>	1301															
Met	Met	Gly	Glu	Ala	Arg	Asn	Arg	Thr	Val	Val	Gln	Glu	Phe	Ile	Leu	
1				5					10					15		
Glu	Gly	Phe	Pro	Ala	Val	Gln	His	Leu	Gly	Asn	Val	Leu	Phe	Leu	Val	
			20					25					30			
His	Leu	Leu	Ala	Tyr	Leu	Ala	Ser	Ile	Met	Ala	Asn	Met	Leu	Ile	Ile	
		35					40					45				
Thr	Ile	Thr	Trp	Ala	Asp	His	His	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	
	50					55					60					
Leu	Asn	Ser	Phe	Ser	Phe	Cys	Glu	Cys	Cys	Phe	Ile	Thr	Thr	Val	Ile	
65					70					75					80	
Pro	Lys	Leu	Leu	Val	Ile	Phe	Leu	Ser	Gly	Arg	Gln	Ile	Ile	Pro	Phe	
				85					90					95		
Thr	Thr	Cys	Leu	Met	Gln	Ser	Phe	Ser	Phe	Leu	Phe	Leu	Gly	Ser	Thr	
			100					105					110			
Val	Phe	Phe	Leu	Met	Ala	Val	Met	Ser	Leu	Asp	Xaa	Tyr	Leu	Ala	Ile	
		115					120					125				
Cys	Lys	Pro	Leu	His	Tyr	Ser	Thr	Ile	Met	Ser	Leu	Arg	Thr	Ser	Phe	
	130					135					140					
His	Leu	Val	Thr	Val	Cys	Phe	Val	Val	Gly	Phe	Thr	Leu	Ile	Thr	Gly	
145					150					155					160	
Leu	Met	Val	Lys	Val	Ser	Gln	Leu	Ser	Phe	Cys	Gly	Pro	His	Val	Ile	
				165					170					175		
Pro	His	Phe	Phe	Arg	Asp	Leu	Gly	Pro	Leu	Ile	Gln	Leu	Ser	Cys	Ser	
			180					185					190			
Asp	Thr	Arg	Ser	Thr	Glu	Thr	Leu	Ala	Phe	Val	Leu	Val	Ser	Phe	Val	
		195					200					205				
Leu	Phe	Thr	Ser	Leu	Ile	Ile	Thr	Ile	Ile	Ala	Tyr	Gly	Asn	Ile	Val	
	210					215					220					
Val	Thr	Ile	Val	Arg	Leu	Pro	Ser	Ala	Lys	Glu	Arg	Gln	Lys	Ala	Phe	
225					230					235					240	
Ser	Thr	Cys	Ser	Ser	His	Leu	Ile	Val	Leu	Ser	Leu	Val	Tyr	Gly	Ser	
				245					250					255		
Cys	Val	Phe	Ile	Tyr	Val	Lys	Pro	Lys	Gln	Met	Asp	Arg	Leu	Asp	Ser	
			260					265					270			
Asn	Arg	Met	Ala	Ala	Leu	Val	Asn	Thr	Val	Val	Thr	Pro	Leu	Leu	Asn	
		275					280					285				
Pro	Ile	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Gln	Val	His	Gln	Ala	Leu	Arg	
	290					295						300				

Asp Ala Gln Ser Arg Met Lys Leu Xaa Lys Gln Asn His Asn Leu Gln
 305 310 315 320
 Xaa Arg Asn Ala Pro Phe Leu Asp Leu Ile Gln Ser Phe Ser Cys Phe
 325 330 335
 Trp Asn

<210> 1302
 <211> 309
 <212> PRT
 <213> Unknown (H38g219 protein)

<220>
 <223> Synthetic construct

<400> 1302
 Met Ala Ser Thr Ser Asn Val Thr Glu Leu Ile Phe Thr Gly Leu Phe
 1 5 10 15
 Gln Asp Pro Ala Val Gln Ser Val Cys Phe Val Val Phe Leu Pro Val
 20 25 30
 Tyr Leu Ala Thr Val Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser
 35 40 45
 Ile Ser Lys Ser Leu Asp Ser Pro Met Tyr Phe Phe Leu Ser Cys Leu
 50 55 60
 Ser Leu Val Glu Ile Ser Tyr Ser Ser Thr Ile Ala Pro Lys Phe Ile
 65 70 75 80
 Ile Asp Leu Leu Ala Lys Ile Lys Thr Ile Ser Leu Glu Gly Cys Leu
 85 90 95
 Thr Gln Ile Phe Phe Phe His Phe Phe Gly Val Ala Glu Ile Leu Leu
 100 105 110
 Ile Val Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Met Asn Ile Ile Ser Arg Gln Leu Cys His Leu Leu Val Ala
 130 135 140
 Gly Ser Trp Leu Gly Gly Phe Cys His Ser Ile Ile Gln Ile Leu Val
 145 150 155 160
 Ile Ile Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Tyr Phe
 165 170 175
 Cys Asp Leu Gln Pro Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Met
 180 185 190
 Glu Gly Val Ile Val Leu Ala Asn Ser Gly Leu Phe Ser Val Phe Ser
 195 200 205
 Phe Leu Ile Leu Val Ser Ser Tyr Ile Val Ile Leu Val Asn Leu Arg
 210 215 220
 Asn His Ser Ala Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ala Ser
 225 230 235 240
 His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Ala Ile Phe Leu Tyr
 245 250 255
 Met Arg Pro Ser Ser Thr Phe Thr Glu Asp Lys Leu Val Ala Val Phe
 260 265 270
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Glu Val Lys Ile Ala Ile Arg Arg Leu Trp Ser Lys Lys Glu
 290 295 300
 Asn Pro Gly Arg Glu
 305

<210> 1303
 <211> 322
 <212> PRT
 <213> Unknown (H38g220 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1303

```

Met Ala Lys Gly Asn His Ser Ser Val Thr Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Thr Asp Asn Gln Glu Leu Gln Val Ile Leu Phe Gly Val Phe Leu
          20           25           30
Leu Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Gly Leu Ile Val Leu
          35           40           45
Ile His Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50           55           60
His Leu Ala Phe Val Asp Phe Tyr Gly Thr Ser Ala Ile Thr Pro Asn
 65           70           75           80
Thr Leu Val Asn Ser Leu His Glu Ile Lys Ser Met Ser Phe Tyr Ala
          85           90           95
Cys Ala Thr Gln Val Cys Cys Phe Ile Thr Leu Ser Val Trp Glu Val
          100          105          110
Ile Val Ala Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
          115          120          125
Leu Leu Tyr Val Val Leu Met Pro Arg Arg Leu Cys Ile Gln Met Val
          130          135          140
Thr Gly Leu Tyr Ile Tyr Gly Phe Thr Met Gly Leu Ile Gln Ala Val
          145          150          155          160
Ala Thr Phe His Met Ser Phe Cys Asp Ser Asn Val Val Asn Gln Phe
          165          170          175
Tyr Cys Asp Asp Val Pro Leu Ile Ala Leu Ala Cys Ser Asp Thr Gln
          180          185          190
Val Lys Glu Leu Met Leu Phe Ile Ile Ala Ala Phe Asn Val Phe Cys
          195          200          205
Ser Leu Ile Ile Val Leu Ile Ser Tyr Val Phe Ile Val Phe Ala Ile
          210          215          220
Leu Arg Ile His Ser Ala Val Gly Arg Gln Lys Ala Phe Ser Thr Cys
          225          230          235          240
Ala Ser His Met Phe Ser Ile Ser Ile Tyr Tyr Gly Thr Leu Ser Phe
          245          250          255
Met Tyr Leu Gln Pro Lys Ser Ser His Ser Leu Asp Lys Asp Lys Phe
          260          265          270
Ala Ser Val Phe Tyr Ala Val Val Ile Pro Met Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Asn Gln Glu Val Lys Asn Ala Met Lys Lys Ile Ile
          290          295          300
Glu Lys Met Cys Ser Ser Asn Gln Gln Xaa Asn Leu Leu Val Leu Lys
          305          310          315          320
Glu Ile

```

<210> 1304

<211> 317

<212> PRT

<213> Unknown (H38g221 protein)

<220>

<223> Synthetic construct

<400> 1304

```

Met Ser Gln Val Thr Asn Thr Thr Gln Glu Gly Ile Tyr Phe Ile Leu
 1          5          10          15
Thr Asp Ile Pro Gly Phe Glu Ala Ser His Ile Trp Ile Ser Ile Pro
          20          25          30
Val Cys Cys Leu Tyr Thr Ile Ser Ile Met Gly Asn Thr Thr Ile Leu
          35          40          45
Thr Val Ile Arg Thr Glu Pro Ser Val His Gln Arg Met Tyr Leu Phe
          50          55          60
Leu Ser Met Leu Ala Leu Thr Asp Leu Gly Leu Thr Leu Thr Thr Leu
65          70          75          80
Pro Thr Val Met Gln Leu Leu Trp Phe Asn Val Arg Arg Ile Ser Ser
          85          90          95
Glu Ala Cys Phe Ala Gln Phe Phe Phe Leu His Gly Phe Ser Phe Met
          100          105          110
Glu Ser Ser Val Leu Leu Ala Met Ser Val Asp Cys Tyr Val Ala Ile
          115          120          125
Cys Cys Pro Leu His Tyr Ala Ser Ile Leu Thr Asn Glu Val Ile Gly
130          135          140
Arg Thr Gly Leu Ala Ile Ile Cys Cys Cys Val Leu Ala Val Leu Pro
145          150          155          160
Ser Leu Phe Leu Leu Lys Arg Leu Pro Phe Cys His Ser His Leu Leu
          165          170          175
Ser Arg Ser Tyr Cys Leu His Gln Asp Met Ile Arg Leu Val Cys Ala
          180          185          190
Asp Ile Arg Leu Asn Ser Trp Tyr Gly Phe Ala Leu Ala Leu Ile
195          200          205
Ile Ile Val Asp Pro Leu Leu Ile Val Ile Ser Tyr Thr Leu Ile Leu
210          215          220
Lys Asn Ile Leu Gly Thr Ala Thr Trp Ala Glu Arg Leu Arg Ala Leu
225          230          235          240
Asn Asn Cys Leu Ser His Ile Leu Ala Val Leu Val Leu Tyr Ile Pro
          245          250          255
Met Val Gly Val Ser Met Thr His Arg Phe Ala Lys His Ala Ser Pro
          260          265          270
Leu Val His Val Ile Met Ala Asn Ile Tyr Leu Leu Ala Pro Pro Val
          275          280          285
Met Asn Pro Ile Ile Tyr Ser Val Lys Asn Lys Gln Ile Gln Trp Gly
290          295          300
Met Leu Asn Phe Leu Ser Leu Lys Asn Met His Ser Arg
305          310          315

```

<210> 1305

<211> 315

<212> PRT

<213> Unknown (H38g222 protein)

<220>

<223> Synthetic construct

<400> 1305

```

Met Asn Pro Ala Asn His Ser Gln Val Ala Gly Phe Val Leu Leu Gly
 1          5          10          15
Leu Ser Gln Val Trp Glu Leu Arg Phe Val Phe Phe Thr Val Phe Ser
          20          25          30
Ala Val Tyr Phe Met Thr Val Val Gly Asn Leu Leu Ile Val Val Ile
          35          40          45
Val Thr Ser Asp Pro His Leu His Thr Thr Met Tyr Phe Leu Leu Gly
          50          55          60
Asn Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Ile Thr Ala Pro Arg
65          70          75          80
Met Leu Val Asp Leu Leu Ser Gly Asn Pro Thr Ile Ser Phe Gly Gly

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```

      85      90      95
Cys Leu Thr Gln Leu Phe Phe Phe His Phe Ile Gly Gly Ile Lys Ile
      100      105      110
Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln
      115      120      125
Pro Leu His Tyr Thr Leu Ile Met Asn Gln Thr Val Cys Ala Leu Leu
      130      135      140
Met Ala Ala Ser Trp Val Gly Gly Phe Ile His Ser Ile Val Gln Ile
      145      150      155      160
Ala Leu Thr Ile Gln Leu Pro Phe Cys Gly Pro Asp Lys Leu Asp Asn
      165      170      175
Phe Tyr Cys Asp Val Pro Gln Leu Ile Lys Leu Ala Cys Thr Asp Thr
      180      185      190
Phe Val Leu Glu Leu Leu Met Val Ser Asn Asn Gly Leu Val Thr Leu
      195      200      205
Met Trp Phe Leu Val Leu Leu Gly Ser Tyr Thr Ala Leu Leu Val Met
      210      215      220
Leu Arg Ser His Ser Arg Glu Gly Arg Ser Lys Ala Leu Ser Thr Cys
      225      230      235      240
Ala Ser His Ile Ala Val Val Thr Leu Ile Phe Val Pro Cys Ile Tyr
      245      250      255
Val Tyr Thr Arg Pro Phe Arg Thr Phe Pro Met Asp Lys Ala Val Ser
      260      265      270
Val Leu Tyr Thr Ile Val Thr Pro Met Leu Asn Pro Ala Ile Tyr Thr
      275      280      285
Leu Arg Asn Lys Glu Val Ile Met Ala Met Lys Lys Leu Trp Arg Arg
      290      295      300
Lys Lys Asp Pro Ile Gly Pro Leu Glu His Arg
      305      310      315

```

<210> 1306

<211> 320

<212> PRT

<213> Unknown (H38g223 protein)

<220>

<223> Synthetic construct

<400> 1306

```

Met Ser Phe Leu Asn Gly Thr Ser Leu Thr Pro Ala Ser Phe Ile Leu
  1      5      10      15
Asn Gly Ile Pro Gly Leu Glu Asp Val His Leu Trp Ile Ser Phe Pro
      20      25      30
Leu Cys Thr Met Tyr Ser Ile Ala Ile Thr Gly Asn Phe Gly Leu Met
      35      40      45
Tyr Leu Ile Tyr Cys Asp Glu Ala Leu His Arg Pro Met Tyr Val Phe
      50      55      60
Leu Ala Leu Leu Ser Phe Thr Asp Val Leu Met Cys Thr Ser Thr Leu
      65      70      75      80
Pro Asn Thr Leu Phe Ile Leu Trp Phe Asn Leu Lys Glu Ile Asp Phe
      85      90      95
Lys Ala Cys Leu Ala Gln Met Phe Phe Val His Thr Phe Thr Gly Met
      100      105      110
Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp His Cys Val Ala Ile
      115      120      125
Cys Phe Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Ser Val Ile Ala
      130      135      140
Lys Ala Gly Phe Leu Thr Phe Leu Arg Gly Val Met Leu Val Ile Pro
      145      150      155      160
Ser Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Lys Gly Asn Val Ile
      165      170      175

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```

Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Ile Ser Cys Gly
      180                      185                      190
Asn Val Arg Val Asn Ala Ile Tyr Gly Leu Ile Val Ala Leu Leu Ile
      195                      200                      205
Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
      210                      215                      220
Gln Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
      225                      230                      235                      240
Ser Thr Cys Thr Ala His Phe Cys Ala Ile Val Leu Thr Tyr Val Pro
      245                      250                      255
Ala Phe Phe Thr Phe Phe Thr His His Phe Gly Gly His Thr Ile Pro
      260                      265                      270
Leu His Ile His Ile Ile Met Ala Asn Leu Tyr Leu Leu Met Pro Pro
      275                      280                      285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Arg Gln Val Arg Glu
      290                      295                      300
Ser Val Ile Arg Phe Phe Leu Lys Gly Lys Asp Asn Ser His Asn Phe
      305                      310                      315                      320

```

<210> 1307

<211> 305

<212> PRT

<213> Unknown (H38g224 protein)

<220>

<223> Synthetic construct

<400> 1307

```

Met Val Ala Thr Asn Asn Val Thr Glu Ile Ile Phe Val Gly Phe Ser
  1                      5                      10                      15
Gln Asn Trp Ser Glu Gln Arg Val Ile Ser Val Met Phe Leu Leu Met
      20                      25                      30
Tyr Thr Ala Val Val Leu Gly Asn Gly Leu Ile Val Val Thr Ile Leu
      35                      40                      45
Ala Ser Lys Val Leu Thr Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu
      50                      55                      60
Ser Phe Val Glu Ile Cys Tyr Cys Ser Val Met Ala Pro Lys Leu Ile
      65                      70                      75                      80
Phe Asp Ser Phe Ile Lys Arg Lys Val Ile Ser Leu Lys Gly Cys Leu
      85                      90                      95
Thr Gln Met Phe Ser Leu His Phe Phe Gly Gly Thr Glu Ala Phe Leu
      100                      105                      110
Leu Met Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115                      120                      125
His Tyr Met Ala Ile Met Asn Gln Arg Met Cys Gly Leu Leu Val Arg
      130                      135                      140
Ile Ala Trp Gly Gly Gly Leu Leu His Ser Val Gly Gln Thr Phe Leu
      145                      150                      155                      160
Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Ile Met Asp His Tyr Phe
      165                      170                      175
Cys Asp Val His Pro Val Leu Glu Leu Ala Cys Ala Asp Thr Phe Phe
      180                      185                      190
Ile Ser Leu Leu Ile Ile Thr Asn Gly Gly Ser Ile Ser Val Val Ser
      195                      200                      205
Phe Phe Val Leu Met Ala Ser Tyr Leu Ile Ile Leu His Phe Leu Arg
      210                      215                      220
Ser His Asn Leu Glu Gly Gln His Lys Ala Leu Ser Thr Cys Ala Ser
      225                      230                      235                      240
His Val Thr Val Val Asp Leu Phe Phe Ile Pro Cys Ser Leu Val Tyr
      245                      250                      255
Ile Arg Pro Cys Val Thr Leu Pro Ala Asp Lys Ile Val Ala Val Phe

```

260 265 270
 Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val Ile Tyr Ser Phe Arg
 275 280 285
 Asn Ala Glu Val Lys Asn Ala Met Arg Arg Phe Ile Gly Gly Lys Val
 290 295 300
 Ile
 305

<210> 1308
 <211> 313
 <212> PRT
 <213> Unknown (H38g225 protein)

<220>
 <223> Synthetic construct

<400> 1308
 Met Ala Pro Glu Asn Phe Thr Arg Val Thr Glu Phe Ile Leu Thr Gly
 1 5 10 15
 Val Ser Ser Cys Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu
 20 25 30
 Val Leu Tyr Gly Leu Thr Met Ala Gly Asn Leu Gly Ile Ile Thr Leu
 35 40 45
 Thr Ser Val Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Gln
 50 55 60
 His Leu Ala Leu Ile Asn Leu Gly Asn Ser Thr Val Ile Ala Pro Lys
 65 70 75 80
 Met Leu Ile Asn Phe Leu Val Lys Lys Lys Thr Thr Ser Phe Tyr Glu
 85 90 95
 Cys Ala Thr Gln Leu Gly Gly Phe Leu Phe Phe Ile Val Ser Glu Val
 100 105 110
 Ile Met Leu Ala Leu Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg Leu Cys Leu Leu Leu
 130 135 140
 Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr Ala Ile Val Val Ser
 145 150 155 160
 Ser Tyr Val Phe Ser Val Ser Tyr Cys Ser Ser Asn Ile Ile Asn His
 165 170 175
 Phe Tyr Cys Asp Asn Val Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
 180 185 190
 Tyr Leu Pro Glu Thr Val Val Phe Ile Ser Ala Ala Thr Asn Val Val
 195 200 205
 Gly Ser Leu Ile Ile Val Leu Val Ser Tyr Phe Asn Ile Val Leu Ser
 210 215 220
 Ile Leu Lys Ile Cys Ser Ser Glu Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Met Met Ala Val Thr Ile Phe Tyr Gly Thr Leu Leu
 245 250 255
 Phe Met Tyr Val Gln Pro Arg Ser Asn His Ser Leu Asp Thr Asp Asp
 260 265 270
 Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Thr Ala Leu Gln Arg
 290 295 300
 Phe Met Thr Asn Leu Cys Tyr Ser Phe
 305 310

<210> 1309
 <211> 326
 <212> PRT

<213> Unknown (H38g226 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1309

Met	Lys	Ile	Ser	Asn	Asn	Ser	Leu	Gly	Phe	Leu	Pro	Thr	Thr	Phe	Ile
1				5					10					15	
Leu	Val	Gly	Ile	Pro	Gly	Leu	Glu	Ser	Glu	His	Leu	Trp	Ile	Ser	Val
		20					25						30		
Pro	Phe	Ser	Leu	Ile	Tyr	Ile	Ile	Ile	Phe	Leu	Gly	Asn	Gly	Ile	Ile
		35					40					45			
Leu	His	Val	Ile	Arg	Thr	Asp	Ile	Ala	Leu	His	Gln	Pro	Met	Tyr	Leu
	50				55						60				
Phe	Leu	Ala	Met	Leu	Ala	Leu	Ala	Glu	Val	Arg	Val	Ser	Ala	Ser	Thr
65				70					75						80
Leu	Pro	Thr	Val	Leu	Gly	Ile	Phe	Leu	Phe	Gly	Asn	Thr	Glu	Ile	Ser
			85					90						95	
Leu	Glu	Ala	Phe	Phe	Phe	Gln	Met	Phe	Ser	Ile	His	Ser	Leu	Ser	Met
		100						105					110		
Met	Glu	Ser	Ala	Val	Leu	Leu	Ala	Met	Ser	Leu	Asp	Arg	Phe	Ile	Ala
		115					120					125			
Ile	Tyr	Ser	Pro	Leu	Ser	Tyr	Thr	Ala	Ile	Leu	Thr	Leu	Pro	Arg	Val
	130					135					140				
Phe	Gly	Thr	Gly	Ala	Ile	Ile	Val	Leu	Lys	Ser	Ile	Met	Leu	Met	Ala
145				150					155						160
Pro	Leu	Pro	Ile	Leu	Leu	Trp	Arg	Leu	Pro	Phe	Cys	Gly	His	Asn	Ala
			165					170						175	
Leu	Ser	His	Ser	Tyr	Cys	Leu	His	Pro	Asn	Leu	Ile	Tyr	Leu	Ser	Cys
		180					185						190		
Gly	Asn	Ile	Ser	Val	Asn	Asn	Ile	Tyr	Gly	Ile	Phe	Ile	Val	Thr	Ser
	195						200					205			
Thr	Phe	Gly	Leu	Asp	Ser	Leu	Leu	Ile	Val	Ile	Ser	Tyr	Gly	Leu	Ile
	210					215					220				
Leu	His	Thr	Val	Leu	Gly	Ile	Ala	Thr	Gly	Glu	Gly	Arg	Lys	Lys	Ala
225				230					235						240
Leu	Asn	Thr	Cys	Gly	Ser	His	Val	Cys	Ala	Val	Leu	Ala	Tyr	Tyr	Val
			245					250						255	
Pro	Met	Ile	Gly	Leu	Ser	Ile	Val	His	Arg	Leu	Gly	His	Arg	Val	Ser
		260						265					270		
Pro	Leu	Leu	Gln	Ala	Met	Met	Ala	Asn	Ala	Tyr	Leu	Phe	Phe	Pro	Pro
	275						280					285			
Val	Val	Asn	Pro	Ile	Val	Tyr	Ser	Ile	Lys	Thr	Lys	Glu	Ile	His	Gly
	290					295					300				
Ala	Ile	Val	Arg	Met	Leu	Leu	Glu	Lys	Arg	Arg	Arg	Val	Xaa	Pro	Lys
305					310					315					320
Thr	Ile	Val	Gly	Arg	Asn										
				325											

<210> 1310

<211> 311

<212> PRT

<213> Unknown (H38g227 protein)

<220>

<223> Synthetic construct

<400> 1310

```

Met Ser Lys Thr Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1          5          10          15
His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
          20          25          30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
          35          40          45
Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
          50          55          60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
          65          70          75          80
Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
          85          90          95
Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe
          100          105          110
Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
          115          120          125
Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala
          130          135          140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile
          145          150          155          160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr
          165          170          175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
          180          185          190
Ala Asn Glu Met Val Ile Phe Val Asp Ile Gly Leu Val Ala Ser Gly
          195          200          205
Cys Phe Leu Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
          210          215          220
Leu Arg Ile His Thr Ser Glu Gly Arg His Arg Ala Phe Gln Thr Cys
          225          230          235          240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Phe
          245          250          255
Ile Tyr Leu Arg Pro Gly Ser Arg Asp Val Val Asp Gly Val Val Ala
          260          265          270
Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
          275          280          285
Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys
          290          295          300
Val Ala His Ser Gln Gly Glu
          305          310

```

<210> 1311

<211> 312

<212> PRT

<213> Unknown (H38g228 protein)

<220>

<223> Synthetic construct

<400> 1311

```

Met Pro Ser Ile Asn Asp Thr His Phe Tyr Pro Pro Phe Phe Leu Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Asp Thr Leu His Ile Trp Ile Ser Phe Pro
          20          25          30
Phe Cys Ile Val Tyr Leu Ile Ala Ile Val Gly Asn Met Thr Ile Leu
          35          40          45
Phe Val Ile Lys Thr Glu His Ser Leu His Gln Pro Met Phe Tyr Phe
          50          55          60
Leu Ala Met Leu Ser Met Ile Asp Leu Gly Leu Ser Thr Ser Thr Ile
          65          70          75          80

```

```

Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gln Glu Ile Ser Phe
      85                      90                      95
Gly Gly Cys Leu Leu Gln Met Phe Phe Ile His Met Phe Thr Gly Met
      100                      105                      110
Glu Thr Val Leu Leu Val Val Met Ala Tyr Asp Arg Phe Val Ala Ile
      115                      120                      125
Cys Asn Pro Leu Gln Tyr Thr Met Ile Leu Thr Asn Lys Thr Ile Ser
      130                      135                      140
Ile Leu Ala Ser Val Val Val Gly Arg Asn Leu Val Leu Val Thr Pro
      145                      150                      155                      160
Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly His Asn Ile Val
      165                      170                      175
Pro His Thr Tyr Cys Glu His Arg Gly Leu Ala Gly Leu Ala Cys Ala
      180                      185                      190
Pro Ile Lys Ile Asn Ile Ile Tyr Gly Leu Met Val Ile Ser Tyr Ile
      195                      200                      205
Ile Val Asp Val Ile Leu Ile Ala Ser Ser Tyr Val Leu Ile Leu Arg
      210                      215                      220
Ala Val Phe Arg Leu Pro Ser Gln Asp Val Arg Leu Lys Ala Phe Asn
      225                      230                      235                      240
Thr Cys Gly Ser His Val Cys Val Met Leu Cys Phe Tyr Thr Pro Ala
      245                      250                      255
Phe Phe Ser Phe Met Thr His Arg Phe Gly Gln Asn Ile Pro His Tyr
      260                      265                      270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Ala Leu
      275                      280                      285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Gln Ile
      290                      295                      300
Val Lys Ile Phe Val Gln Lys Glu
      305                      310

```

<210> 1312

<211> 303

<212> PRT

<213> Unknown (H38g229 protein)

<220>

<223> Synthetic construct

<400> 1312

```

Met Thr Glu Phe Ile Phe Leu Val Leu Ser Pro Asn Gln Glu Val Gln
  1                      5                      10                      15
Arg Val Cys Phe Val Ile Phe Leu Phe Leu Tyr Thr Ala Ile Val Leu
      20                      25                      30
Gly Asn Phe Leu Ile Val Leu Thr Val Met Thr Ser Arg Ser Leu Gly
      35                      40                      45
Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu Ser Phe Met Glu Ile Cys
      50                      55                      60
Tyr Ser Ser Ala Thr Ala Pro Lys Leu Ile Ser Asp Leu Leu Ala Glu
      65                      70                      75                      80
Arg Lys Val Ile Ser Trp Trp Gly Cys Met Ala Gln Leu Phe Phe Leu
      85                      90                      95
His Phe Phe Gly Thr Glu Ile Phe Leu Leu Thr Val Met Ala Tyr
      100                      105                      110
Asp His Tyr Val Ala Ile Cys Lys Pro Leu Ser Tyr Thr Thr Ile Met
      115                      120                      125
Asn Trp Gln Val Cys Thr Val Leu Val Gly Ile Ala Trp Val Gly Gly
      130                      135                      140
Phe Met His Ser Phe Ala Gln Ile Leu Leu Ile Phe His Leu Leu Phe
      145                      150                      155                      160
Cys Gly Pro Asn Val Ile Asn His Tyr Phe Cys Asp Leu Val Pro Leu

```



```

                165                170                175
Leu Lys Leu Ala Cys Ser Asp Thr Phe Leu Ile Gly Leu Leu Ile Val
                180                185                190
Ala Asn Gly Gly Thr Leu Ser Val Ile Ser Phe Gly Val Leu Leu Ala
                195                200                205
Ser Tyr Met Val Ile Leu Leu His Leu Arg Thr Trp Ser Ser Glu Gly
                210                215                220
Trp Cys Lys Ala Leu Ser Thr Cys Gly Ser His Phe Ala Val Val Ile
225                230                235                240
Leu Phe Phe Gly Pro Cys Val Phe Asn Ser Leu Arg Pro Ser Thr Thr
                245                250                255
Leu Pro Ile Asp Lys Met Val Ala Val Phe Tyr Thr Val Ile Thr Ala
                260                265                270
Ile Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Ala Glu Met Arg Lys
                275                280                285
Ala Met Lys Arg Leu Trp Ile Arg Thr Leu Arg Leu Asn Glu Lys
                290                295                300

```

<210> 1313

<211> 316

<212> PRT

<213> Unknown (H38g230 protein)

<220>

<223> Synthetic construct

<400> 1313

```

Leu Ile Ala Thr Gly Asn Trp Thr Arg Ile Ser Glu Phe Ile Leu Met
1                5                10                15
Ser Phe Ser Ser Leu Pro Thr Glu Ile Gln Ser Leu Leu Phe Leu Thr
                20                25                30
Phe Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Cys Leu Ile Ile
35                40                45
Leu Val Thr Leu Ala Asp Pro Met Leu His Ser Pro Met Tyr Phe Phe
50                55                60
Leu Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val
65                70                75                80
Pro Lys Met Leu Gly Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe
85                90                95
Leu Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe Phe Gly Val Ala
100                105                110
Glu Cys Phe Leu Gln Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile
115                120                125
Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala
130                135                140
Lys Leu Ala Ala Ala Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val
145                150                155                160
Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val
165                170                175
Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu Val Cys Ala
180                185                190
Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val
195                200                205
Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala
210                215                220
Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe
225                230                235                240
Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser
245                250                255
Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly
260                265                270

```

Thr Lys Leu Leu Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn
 275 280 285
 Pro Ile Ile Tyr Ser Leu Arg Asn Asn Glu Val Lys Asn Ala Leu Ser
 290 295 300
 Arg Thr Val Ser Lys Ala Leu Gly Pro Gln Lys Leu
 305 310 315

<210> 1314
 <211> 309
 <212> PRT
 <213> Unknown (H38g231 protein)

<220>
 <223> Synthetic construct

<400> 1314
 Met Pro Asn Phe Thr Asp Val Thr Glu Phe Thr Leu Leu Gly Leu Thr
 1 5 10 15
 Cys Arg Gln Glu Leu Gln Val Leu Phe Phe Val Val Phe Leu Ala Val
 20 25 30
 Tyr Met Ile Thr Leu Leu Gly Asn Ile Gly Met Ile Ile Leu Ile Ser
 35 40 45
 Ile Ser Pro Gln Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His Leu
 50 55 60
 Ser Phe Ala Asp Val Cys Phe Ser Ser Asn Val Thr Pro Lys Met Leu
 65 70 75 80
 Glu Asn Leu Leu Ser Glu Thr Lys Thr Ile Ser Tyr Val Gly Cys Leu
 85 90 95
 Val Gln Cys Tyr Phe Phe Ile Ala Val Val His Val Glu Val Tyr Ile
 100 105 110
 Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Gly Cys Asn Pro Leu
 115 120 125
 Leu Tyr Gly Ser Lys Met Ser Arg Thr Val Cys Val Arg Leu Ile Ser
 130 135 140
 Val Pro Tyr Val Tyr Gly Phe Ser Val Ser Leu Ile Cys Thr Leu Trp
 145 150 155 160
 Thr Tyr Gly Leu Tyr Phe Cys Gly Asn Phe Glu Ile Asn His Phe Tyr
 165 170 175
 Cys Ala Asp Pro Pro Leu Ile Gln Ile Ala Cys Gly Arg Val His Ile
 180 185 190
 Lys Glu Ile Thr Met Ile Val Ile Ala Gly Ile Asn Phe Thr Tyr Ser
 195 200 205
 Leu Ser Val Val Leu Ile Ser Tyr Thr Leu Ile Val Val Ala Val Leu
 210 215 220
 Arg Met Arg Ser Ala Asp Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Ala Val Ser Met Phe Tyr Gly Thr Pro Ile Phe Met
 245 250 255
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val
 260 265 270
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Val Asn Lys Ala Ile Thr
 290 295 300
 Lys Thr Tyr Val Arg
 305

<210> 1315
 <211> 320
 <212> PRT
 <213> Unknown (H38g232 protein)

<220>

<223> Synthetic construct

<400> 1315

```

Met Leu His Thr Asn Asn Thr Gln Phe His Pro Ser Thr Phe Leu Val
 1           5           10           15
Val Gly Val Pro Gly Leu Glu Asp Val His Val Trp Ile Gly Phe Pro
          20           25           30
Phe Phe Ala Val Tyr Leu Thr Ala Leu Leu Gly Asn Ile Ile Ile Leu
          35           40           45
Phe Val Ile Gln Thr Glu Gln Ser Leu His Gln Pro Met Phe Tyr Phe
          50           55           60
Leu Ala Met Leu Ala Gly Thr Asp Leu Gly Leu Ser Thr Ala Thr Ile
65           70           75           80
Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gly Glu Ile Ala Phe
          85           90           95
Gly Ala Cys Ile Thr Gln Met Tyr Thr Ile His Ile Cys Thr Gly Leu
          100          105          110
Glu Ser Val Val Leu Thr Val Thr Gly Ile Asp Arg Tyr Ile Ala Ile
          115          120          125
Cys Asn Pro Leu Arg Tyr Ser Met Ile Leu Thr Asn Lys Val Ile Ala
          130          135          140
Ile Leu Gly Ile Val Ile Ile Val Arg Thr Leu Val Phe Val Thr Pro
145          150          155          160
Phe Thr Phe Leu Thr Leu Arg Leu Pro Phe Cys Gly Val Arg Ile Ile
          165          170          175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala Lys Leu Ala Cys Ala
          180          185          190
Ser Ile Asn Val Ile Tyr Gly Leu Ile Ala Phe Ser Val Gly Tyr Ile
          195          200          205
Asp Ile Ser Val Ile Gly Phe Ser Tyr Val Gln Ile Leu Arg Ala Val
          210          215          220
Phe His Leu Pro Ala Trp Asp Ala Arg Leu Lys Ala Leu Ser Thr Cys
225          230          235          240
Gly Ser His Val Cys Val Met Leu Ala Phe Tyr Leu Pro Ala Leu Phe
          245          250          255
Ser Phe Met Thr His Arg Phe Gly His Asn Ile Pro His Tyr Ile His
          260          265          270
Ile Leu Leu Ala Asn Leu Tyr Val Val Phe Pro Pro Ala Leu Asn Ser
          275          280          285
Val Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gln Val Leu Arg
          290          295          300
Ile Leu Asn Pro Lys Ser Phe Trp His Phe Asp Pro Lys Arg Ile Phe
305          310          315          320

```

<210> 1316

<211> 312

<212> PRT

<213> Unknown (H38g233 protein)

<220>

<223> Synthetic construct

<400> 1316

```

Met Glu Gln His Asn Leu Thr Thr Val Asn Glu Phe Ile Leu Thr Gly
 1           5           10           15
Ile Thr Asp Ile Ala Glu Leu Gln Ala Pro Leu Phe Ala Leu Phe Leu
          20           25           30
Met Ile Tyr Val Ile Ser Val Met Gly Asn Leu Gly Met Ile Val Leu
          35           40           45

```

Thr Lys Leu Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 His Leu Ala Phe Met Asp Leu Gly Tyr Ser Thr Val Gly Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Val Val Asp Lys Asn Ile Ile Ser Tyr Tyr Phe
 85 90 95
 Cys Ala Thr Gln Leu Ala Phe Phe Leu Val Phe Ile Gly Ser Glu Leu
 100 105 110
 Phe Ile Leu Ser Ala Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Ile Met Ser Arg Arg Val Cys Gln Val Leu
 130 135 140
 Val Ala Ile Pro Tyr Leu Tyr Cys Thr Phe Ile Ser Leu Leu Val Thr
 145 150 155 160
 Ile Lys Ile Phe Thr Leu Ser Phe Cys Gly Tyr Asn Val Ile Ser His
 165 170 175
 Phe Tyr Cys Asp Ser Leu Pro Leu Leu Pro Leu Leu Cys Ser Asn Thr
 180 185 190
 His Glu Ile Glu Leu Ile Ile Leu Ile Phe Ala Ala Ile Asp Leu Ile
 195 200 205
 Ser Ser Leu Leu Ile Val Leu Leu Ser Tyr Leu Leu Ile Leu Val Ala
 210 215 220
 Ile Leu Arg Met Asn Ser Ala Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Thr Leu Leu Phe
 245 250 255
 Met Tyr Val Gln Pro Lys Ser Ser His Ser Phe Asp Thr Asp Lys Val
 260 265 270
 Ala Ser Ile Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Tyr Ala Leu Arg Arg Thr Trp
 290 295 300
 Asn Asn Leu Cys Asn Ile Phe Val
 305 310

<210> 1317

<211> 315

<212> PRT

<213> Unknown (H38g234 protein)

<220>

<223> Synthetic construct

<400> 1317

Met Met Trp Glu Asn Trp Thr Ile Val Ser Glu Phe Val Leu Val Ser
 1 5 10 15
 Phe Ser Ala Leu Ser Thr Glu Leu Gln Ala Leu Leu Phe Leu Leu Phe
 20 25 30
 Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Val Leu Ile Ile Leu
 35 40 45
 Val Thr Ile Ala Asp Ser Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu
 50 55 60
 Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro
 65 70 75 80
 Lys Met Leu Gly Thr Leu Ile Ile Gln Asp Thr Thr Ile Ser Phe Leu
 85 90 95
 Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe Gly Ala Ala Glu
 100 105 110
 Cys Cys Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Asp Pro Leu His Tyr Pro Val Ile Met Gly His Ile Ser Cys Ala Gln

```

      130              135              140
Leu Ala Ala Ala Ser Trp Phe Ser Gly Phe Ser Val Ala Thr Val Gln
145              150              155              160
Thr Thr Trp Ile Phe Ser Phe Pro Phe Cys Gly Pro Asn Arg Val Asn
      165              170              175
His Phe Phe Cys Asp Ser Pro Pro Val Ile Ala Leu Val Cys Ala Asp
      180              185              190
Thr Ser Val Phe Glu Leu Glu Ala Leu Thr Ala Thr Val Pro Phe Ile
      195              200              205
Leu Phe Pro Phe Leu Leu Ile Leu Gly Ser Tyr Val Arg Ile Leu Ser
      210              215              220
Thr Ile Phe Arg Met Pro Ser Ala Glu Gly Lys His Gln Ala Phe Ser
225              230              235              240
Thr Cys Ser Ala His Leu Leu Val Val Ser Leu Phe Tyr Ser Thr Ala
      245              250              255
Ile Leu Thr Tyr Phe Arg Pro Gln Ser Ser Ala Ser Ser Glu Ser Lys
      260              265              270
Lys Leu Leu Ser Leu Ser Ser Thr Val Val Thr Pro Met Leu Asn Pro
      275              280              285
Ile Ile Tyr Ser Ser Arg Asn Lys Glu Val Lys Ala Ala Leu Lys Arg
      290              295              300
Leu Ile His Arg Thr Leu Gly Ser Gln Lys Leu
305              310              315

```

<210> 1318

<211> 310

<212> PRT

<213> Unknown (H38g235 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1318

```

Met Ala Lys Thr Asn Asn Ser Glu Val Thr Glu Phe Ile Leu Leu Gly
 1              5              10              15
Leu Thr Asp Asn Pro Glu Leu Gln Ala Leu Phe Trp Gly Ile Phe Leu
      20              25              30
Val Ile Asn Leu Ser Ser Val Met Gly Ser Leu Gly Leu Ile Met Leu
      35              40              45
Ile His Ile Ser Pro Gln Leu His Thr Ala Met Tyr Phe Phe Leu Ser
      50              55              60
His Val Ala Phe Val Tyr Phe Cys Tyr Thr Ser Ser Ile Thr Pro Asn
65              70              75              80
Ser Leu Val Asn Leu Leu Gln Glu Thr Lys Arg Ile Ser Leu Pro Thr
      85              90              95
Cys Ala Ser Gln Leu His Cys Phe Ile Met Phe Val Val Cys Asp Met
      100              105              110
Tyr Val Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115              120              125
Pro Leu Leu Tyr Ser Ile Ile Met Asn Arg Arg Val Cys Ile Gln Met
      130              135              140
Val Val Ser Thr Tyr Leu Tyr Gly Phe Ser Val Arg Leu Leu Gln Ala
145              150              155              160
Ile Leu Thr Phe His Leu Ser Phe Xaa Asp Ser Asn Ile Ile Asn Asn
      165              170              175
Ser Tyr Cys Asp Asp Val Pro Leu Ala Cys Leu Pro Tyr His Lys Asn
      180              185              190

```

His Tyr Lys Asp Val Lys Glu Leu Ile Leu Phe Thr Leu Ala Gly Phe
 195 200 205
 Asn Thr Leu Phe Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile Ser Val
 210 215 220
 Leu Ser Ala Ile Leu Arg Ile Asn Ser Ala Glu Ser Arg Gln Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Asp Ser His Leu Thr Ser Ile Ile Ile Phe Tyr Gly
 245 250 255
 Ile Ile Thr Phe Met Tyr Met Gln Xaa Lys Thr Asn Asn Ser Leu Asp
 260 265 270
 Thr Asp Lys Ile Ala Ser Val Phe Cys Ile Val Lys Ile Pro Ser Ile
 275 280 285
 Tyr Ser Leu Arg Asn His Glu Val Lys Asp Ala Leu Lys Met Ile Met
 290 295 300
 Glu Asn Leu Cys Leu Thr
 305 310

<210> 1319

<211> 184

<212> PRT

<213> Unknown (H38g236 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(184)

<223> Xaa = Any Amino Acid

<400> 1319

Leu Val Lys Val Lys Lys Asn Xaa Asn Ile Phe Leu Ser Thr Ala Tyr
 1 5 10 15
 His Phe Phe Pro Thr Leu Ser Val Asn Asn Asn Lys Phe Leu Xaa Ile
 20 25 30
 Ile Asn Asn Asn Phe Xaa Val Xaa Phe Asn Leu His Ser Glu Thr Ser
 35 40 45
 His Ser Xaa Val Tyr Ser Leu Val Leu Ser Ser Lys Val Cys Ile Leu
 50 55 60
 Leu Ala Ala Gly Val Val Gly Gly Ile Leu Ser Arg Arg Ile Val Cys
 65 70 75 80
 Gly Pro Thr Val Ser Leu Ser Ser Ser Arg Ser Asn Ala Ile Asn His
 85 90 95
 Phe Phe Cys Asn Lys Ser Leu Gly Leu Gly Leu Ser Cys Tyr Asn Ile
 100 105 110
 Tyr Ile Ser Thr Ala Val Pro Ala Phe Val Gly Val Xaa Val Leu His
 115 120 125
 Ser Leu Pro Tyr Leu Val Ile Met Phe Ser Trp Thr Tyr Ile Leu Val
 130 135 140
 Ala Ile Lys Arg Met Ser Ser Val Gly Arg Lys Glu Leu Ser Ile Cys
 145 150 155 160
 Val Ser His Leu Lys Thr Ser Thr Ile Phe His Thr Ala Leu Phe Tyr
 165 170 175
 Val Tyr Leu Gln Pro Asp Phe Phe
 180

<210> 1320

<211> 321

<212> PRT

<213> Unknown (H38g237 protein)

<220>

<223> Synthetic construct

<400> 1320

```

Met Ser Gly Asp Asn Ser Ser Ser Leu Thr Pro Gly Phe Phe Ile Leu
 1           5           10           15
Asn Gly Val Pro Gly Leu Glu Ala Thr His Ile Trp Ile Ser Leu Pro
      20           25           30
Phe Cys Phe Met Tyr Ile Ile Ala Val Val Gly Asn Cys Gly Leu Ile
      35           40           45
Cys Leu Ile Ser His Glu Glu Ala Leu His Arg Pro Met Tyr Tyr Phe
 50           55           60
Leu Ala Leu Leu Ser Phe Thr Asp Val Thr Leu Cys Thr Thr Met Val
65           70           75           80
Pro Asn Met Leu Cys Ile Phe Trp Phe Asn Leu Lys Glu Ile Asp Phe
      85           90           95
Asn Ala Cys Leu Ala Gln Met Phe Phe Val His Met Leu Thr Gly Met
      100          105          110
Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
      115          120          125
Cys Tyr Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Pro Val Ile Ala
130          135          140
Lys Ala Gly Leu Ala Thr Phe Leu Arg Asn Val Met Leu Ile Ile Pro
145          150          155          160
Phe Thr Leu Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Phe Ile
      165          170          175
Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Val Ser Cys Gly
      180          185          190
Asn Phe Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
      195          200          205
Gly Val Phe Asp Ile Cys Cys Ile Ser Val Ser Tyr Thr Met Ile Leu
210          215          220
Gln Ala Val Met Ser Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
225          230          235          240
Ser Thr Cys Thr Ser His Met Cys Ser Ile Val Ile Thr Tyr Val Ala
      245          250          255
Ala Phe Phe Thr Phe Phe Thr His Arg Phe Val Gly His Asn Ile Pro
      260          265          270
Asn His Ile His Ile Ile Val Ala Asn Leu Tyr Leu Leu Leu Pro Pro
      275          280          285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Glu
      290          295          300
Gly Val Ile Lys Phe Leu Leu Gly Asp Lys Val Ser Phe Thr Tyr Asp
305          310          315          320
Lys

```

<210> 1321

<211> 134

<212> PRT

<213> Unknown (H38g238 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(134)

<223> Xaa = Any Amino Acid

<400> 1321

```

Cys Phe Cys Gly Phe Ala Val Leu Thr Ser Cys Leu Phe Cys Leu Thr
 1           5           10           15

```

Pro Glu Arg Xaa His Asn Thr Leu Arg Met Ala Leu Gly Ser His Arg
 20 25 30
 Phe Pro Ser Xaa Pro Ile Lys Lys Asn Tyr Lys Trp Pro His Tyr Gln
 35 40 45
 Pro Glu Leu Leu Pro His Trp Ser Ser Lys Thr Glu Arg Ile Cys Ser
 50 55 60
 Pro Ala Pro Ser Gly Leu Glu Met Leu Arg Asn Ala Lys Pro Leu Gly
 65 70 75 80
 Phe Gln Leu Tyr Leu Ile Xaa Asn Glu Gln Ser Arg Leu Ala Pro Gln
 85 90 95
 Gly Val Pro Gln Lys Thr Xaa Ser Leu Cys Ser Ser Ala Leu Ser Ser
 100 105 110
 Tyr Cys Leu Lys Asp Thr Gly Gly Gly Gly Lys Xaa Ser Gly Glu Arg
 115 120 125
 Ser Ser Phe Pro Arg Glu
 130

<210> 1322

<211> 318

<212> PRT

<213> Unknown (H38g239 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1322

Met Lys Pro Thr Ile Gln Met Ala Ser Gly Asn Leu Thr Trp Val Thr
 1 5 10 15
 Glu Phe Ile Leu Val Gly Val Ser Asp Asp Pro Glu Leu Gln Ile Pro
 20 25 30
 Leu Phe Leu Val Phe Leu Val Leu Tyr Leu Leu Thr Val Ala Gly Asn
 35 40 45
 Leu Gly Ile Ile Thr Leu Thr Ser Val Asp Pro Gln Leu Gln Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Xaa His Leu Ala Ile Ile Asn Leu Cys Asn Ser
 65 70 75 80
 Thr Val Val Ala Pro Lys Met Leu Val Asn Phe Leu Val Thr Lys Lys
 85 90 95
 Thr Ile Ser Tyr Tyr Gly Cys Ala Ala Gln Leu Gly Gly Phe Leu Val
 100 105 110
 Phe Ile Val Ala Glu Ile Phe Thr Leu Ala Ala Met Ala Tyr Asp Arg
 115 120 125
 Tyr Val Ala Ile Trp Ser Pro Leu Leu Tyr Ala Val Val Val Ser Pro
 130 135 140
 Lys Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile
 145 150 155 160
 Thr Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser
 165 170 175
 Ser Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala
 180 185 190
 Leu Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe
 195 200 205
 Ser Gly Thr Asn Leu Leu Phe Ser Met Ile Val Val Leu Ile Ser Tyr
 210 215 220
 Phe Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg
 225 230 235 240
 Gln Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Val

				245					250				255				
Phe	Tyr	Gly	Thr	Leu	Leu	Phe	Met	Tyr	Leu	Gln	Pro	Arg	Ser	Asn	His		
			260					265					270				
Ser	Leu	Asp	Thr	Asp	Lys	Met	Ala	Ser	Val	Phe	Tyr	Thr	Leu	Val	Ile		
		275					280					285					
Pro	Val	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asn	Val	Lys		
	290					295					300						
Asp	Ala	Leu	Lys	Arg	Phe	Leu	Asp	Asn	Pro	Cys	Arg	Ser	Leu				
305					310					315							

<210> 1323

<211> 315

<212> PRT

<213> Unknown (H38g240 protein)

<220>

<223> Synthetic construct

<400> 1323

Met	Leu	Ser	Pro	Asn	His	Thr	Ile	Val	Thr	Glu	Phe	Ile	Leu	Leu	Gly		
1				5					10					15			
Leu	Thr	Asp	Asp	Pro	Val	Leu	Glu	Lys	Ile	Leu	Phe	Gly	Val	Phe	Leu		
		20						25				30					
Ala	Ile	Tyr	Leu	Ile	Thr	Leu	Ala	Gly	Asn	Leu	Cys	Met	Ile	Leu	Leu		
	35					40					45						
Ile	Arg	Thr	Asn	Ser	Gln	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly		
	50				55					60							
His	Leu	Ser	Phe	Val	Asp	Ile	Cys	Tyr	Ser	Ser	Asn	Val	Thr	Pro	Asn		
65				70					75					80			
Met	Leu	His	Asn	Phe	Leu	Ser	Glu	Gln	Lys	Thr	Ile	Ser	Tyr	Ala	Gly		
			85					90					95				
Cys	Phe	Thr	Gln	Cys	Leu	Leu	Phe	Ile	Ala	Leu	Val	Ile	Thr	Glu	Phe		
		100						105				110					
Tyr	Phe	Leu	Ala	Ser	Met	Ala	Leu	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Ser		
	115				120						125						
Pro	Leu	His	Tyr	Ser	Ser	Arg	Met	Ser	Lys	Asn	Ile	Cys	Ile	Ser	Leu		
	130				135					140							
Val	Thr	Val	Pro	Tyr	Met	Tyr	Gly	Phe	Leu	Asn	Gly	Leu	Ser	Gln	Thr		
145				150					155					160			
Leu	Leu	Thr	Phe	His	Leu	Ser	Phe	Cys	Gly	Ser	Leu	Glu	Ile	Asn	His		
			165					170					175				
Phe	Tyr	Cys	Ala	Asp	Pro	Pro	Leu	Ile	Met	Leu	Ala	Cys	Ser	Asp	Thr		
		180						185					190				
Arg	Val	Lys	Lys	Met	Ala	Met	Phe	Val	Val	Ala	Gly	Phe	Thr	Leu	Ser		
	195				200					205							
Ser	Ser	Leu	Phe	Ile	Ile	Leu	Leu	Ser	Tyr	Leu	Phe	Ile	Phe	Ala	Ala		
	210				215					220							
Ile	Phe	Arg	Ile	Arg	Ser	Ala	Glu	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr		
225				230					235					240			
Cys	Ala	Ser	His	Leu	Thr	Ile	Val	Thr	Leu	Phe	Tyr	Gly	Thr	Leu	Phe		
			245					250					255				
Cys	Met	Tyr	Val	Arg	Pro	Pro	Ser	Glu	Lys	Ser	Val	Glu	Glu	Ser	Lys		
		260						265					270				
Ile	Ile	Ala	Val	Phe	Tyr	Thr	Phe	Leu	Ser	Pro	Met	Leu	Asn	Pro	Leu		
	275					280					285						
Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Val	Ile	Leu	Ala	Ile	Gln	Gln	Met		
	290				295					300							
Ile	Arg	Gly	Lys	Ser	Phe	Cys	Lys	Ile	Ala	Val							
305				310					315								

<210> 1324

<211> 313
 <212> PRT
 <213> Unknown (H38g241 protein)

<220>
 <223> Synthetic construct

<400> 1324
 Met Pro Ile Ala Asn Asp Thr Gln Phe His Thr Ser Ser Phe Leu Leu
 1 5 10 15
 Leu Gly Ile Pro Gly Leu Glu Asp Val His Ile Trp Ile Gly Phe Pro
 20 25 30
 Phe Phe Ser Val Tyr Leu Ile Ala Leu Leu Gly Asn Ala Ala Ile Phe
 35 40 45
 Phe Val Ile Gln Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Cys
 50 55 60
 Leu Ala Met Leu Asp Ser Ile Asp Leu Ser Leu Ser Thr Ala Thr Ile
 65 70 75 80
 Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Ile Lys Glu Ile Ser Phe
 85 90 95
 Gly Gly Tyr Leu Ser Gln Met Phe Phe Ile His Phe Phe Thr Val Met
 100 105 110
 Glu Ser Ile Val Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile
 115 120 125
 Cys Lys Pro Leu Trp Tyr Thr Met Ile Leu Thr Ser Lys Ile Ile Ser
 130 135 140
 Leu Ile Ala Gly Ile Ala Val Leu Arg Ser Leu Tyr Met Val Ile Pro
 145 150 155 160
 Leu Val Phe Leu Leu Leu Arg Leu Pro Phe Cys Gly His Arg Ile Ile
 165 170 175
 Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Ala
 180 185 190
 Ser Ile Lys Val Asn Ile Met Phe Gly Leu Gly Ser Ile Ser Leu Leu
 195 200 205
 Leu Leu Asp Val Leu Leu Ile Ile Leu Ser His Ile Arg Ile Leu Tyr
 210 215 220
 Ala Val Phe Cys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn
 225 230 235 240
 Thr Cys Gly Ser His Ile Gly Val Ile Leu Ala Phe Ser Thr Pro Ala
 245 250 255
 Phe Phe Ser Phe Phe Thr His Cys Phe Gly His Asp Ile Pro Gln Tyr
 260 265 270
 Ile His Ile Phe Leu Ala Asn Leu Tyr Val Val Val Pro Pro Thr Leu
 275 280 285
 Asn Pro Val Ile Tyr Gly Val Arg Thr Lys His Ile Arg Glu Thr Val
 290 295 300
 Leu Arg Ile Phe Phe Lys Thr Asp His
 305 310

<210> 1325
 <211> 328
 <212> PRT
 <213> Unknown (H38g242 protein)

<220>
 <223> Synthetic construct

<400> 1325
 Met His Ile Phe Lys Phe Val Leu Asp Phe Asn Met Lys Asn Val Thr
 1 5 10 15
 Glu Val Thr Leu Phe Val Leu Lys Gly Phe Thr Asp Asn Leu Glu Leu

```

      20      25      30
Gln Thr Ile Phe Phe Phe Leu Phe Leu Ala Ile Tyr Leu Phe Thr Leu
      35      40      45
Met Gly Asn Leu Gly Leu Ile Leu Val Val Ile Arg Asp Ser Gln Leu
      50      55      60
His Lys Pro Met Tyr Tyr Phe Leu Ser Met Leu Ser Ser Val Asp Ala
      65      70      75      80
Cys Tyr Ser Ser Val Ile Thr Pro Asn Met Leu Val Asp Phe Thr Thr
      85      90      95
Lys Asn Lys Val Ile Ser Phe Leu Gly Cys Val Ala Gln Val Phe Leu
      100      105      110
Ala Cys Ser Phe Gly Thr Thr Glu Cys Phe Leu Leu Ala Ala Met Ala
      115      120      125
Tyr Asp Arg Tyr Val Ala Ile Tyr Asn Pro Leu Leu Tyr Ser Val Ser
      130      135      140
Met Ser Pro Arg Val Tyr Met Pro Leu Ile Asn Ala Ser Tyr Val Ala
      145      150      155      160
Gly Ile Leu His Ala Thr Ile His Thr Val Ala Thr Phe Ser Leu Ser
      165      170      175
Phe Cys Gly Ala Asn Glu Ile Arg Arg Val Phe Cys Asp Ile Pro Pro
      180      185      190
Leu Leu Ala Ile Ser Tyr Ser Asp Thr His Thr Asn Gln Leu Leu Leu
      195      200      205
Phe Tyr Phe Val Gly Ser Ile Glu Leu Val Thr Ile Leu Ile Val Leu
      210      215      220
Ile Ser Tyr Gly Leu Ile Leu Leu Ala Ile Leu Lys Met Tyr Ser Ala
      225      230      235      240
Glu Gly Arg Arg Lys Val Phe Ser Thr Cys Gly Ala His Leu Thr Gly
      245      250      255
Val Ser Ile Tyr Tyr Gly Thr Ile Leu Phe Met Tyr Val Arg Pro Ser
      260      265      270
Ser Ser Tyr Ala Ser Asp His Asp Met Ile Val Ser Ile Phe Tyr Thr
      275      280      285
Ile Val Ile Pro Leu Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys
      290      295      300
Asp Val Lys Asp Ser Met Lys Lys Met Phe Gly Lys Asn Gln Val Ile
      305      310      315      320
Asn Lys Val Tyr Phe His Thr Lys
      325

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<210> 1326

<211> 329

<212> PRT

<213> Unknown (H38g243 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1326

```

Met Asn Gly Ala Asn Ser Ser Ser Leu Thr Pro Arg Tyr Phe Ile Leu
      1      5      10      15
Ser Gly Val Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Leu Pro
      20      25      30
Phe Cys Phe Met Tyr Ile Ile Val Val Leu Gly Asn Cys Gly Leu Ile
      35      40      45
Tyr Leu Ile Ser His Glu Glu Ala Leu His Gln Pro Thr Tyr Tyr Phe
      50      55      60

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Leu Asp Leu Leu Ser Leu Thr Asp Val Thr Gly Cys Thr Ser Phe Val
65          70          75          80
Pro Asn Met Leu Cys Ile Phe Trp Phe Gly Leu Lys Glu Ile Asp Phe
          85          90          95
Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Met Leu Thr Gly Met
          100          105          110
Glu Ser Gly Ala Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Tyr Pro Leu His Tyr Ser Thr Ile Phe Thr Asn Thr Val Ile Thr
          130          135          140
Lys Val Gly Leu Val Thr Phe Ile Gln Ser Val Leu Leu Met Ile Pro
145          150          155          160
Phe Ala Phe Leu Ile Lys Cys Leu Pro Tyr Cys Arg Gly Asn Leu Ile
          165          170          175
His His Thr Tyr Cys Xaa His Met Ser Val Ala Lys Leu Ser Cys Gly
          180          185          190
Asn Val Gln Ile Asn Ala Ile Tyr Gly Leu Ile Ala Ala Ile Leu Ile
          195          200          205
Gly Gly Phe Asp Met Phe Cys Ile Ser Met Ser Tyr Thr Met Ile Ile
          210          215          220
Arg Ala Val Val Asn Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
225          230          235          240
Ser Thr Cys Thr Ala His Ile Cys Ala Ile Phe Ile Thr Tyr Val Pro
          245          250          255
Ala Phe Phe Asn Phe Phe Thr His Arg Phe Gly Gly His Thr Ile Pro
          260          265          270
His His Val His Ile Phe Ile Ala Asn Leu Tyr Leu Met Leu Pro Pro
          275          280          285
Thr Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu
          290          295          300
Gly Val Ile Lys Leu Phe Arg Glu Lys Val Tyr Phe Lys Tyr Asp
305          310          315          320
Ile Asn Leu Xaa Tyr Arg Ser Leu Asn
          325

```

<210> 1327

<211> 301

<212> PRT

<213> Unknown (H38g244 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(301)

<223> Xaa = Any Amino Acid

<400> 1327

```

Met Ala Ser Thr Asn Asn Val Thr Glu Ser Met Ile Thr Ser Leu Phe
1          5          10          15
Gln Asp Pro Ala Val Gln Arg Val Cys Phe Val Val Phe Leu Pro Val
          20          25          30
Tyr Leu Ala Met Glu Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser
          35          40          45
Ile Ser Lys Ser Leu His Ser Pro Val Tyr Phe Phe Leu Ser Tyr Leu
          50          55          60
Ser Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr
65          70          75          80
Asp Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala
          85          90          95
Gln Ile Phe Leu His Phe Phe Gly Ile Pro Trp Ile Phe Leu Leu Pro

```

100	105	110
Leu Met Thr Asn Asp Gln Tyr Met Ala Asn Cys Lys Leu Tyr Tyr Tyr		
115	120	125
Thr Thr Ile Met Ser Cys Arg Val Cys His Leu Leu Val Ala Gly Phe		
130	135	140
Trp Leu Arg Gly Ile Ile His Ser Met Val Gln Ile Leu Val Ser Val		
145	150	155
Gln Leu Phe Phe Cys Gly Pro Asn Met Ile Asp His Ser Phe Cys Asp		
165	170	175
Leu Gln Val Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Val Glu Gly		
180	185	190
Val Ile Val Leu Ala Asn Ser Glu Leu Val Ser Val Phe Phe Leu Ile		
195	200	205
Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Asn Leu Arg Asn His Ser		
210	215	220
Ala Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ala Ser Tyr Leu Val		
225	230	235
Phe Xaa Thr Cys Ile Phe Leu Tyr Val Xaa Leu Ser Ser Thr Phe Thr		
245	250	255
Lys Asp Lys Leu Val Ala Val Phe Tyr Val Val Ile Thr Pro Met Leu		
260	265	270
Asn Pro Phe Ile Tyr Thr Leu Gly Asn Ala Glu Met Lys Ile Thr Met		
275	280	285
Arg Arg Leu Leu Gly Arg Thr Val Asn Ser Gly Met Glu		
290	295	300

<210> 1328

<211> 324

<212> PRT

<213> Unknown (H38g245 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1328

Gly Ser Xaa Lys Gln Xaa Lys Ser Xaa Pro Pro Ile Phe Phe Leu Thr		
1	5	10
Gly Ile Pro Gly Leu Glu Ala Gln His Gly Trp Leu Ser Ile Pro Phe		
20	25	30
Phe Thr Met Tyr Ile Val Ala Ile Val Gly Asn Ile Leu Ile Met Ala		
35	40	45
Ala Val Gln Glu Asp Ser Ala Leu His Glu Pro Met Tyr Leu Phe Leu		
50	55	60
Ser Met Leu Ala Val Thr Glu Val Gly Val Ser Val Ser Thr Leu Pro		
65	70	75
Thr Val Thr Gly Ile Leu Trp Phe Asp Ala His Arg Val Asp Phe Asp		
85	90	95
Gly Cys Leu Ala Gln Met Phe Phe Ile His Thr Phe Ser Cys Met Glu		
100	105	110
Ser Gly Val Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Tyr		
115	120	125
Asn Leu Leu Arg Tyr Thr Ala Ile Leu Thr Leu Pro Arg Ile Ile Cys		
130	135	140
Met Gly Leu Gly Ile Thr Leu Lys Ser Val Ala Leu Met Ala Pro Leu		
145	150	155
Pro Ile Leu Leu Arg Gln Leu Pro Tyr Cys His Thr Asn Val Leu Ser		
165	170	175

His Ser Tyr Cys Leu His Ser Asp Leu Ile Gln Leu Pro Cys Ala Asp
 180 185 190
 Thr Lys Leu Asn Ser Ile Leu Gly Leu Ala Ile Val Leu Ala Asn Phe
 195 200 205
 Gly Leu Asp Ser Leu Leu Ile Val Val Ser Tyr Val Leu Ile Leu Tyr
 210 215 220
 Thr Val Met Gly Ile Ala Ser Gly Glu Gly Arg Trp Lys Ala Leu Asn
 225 230 235 240
 Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Tyr Tyr Val Pro Met
 245 250 255
 Ile Gly Val Ser Val Met His Arg Ala Ala Lys His Ala Ser Pro Ile
 260 265 270
 Val His Thr Leu Met Ser Ser Ile Cys Leu Leu Val Pro Pro Val Leu
 275 280 285
 Asn Pro Ile Ile Tyr Ser Val Lys Thr Gln Thr Ile Arg Gln Gly Ile
 290 295 300
 Leu Thr Leu Phe Ser Cys Lys Arg Glu Leu Leu Xaa Ile Thr Ala Arg
 305 310 315 320
 Ser Gln Glu Leu

<210> 1329

<211> 292

<212> PRT

<213> Unknown (H38g246 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(292)

<223> Xaa = Any Amino Acid

<400> 1329

Thr Leu Phe Ile Ile Ser Lys Phe Gln Gly Cys Xaa Lys Val Gly Leu
 1 5 10 15
 Tyr Thr Gln Ser Leu Tyr Leu Leu Ala Glu Tyr Phe His Arg Gly Gln
 20 25 30
 Leu Met Lys Met Leu Thr Ser Thr Asn Leu Ser Leu Ser Val Val Thr
 35 40 45
 Ile Gly Ile Phe Gln Phe Asn Val Arg Glu Ile Val Phe Gly Ala Phe
 50 55 60
 Leu Val Tyr Ile Gln Met Phe Met Thr Tyr Leu Cys Thr Gly Leu Glu
 65 70 75 80
 Ser Gly Val Leu Ile Ile Leu Ala Ile Asp His Tyr Val Val Ile Arg
 85 90 95
 Asn Pro Leu Arg Tyr Thr Met Ile Leu Met Asn Asn Val Val Ala Ile
 100 105 110
 Leu Gly Val Met Ile Ile Arg Ser Leu Ile Phe Ile Ile Pro Phe Glu
 115 120 125
 Phe Leu Ile Leu Leu Leu Ser Phe Cys Ala Ala His Ile Ile Pro His
 130 135 140
 Thr Lys Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ala Ser Val
 145 150 155 160
 Arg Ala Asn Asn Met Phe Gly Met Val Ala Phe Ser Val Gly Phe Ile
 165 170 175
 Asp Leu Ile Ala Ile Gly Phe Ser Tyr Val Lys Lys Leu Arg Ala Leu
 180 185 190
 Phe His Leu Pro Pro Trp Asn Gly Gln Phe Glu Ala Leu Asn Thr Cys
 195 200 205
 Gly Ser His Val Cys Met Leu Ile Phe Tyr Ile Pro Val Phe Phe Phe

```

      210              215              220
Xaa Tyr Thr Ala Trp Xaa Lys His Pro Cys Tyr Ile Arg Ile Phe Leu
225              230              235              240
Ala Asn Val Tyr Thr Val Val Leu Pro Val Phe Asn Pro Val Ile Tyr
      245              250              255
Gly Ile Arg Lys Lys Gln Ile Pro Asp Xaa Gly Ile Asp L u Lys Thr
      260              265              270
Phe Asp Asp Gln Ser Leu Leu Val Met Met Ile Tyr Ile Leu Gly Tyr
      275              280              285
Ile Cys Lys Tyr
      290

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<210> 1330

<211> 312

<212> PRT

<213> Unknown (H38g247 protein)

<220>

<223> Synthetic construct

<400> 1330

```

Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1              5              10              15
Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Phe Leu Phe Phe Ser
      20              25              30
Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr
      35              40              45
Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala
      50              55              60
Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys
      65              70              75              80
Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly
      85              90              95
Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met
      100              105              110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
      115              120              125
Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe
      130              135              140
Leu Val Ile Ser Trp Ile Ile Gly Ile Ile His Ser Val Ile Gln Leu
      145              150              155              160
Ala Phe Val Val Asp Leu Leu Phe Cys Gly Pro Asn Glu Leu Asp Ser
      165              170              175
Phe Phe Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Ile Glu Thr
      180              185              190
Tyr Thr Leu Gly Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu
      195              200              205
Ala Ser Phe Leu Ile Leu Ile Ile Ser Tyr Ile Phe Ile Leu Val Thr
      210              215              220
Val Gln Lys Lys Ser Ser Gly Gly Ile Phe Lys Ala Phe Ser Met Leu
      225              230              235              240
Ser Ala His Val Ile Val Val Val Leu Val Phe Gly Pro Leu Ile Phe
      245              250              255
Phe Tyr Ile Phe Pro Phe Pro Thr Ser His Leu Asp Lys Phe Leu Ala
      260              265              270
Ile Phe Asp Ala Val Ile Thr Pro Val Leu Asn Pro Val Ile Tyr Thr
      275              280              285
Phe Arg Asn Lys Glu Met Met Val Ala Met Arg Arg Cys Ser Gln
      290              295              300
Phe Val Asn Tyr Ser Lys Ile Phe
      305              310

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<210> 1331
 <211> 168
 <212> PRT
 <213> Unknown (H38g248 protein)

<220>
 <223> Synthetic construct

<400> 1331
 Lys Gln Ser Ser Gly Asp Ser Gly Asn Gln Thr Thr Trp Leu Ile Leu
 1 5 10 15
 Val Gly Phe Gly Glu Leu Gln Tyr Leu Gly Phe Leu Pro Phe Thr Leu
 20 25 30
 Phe Leu Ala Ile Tyr Val Val Thr Val Val Gly Asn Ala Leu Ile Met
 35 40 45
 Leu Ala Val Ala Ser Ser Arg Thr Leu His Pro Pro Met Tyr Phe Phe
 50 55 60
 Leu Cys His Phe Ser Leu Leu Glu Ile Gly Tyr Thr Ser Asn Val Ile
 65 70 75 80
 Leu Trp Leu Leu Gln Ser Phe Leu Glu Gly Lys Glu Val Ile Ser Leu
 85 90 95
 Val Ser Cys Leu Ala Gln Phe Tyr Val Phe Ser Ser Leu Ala Ala Ala
 100 105 110
 Glu Cys Leu Leu Leu Ser Ala Val Ser Tyr Asp Cys Tyr Leu Ala Ile
 115 120 125
 Cys Cys Pro Leu His Tyr Pro Ala Leu Met Ser Thr Trp Phe Cys His
 130 135 140
 Cys Leu Ala Ala Gly Ala Trp Phe Ser Gly Phe Phe Ser Ser Ala Phe
 145 150 155 160
 Thr Met Ala Leu Ala Ala Pro Leu
 165

<210> 1332
 <211> 321
 <212> PRT
 <213> Unknown (H38g249 protein)

<220>
 <223> Synthetic construct

<400> 1332
 Met Leu Thr Leu Asn Lys Thr Asp Leu Ile Pro Ala Ser Phe Ile Leu
 1 5 10 15
 Asn Gly Val Pro Gly Leu Glu Asp Thr Gln Leu Trp Ile Ser Phe Pro
 20 25 30
 Phe Cys Ser Met Tyr Val Val Ala Met Val Gly Asn Cys Gly Leu Leu
 35 40 45
 Tyr Leu Ile His Tyr Glu Asp Ala Leu His Lys Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ala Met Leu Ser Phe Thr Asp Leu Val Met Cys Ser Ser Thr Ile
 65 70 75 80
 Pro Lys Ala Leu Cys Ile Phe Trp Phe His Leu Lys Asp Ile Gly Phe
 85 90 95
 Asp Glu Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Thr Gly Met
 100 105 110
 Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg Tyr Ser Thr Ile Leu Thr Asn Pro Val Ile Ala
 130 135 140
 Lys Val Gly Thr Ala Thr Phe Leu Arg Gly Val Leu Leu Ile Ile Pro


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145          150          155          160
Phe Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Ile Leu
          165          170          175
Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Leu Ser Cys Gly
          180          185          190
Asn Val Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
          195          200          205
Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
          210          215          220
Arg Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
225          230          235          240
Asn Thr Cys Thr Ala His Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro
          245          250          255
Ala Phe Phe Ser Phe Phe Ser His Arg Phe Gly Glu His Ile Ile Pro
          260          265          270
Pro Ser Cys His Ile Ile Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro
          275          280          285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp
          290          295          300
Cys Val Ile Arg Ile Leu Ser Gly Ser Lys Asp Thr Lys Ser Tyr Ser
305          310          315          320
Met

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<210> 1333

<211> 315

<212> PRT

<213> Unknown (H38g250 protein)

<220>

<223> Synthetic construct

<400> 1333

```

Met Thr Thr His Arg Asn Asp Thr Leu Ser Thr Glu Ala Ser Asp Phe
1          5          10          15
Leu Leu Asn Cys Phe Val Arg Ser Pro Ser Trp Gln His Trp Leu Ser
          20          25          30
Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Val Gly Ala Asn Thr Thr
          35          40          45
Leu Leu Met Thr Ile Trp Leu Glu Ala Ser Leu His Gln Pro Leu Tyr
          50          55          60
Tyr Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr
65          70          75          80
Val Ile Pro Lys Val Leu Thr Ile Phe Trp Phe Asp Leu Arg Pro Ile
          85          90          95
Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Ile Met Asn Cys Phe Leu
          100          105          110
Ala Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val
          115          120          125
Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp His Phe
130          135          140
Val Val Lys Ala Ala Met Phe Ile Leu Thr Arg Asn Val Leu Met Thr
145          150          155          160
Leu Pro Ile Pro Ile Leu Ser Ala Gln Leu Arg Tyr Cys Gly Arg Asn
          165          170          175
Val Ile Glu Asn Cys Ile Cys Ala Asn Met Ser Val Ser Arg Leu Ser
          180          185          190
Cys Asp Asp Val Thr Ile Asn His Leu Tyr Gln Phe Ala Gly Gly Trp
          195          200          205
Thr Leu Leu Gly Ser Asp Leu Ile Leu Ile Phe Leu Ser Tyr Thr Phe
210          215          220

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Ile Leu Arg Ala Val Leu Arg Leu Lys Ala Glu Gly Ala Val Ala Lys
225                230                235                240
Ala Leu Ser Thr Cys Gly Ser His Phe Met Leu Ile Leu Phe Phe Ser
                245                250                255
Thr Ile Leu Leu Val Phe Val Leu Thr His Val Ala Lys Lys Lys Val
                260                265                270
Ser Pro Asp Val Pro Val Leu Leu Asn Val Leu His His Val Ile Pro
                275                280                285
Ala Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Gln Glu Ile Lys
                290                295                300
Gln Gly Met Gln Arg Leu Leu Lys Lys Gly Cys
305                310                315

```

<210> 1334

<211> 302

<212> PRT

<213> Unknown (H38g251 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(302)

<223> Xaa = Any Amino Acid

<400> 1334

```

Leu Ser Ser Met Cys Leu Thr Ile Val Met His Cys Glu Phe Phe Leu
1          5          10          15
Met Asp Leu Thr Asp Asp Pro Gln Leu His Pro Thr Phe Ser Ala Leu
                20          25          30
Phe Leu Pro Ile Tyr Val Val Met Val Met Ala Asn Leu Gly Leu Leu
                35          40          45
Ala Phe Ile Val Val Ser Pro Gln Phe Leu Thr Pro Met Tyr Phe Phe
                50          55          60
Leu Ser Asn Trp Ser Ser Val Asp Phe Cys Tyr Ser Ser Val Thr Val
65          70          75          80
Pro Lys Ile Ser Met Gly Phe Phe Ser Asp Cys Gln Val Phe Ser Phe
                85          90          95
Ser Gly Cys Met Ala Gln Leu Ser Cys Phe Xaa Ile Phe Ala Asp Thr
                100          105          110
Glu Phe Phe Leu Leu Ala Ser Met Val Tyr Tyr Arg Xaa Glu Ala Val
                115          120          125
Cys Asn Pro Leu Leu Tyr His Ile Thr Met Ser Pro Lys Leu Cys Leu
                130          135          140
Gln Leu Val Ala Thr Ser Met Asn Met Val Leu Pro Ser Ser Thr Ile
145          150          155          160
Phe His Leu Ile Phe Cys Lys Ser Arg Ala Ile Ile His Xaa Phe Cys
                165          170          175
Tyr Phe Ser Pro Pro Pro Arg Leu Xaa Lys Leu Ser Cys Ser Asp Met
                180          185          190
Gln Gly Leu Gln Leu Leu Thr Phe Ala Ser Ser Ser Phe Asn Val Ser
                195          200          205
Val Ser Arg Thr Ile Phe Leu Val Ser Tyr Leu Ile Met Arg Met Pro
                210          215          220
Ser Val Xaa Gly Lys His Cys Ala Ser His Leu Thr Ala Val Ser Leu
225          230          235          240
Cys Tyr Gly Thr Thr Val Phe Leu His Leu His Leu Ser Leu Lys Cys
                245          250          255
Ser Pro Asp Arg Asp Met Leu Val Ser Val Leu His Ser Ala Ile Leu
                260          265          270
Met Leu Asn Pro Met Val Gln Ser Leu Arg Asn Lys Asp Val Lys Lys

```

275	280	285
Thr Phe Gly Thr Ser Ser Xaa Arg Phe Thr Ile Pro Leu Leu		
290	295	300

<210> 1335
 <211> 324
 <212> PRT
 <213> Unknown (H38g252 protein)

<220>
 <223> Synthetic construct

<400> 1335
 Met Pro Leu Phe Asn Ser Leu Cys Trp Phe Pro Thr Ile His Val Thr
 1 5 10 15
 Pro Pro Ser Phe Ile Leu Asn Gly Ile Pro Gly Leu Glu Arg Val His
 20 25 30
 Val Trp Ile Ser Leu Pro Leu Cys Thr Met Tyr Ile Ile Phe Leu Val
 35 40 45
 Gly Asn Leu Gly Leu Val Tyr Leu Ile Tyr Tyr Glu Glu Ser Leu His
 50 55 60
 His Pro Met Tyr Phe Phe Phe Gly His Ala Leu Ser Leu Ile Asp Leu
 65 70 75 80
 Leu Thr Cys Thr Thr Leu Pro Asn Ala Leu Cys Ile Phe Trp Phe
 85 90 95
 Ser Leu Lys Glu Ile Asn Phe Asn Ala Cys Leu Ala Gln Met Phe Phe
 100 105 110
 Val His Gly Phe Thr Gly Val Glu Ser Gly Val Leu Met Leu Met Ala
 115 120 125
 Leu Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr Ala Thr Thr
 130 135 140
 Leu Thr Asn Pro Ile Ile Ala Lys Ala Glu Leu Ala Thr Phe Leu Arg
 145 150 155 160
 Gly Val Leu Leu Met Ile Pro Phe Pro Phe Leu Val Lys Arg Leu Pro
 165 170 175
 Phe Cys Gln Ser Asn Ile Ile Ser His Thr Tyr Cys Asp His Met Ser
 180 185 190
 Val Val Lys Leu Ser Cys Ala Ser Ile Lys Val Asn Val Ile Tyr Gly
 195 200 205
 Leu Met Val Ala Leu Leu Ile Gly Val Phe Asp Ile Cys Cys Ile Ser
 210 215 220
 Leu Ser Tyr Thr Leu Ile Leu Lys Ala Ala Ile Ser Leu Ser Ser Ser
 225 230 235 240
 Asp Ala Arg Gln Lys Ala Phe Ser Thr Cys Thr Ala His Ile Ser Ala
 245 250 255
 Ile Ile Ile Thr Tyr Val Pro Ala Phe Phe Thr Phe Phe Ala His Arg
 260 265 270
 Phe Gly Gly His Thr Ile Pro Pro Ser Leu His Ile Ile Val Ala Asn
 275 280 285
 Leu Tyr Leu Leu Leu Pro Pro Thr Leu Asn Pro Ile Val Tyr Gly Val
 290 295 300
 Lys Thr Lys Gln Ile Arg Lys Ser Val Ile Lys Phe Phe Gln Gly Asp
 305 310 315 320
 Lys Gly Ala Gly

<210> 1336
 <211> 274
 <212> PRT
 <213> Unknown (H38g253 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(274)

<223> Xaa = Any Amino Acid

<400> 1336

```

Glu Arg Asn Pro Ser Val Ala Glu Lys Cys Leu Gln Gly Met Thr Asp
 1           5           10           15
Ser Ser His His Tyr Leu Xaa Leu Arg Leu Pro Leu Phe Arg Leu Leu
          20           25           30
Ile Leu Leu Tyr Thr Ile Ile Thr Ile Gly Asn Leu Gly Thr Val Ile
          35           40           45
Leu Ile Gly Ile Ser Leu Gly Leu Tyr Val Cys Pro Pro Arg Phe Leu
          50           55           60
Leu Phe Thr Phe Ser Met Leu Arg Val Leu Val Lys Cys Phe Xaa Ser
65           70           75           80
Thr Val Leu Pro Phe Ser Phe Trp Ser Leu Glu Ala Gln Ile Asn Phe
          85           90           95
Phe Ser Ile Leu Cys Ile Thr Glu Phe Phe Pro Leu Ala Thr Met Ala
          100          105          110
Tyr Asp Asp Asn Val Ala Thr Cys Glu Pro Leu Phe His Pro Phe Thr
          115          120          125
Ser Leu Arg Leu Asn Ser Ala Phe Val Xaa Glu Lys Leu Tyr Leu Arg
          130          135          140
Ala Phe Thr Ser Ala Leu Pro Ser Thr Leu Pro Phe His Leu Pro Phe
145          150          155          160
Phe Asn Ser His Leu Cys Ser Leu Gln Xaa His Tyr Phe Leu Gly Gln
          165          170          175
Val Val Leu Xaa Asn Met Thr Pro Asn Phe Lys Leu Pro Asp Phe Ser
          180          185          190
Asn Ser Asn Val Asn Leu Val Ser Leu Cys Cys Pro Thr Ile Cys Cys
          195          200          205
Tyr Pro Ile Ile Leu Arg Ser Leu Ser Ser His Asn Xaa Ser Glu Asn
          210          215          220
Lys Leu Leu Ile Ile Ile Phe Phe Gln Asn Ser Thr Xaa Leu Leu Phe
225          230          235          240
Ile Phe Cys Ser Asp Glu Asn Val Tyr Xaa Thr Ile Xaa Gly Ile Thr
          245          250          255
Asp Xaa Phe Ile Lys Ser Lys His Cys Val His Ile Pro Leu Met Gln
          260          265          270
Ile Leu

```

<210> 1337

<211> 315

<212> PRT

<213> Unknown (H38g254 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1337

```

Met Ser Ser Leu Asn Val Thr Glu Pro His Leu Ser Ser Phe Leu Leu
 1           5           10           15
Leu Gly Ile Pro Gly Leu Glu Ala Ala Gln Arg Trp Leu Gly Phe Pro

```

```

      20      25      30
Phe Cys Val Val Tyr Leu Ile Ala Leu Val Gly Asn Leu Ile Ile Leu
      35      40      45
Phe Val Ile Trp Thr Asp Lys Asn Leu His Gln Pro Met Phe Tyr Phe
      50      55      60
Leu Ala Met Leu Ser Val Ile Asp Leu Ser Leu Ser Thr Ser Thr Ile
      65      70      75      80
Pro Lys Met Leu Gly Ile Phe Trp Phe Ser Leu Gln Glu Leu Cys Phe
      85      90      95
Gly Cys Cys Val Ala Gln Val Phe Phe Ile His Phe Phe Ser Val Met
      100      105      110
Glu Ser Ile Val Leu Leu Val Met Gly Phe Asp Arg Tyr Val Ala Ile
      115      120      125
Cys Asn Pro Phe Arg Xaa Thr Lys Ile Leu Thr Asn Arg Ile Thr Gly
      130      135      140
Val Ile Ala Met Val Val Val Leu Arg Ser Leu Cys Met Ile Ala Pro
      145      150      155      160
Ile Ile Phe Leu Leu Met Arg Leu Pro Tyr Cys Gly His Arg Ile Ile
      165      170      175
Pro Tyr Thr Tyr Cys Glu His Met Gly Val Ala Arg Leu Ala Cys Ala
      180      185      190
Ser Ile Ser Val Asn Val Ser His Gly Leu Gly Asn Ile Phe Ile Leu
      195      200      205
Phe Leu Asp Met Phe Leu Ile Ile Ile Ser Tyr Ala Arg Ile Leu Cys
      210      215      220
Thr Val Phe His Leu Pro Ser Gln Glu Ala His Leu Lys Ala Leu Asn
      225      230      235      240
Thr Cys Ser Ser His Ile Cys Val Ile Leu Ala Phe Phe Gly Pro Ala
      245      250      255
Leu Phe Ser Phe Leu Thr His Arg Phe Gly His Gly Ile Pro Gln Tyr
      260      265      270
Ile His Ile Leu Leu Ala Asn Leu Tyr Ile Val Val Ile Pro Pro Ala
      275      280      285
Leu Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Glu Arg
      290      295      300
Val Glu Ser Leu Phe Thr Lys Asn Xaa Leu Asn
      305      310      315

```

<210> 1338

<211> 323

<212> PRT

<213> Unknown (H38g255 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1338

```

Val Glu Asn Ser Pro Met Val Thr Asp Phe Ile Phe Leu Gly Met Thr
1      5      10      15
Asp Asn Ser Gln Leu Glu Val Leu Leu Phe Gly Val Phe Leu Ile Ala
      20      25      30
Tyr Ile Ile Thr Val Leu Glu Asn Leu Gly Leu Val Val Leu Ile Arg
      35      40      45
Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Gln
      50      55      60
Ser Phe Leu Asp Val Cys Phe Ser Ser Ile Thr Ile Pro Gln Asn Leu
      65      70      75      80

```

<210> 1339
<211> 311
<212> PRT
<213> Unknown (H38g256 protein)

<400> 1339

Trp	Leu	Asp	Glu	Lys	Lys	Gln	Asp	Ser	Asn	Val	Thr	Glu	Leu	Val	Leu
1				5					10					15	
Leu	Gly	Leu	Ser	Ser	Ser	Trp	Glu	Leu	Gln	Leu	Phe	Leu	Leu	Leu	Leu
			20					25					30		
Phe	Leu	Phe	Phe	Tyr	Ile	Ala	Ile	Val	Leu	Gly	Asn	Leu	Leu	Ile	Val
		35					40					45			
Val	Thr	Val	Gln	Ala	His	Ala	His	Leu	Leu	Gln	Ser	Pro	Met	Tyr	Tyr
	50					55					60				
Phe	Leu	Gly	His	Leu	Ser	Phe	Ile	Asp	Leu	Cys	Leu	Ser	Cys	Val	Thr
65					70					75					80
Leu	Pro	Lys	Met	Leu	Gly	Asp	Phe	Leu	Gln	Gln	Gly	Lys	Ser	Ile	Ser
				85					90					95	
Phe	Ser	Gly	Cys	Leu	Ala	Gln	Ile	Tyr	Phe	Leu	His	Phe	Leu	Gly	Ala
			100					105					110		
Ser	Glu	Met	Phe	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala
		115					120					125			
Ile	Cys	Asn	Pro	Leu	Arg	Tyr	Leu	Ile	Ile	Met	Asn	Pro	Gln	Leu	Cys
	130					135					140				
Leu	Trp	Leu	Val	Leu	Ala	Cys	Trp	Cys	Gly	Gly	Phe	Ile	His	Ser	Ile

```

145          150          155          160
Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro Asn Glu
          165          170          175
Leu Asp Asn Phe Tyr Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys
          180          185          190
Met Asp Thr Tyr Val Val Glu Val Leu Met Ile Ala Asn Ser Gly Leu
          195          200          205
Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala Val Ile
          210          215          220
Leu Ile Thr Leu Arg Thr His Phe Gly Gln Gly Gln Asn Lys Phe Leu
225          230          235          240
Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe Met Pro
          245          250          255
Cys Ile Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val Asp Lys
          260          265          270
Ile Phe Ser Met Phe Tyr Thr Val Met Thr Pro Met Leu Ser Pro Leu
          275          280          285
Ile Tyr Thr Leu Arg Asn Ala Asp Met Lys Thr Ala Met Lys Lys Leu
          290          295          300
Arg Ile Lys Pro Cys Asp Ile
305          310

```

<210> 1340

<211> 318

<212> PRT

<213> Unknown (H38g257 protein)

<220>

<223> Synthetic construct

<400> 1340

```

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1          5          10          15
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
          20          25          30
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
          35          40          45
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
          50          55          60
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
65          70          75          80
Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
          85          90          95
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
          100          105          110
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
          115          120          125
Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
          130          135          140
Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
145          150          155          160
Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
          165          170          175
Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
          180          185          190
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
          195          200          205
Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
          210          215          220
Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
225          230          235          240

```

Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro
 245 250 255
 Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser
 260 265 270
 Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val
 275 280 285
 Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg
 290 295 300
 Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
 305 310 315

<210> 1341

<211> 320

<212> PRT

<213> Unknown (H38g258 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1341

Met Ser Ser Arg Leu Met Asn Val Phe Ser Met Glu Thr Ile Asn Phe
 1 5 10 15
 Val Ser Cys Leu Ile Leu Met Gly Phe Pro Ser Ser Pro Glu Met Gln
 20 25 30
 Leu Leu Tyr Phe Gly Leu Phe Ser Val Ala Tyr Thr Leu Thr Pro Met
 35 40 45
 Gly Asn Ala Ala Ile Val Cys Ala Val Trp Xaa Asp Gln His Leu His
 50 55 60
 Thr Pro Met Tyr Thr Leu Leu Gly Asn Phe Ser Leu Leu Glu Ile Trp
 65 70 75 80
 Tyr Val Thr Ala Thr Lys Leu Leu Ala Asn Phe Leu Ser Thr Ser Lys
 85 90 95
 Ser Ile Ser Phe Met Ser Cys Phe Ala Gln Phe Tyr Phe Phe Ser Leu
 100 105 110
 Gly Tyr Asp Glu Gly Phe Phe Leu Cys Ile Thr Ala Phe Asp Arg Tyr
 115 120 125
 Leu Ala Ile Cys Arg Pro Leu Arg Tyr Pro Cys Ile Met Thr Lys Gln
 130 135 140
 Val Cys Thr Gly Leu Ile Phe Ala Trp Ser Cys Val Phe Val Ile
 145 150 155 160
 Phe Leu Thr Leu Val Ile Leu Ile Ser Gln Leu Ser Tyr Cys Gly Pro
 165 170 175
 Asn Ile Ile Asn His Phe Ile Cys Asp Pro Val Pro Leu Lys Met Leu
 180 185 190
 Ser Cys Ser Glu Asp Ile Ile Ile Thr Gln Leu Ile Tyr Ser Thr Phe
 195 200 205
 Asn Ser Val Phe Ile Ile Gly Thr Phe Leu Phe Ile Leu Cys Ser Tyr
 210 215 220
 Ala Leu Val Ile Leu Ala Ile Ile Arg Met Pro Ser Glu Ala Gly Lys
 225 230 235 240
 Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Leu
 245 250 255
 Phe Tyr Gly Ser Ile Met Val Met Tyr Val Ser Pro Gly Ser Ala His
 260 265 270
 Pro Ala Lys Asn Glu Lys Ile Ile Thr Leu Phe Phe Ser Val Ile Thr
 275 280 285
 Pro Leu Cys Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys

290		295		300
Asp Tyr Leu Arg Lys Ile Phe Arg Thr Gly Lys Asp Val Asn Lys Ile				
305		310		315
				320

<210> 1342

<211> 309

<212> PRT

<213> Unknown (H38g259 protein)

<220>

<223> Synthetic construct

<400> 1342

Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr				
1		5		15
Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile				
	20		25	30
Tyr Phe Ile Ser Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val Ile				
	35		40	45
Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu				
	50		55	60
Ser Cys Leu Asp Ile Cys Tyr Ser Ser Val Thr Leu Pro Lys Met Leu				
	65		70	75
Gln Asn Phe Leu Ser Ala His Lys Ala Ile Ser Phe Leu Gly Cys Ile				
		85		90
Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Met Leu				
		100		105
Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Lys Pro Leu				
		115		120
Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile				
		130		135
Thr Ile Trp Met Ile Gly Phe Phe His Ala Leu Leu His Ser Leu Met				
		145		150
Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile Tyr His Phe Phe				
		165		170
Cys Asp Val Lys Pro Leu Leu Lys Leu Ser Leu Ile Ser Gly Trp Leu				
		180		185
Ser Thr Val Thr Gly Thr Ile Ala Met Gly Pro Phe Phe Leu Thr Leu				
		195		200
Leu Ser Tyr Phe Tyr Ile Ile Thr His Leu Phe Phe Lys Thr His Ser				
		210		215
Phe Ser Met Leu Arg Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met				
		225		230
Val Val Ile Leu Leu Tyr Ala Pro Val Leu Phe Thr Tyr Ile His His				
		245		250
Ala Ser Gly Thr Ser Met Asp Gln Asp Arg Ile Thr Ala Ile Met Tyr				
		260		265
Thr Val Val Thr Pro Val Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn				
		275		280
Lys Glu Val Lys Gly Ala Phe Asn Arg Ala Met Lys Arg Trp Leu Trp				
		290		295
Pro Lys Glu Ile Leu				300
305				

<210> 1343

<211> 331

<212> PRT

<213> Unknown (H38g260 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1343

```

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Arg
 1           5           10           15
Leu Thr Gln Phe Arg Asp Ile Xaa Leu Val Phe Val Leu Val Leu
      20           25           30
Ile Phe Tyr Phe Phe Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
      35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
      65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
      85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
      100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Thr Ile Cys Leu
      115          120          125
Pro Leu Gln Tyr Ser Thr Val Met Asn Ser Arg Ala Cys Tyr Ala Met
      130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
      145          150          155          160
Val Leu Ile Ile Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
      165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
      180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
      195          200          205
Met Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
      210          215          220
Ile Arg Ala Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys
      225          230          235          240
Thr Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe
      245          250          255
Ile Tyr Thr Cys Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser
      260          265          270
Leu Phe His Thr Val Ile Leu Pro Leu Leu Asn Pro Val Ile Tyr Thr
      275          280          285
Leu His Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys
      290          295          300
His Ile Ala Xaa Lys Arg Ala Lys Lys Lys Arg Arg Lys Ile Asp Cys
      305          310          315          320
Lys Phe Tyr Leu Lys Leu Ile Cys Leu Phe Pro
      325          330

```

<210> 1344

<211> 315

<212> PRT

<213> Unknown (H38g261 protein)

<220>

<223> Synthetic construct

<400> 1344

```

Met Glu Ile Val Ser Thr Gly Asn Glu Thr Ile Thr Glu Phe Val Leu
 1           5           10           15
Leu Gly Phe Tyr Asp Ile Pro Glu Leu His Phe Leu Phe Phe Ile Val

```

<400> 1345																
Met	Ser	Ala	Asn	Thr	Ser	Met	Val	Thr	Glu	Phe	Leu	Leu	Leu	Gly	Phe	
1				5					10					15		
Ser	His	Leu	Ala	Asp	Leu	Gln	Gly	Leu	Leu	Phe	Ser	Val	Phe	Leu	Thr	
			20					25					30			
Ile	Tyr	Leu	Leu	Thr	Val	Ala	Gly	Asn	Phe	Leu	Ile	Val	Val	Leu	Val	
		35					40					45				
Ser	Thr	Asp	Ala	Ala	Leu	Gln	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Arg	Thr	
	50					55					60					
Leu	Ser	Ala	Leu	Glu	Ile	Gly	Tyr	Thr	Ser	Val	Thr	Val	Pro	Leu	Leu	
65				70						75					80	
Leu	His	His	Leu	Leu	Thr	Gly	Arg	Arg	His	Ile	Ser	Arg	Ser	Gly	Cys	
			85						90					95		
Ala	Leu	Gln	Met	Phe	Phe	Phe	Leu	Phe	Gly	Ala	Thr	Glu	Cys	Cys		
			100					105				110				

Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro
 115 120 125
 Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala
 130 135 140
 Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro
 145 150 155 160
 Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe
 165 170 175
 Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser
 180 185 190
 Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys
 195 200 205
 Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile
 210 215 220
 Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe
 245 250 255
 Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu
 260 265 270
 Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile
 275 280 285
 Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile
 290 295 300
 Gln Lys Thr Val Pro Met Glu Ile
 305 310

<210> 1346

<211> 316

<212> PRT

<213> Unknown (H38g263 protein)

<220>

<223> Synthetic construct

<400> 1346

Met Val Asn Gln Ser Ser Pro Met Gly Phe Leu Leu Leu Gly Phe Ser
 1 5 10 15
 Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
 20 25 30
 Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Val
 35 40 45
 Leu Tyr Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asp Leu
 50 55 60
 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
 65 70 75 80
 Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Gly Cys Ser
 85 90 95
 Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
 100 105 110
 Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
 115 120 125
 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
 130 135 140
 Val Ala Trp Val Met Ser Leu Val Gln Ser Ile Val Gln Thr Pro Ser
 145 150 155 160
 Thr Leu His Leu Pro Phe Cys Pro His Gln Gln Ile Asp Asp Phe Leu
 165 170 175
 Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp Thr Ser Tyr
 180 185 190
 Asn Glu Ile Gln Leu Ala Val Ser Ser Val Ile Phe Val Val Val Pro

195	200	205
Leu S r Leu Ile Leu Ala Ser Tyr Gly Ala Thr Ala Gln Ala Val Leu		
210	215	220
Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser		
225	230	235
Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val		
	245	250
Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe		
	260	265
Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr		
	275	280
Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly		
	290	295
Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala		
305	310	315

<210> 1347

<211> 318

<212> PRT

<213> Unknown (H38g264 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1347

Met Lys Ser Glu Leu Asn Arg Asn Tyr Ser Glu Val Thr Glu Phe Ile		
1	5	10
Leu Leu Gly Phe Arg Thr Ser Pro Glu Ala Gln Ile Leu Leu Phe Phe		
	20	25
Leu Phe Leu Leu Ile Tyr Met Val Ile Val Leu Arg Asn Leu Ser Met		
	35	40
Leu Val Val Ile Glu Ile Asp Ser Arg Leu His Thr Pro Val Tyr Phe		
	50	55
Phe Leu Arg Asn Leu Ser Tyr Leu Asp Leu Arg Tyr Ser Thr Val Ile		
	65	70
Ala Pro Lys Leu Thr Thr Leu Phe Ser Lys Glu Lys Lys Ile Ser Tyr		
	85	90
Asn Gly Xaa Ala Thr Gln Leu Phe Phe Phe Ala Leu Phe Val Gly Thr		
	100	105
Glu Gly Phe Phe Leu Asp Met Met Ala Tyr Asp Arg Phe Ser Ala Ile		
	115	120
Cys Ser Pro Phe Phe Tyr Thr Val Cys Met Ser Gln Gln Ala Cys Val		
	130	135
Cys Leu Val Val Gly Ser Ser Ile Cys Gly Cys Ile Asn Ser Met Ile		
	145	150
Gln Thr Gly Phe Thr Phe Ser Leu His Phe Cys Gly Glu Asn Arg Leu		
	165	170
Glu His Phe Phe Cys Asp Val Ser Val Met Ile Lys Ile Ser Cys Ile		
	180	185
Asp Ile Leu Val Asn Glu Val Val Leu Phe Ile Leu Ser Ala Leu Ile		
	195	200
Thr Thr Thr Thr Thr Val Ile Leu Ala Ser Tyr Val His Ile Leu Ser		
	210	215
Thr Val Leu Lys Ile Leu Ser Thr His Gly Arg Arg Lys Thr Phe Ser		
	225	230
Thr Cys Ser Ser His Ile Thr Val Val Ser Leu Phe Tyr Gly Thr Val		
	245	250
		255

Phe Phe Met Tyr Ala Gln Pro Gly Ala Ile Pro Lys Ser Lys Val Ile
 260 265 270
 Val Val Phe Xaa Thr Leu Val Ile Pro Met Leu Asn Thr Leu Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Val Gln Asn Ala Leu Lys Arg Tyr Ile Asp Lys
 290 295 300
 Lys Asn Ile Phe His Trp Pro Leu Ala Ile Tyr Lys Thr Ile
 305 310 315

<210> 1348

<211> 177

<212> PRT

<213> Unknown (H38g265 protein)

<220>

<223> Synthetic construct

<400> 1348

Met Ser Pro Arg Met Cys Leu Ser Phe Leu Ala Val Ala Trp Thr Leu
 1 5 10 15
 Gly Val Ser His Ser Leu Phe Gln Leu Ala Phe Leu Val Asn Leu Pro
 20 25 30
 Phe Cys Gly Pro Asn Val Leu Asp Ser Phe Tyr Cys Asp Leu Pro Arg
 35 40 45
 Leu Leu Arg Leu Ala Cys Thr Asp Thr Tyr Arg Leu Gln Phe Met Val
 50 55 60
 Thr Val Asn Ser Gly Phe Ile Cys Val Gly Thr Phe Phe Ile Leu Leu
 65 70 75 80
 Ile Ser Tyr Ile Phe Ile Leu Phe Thr Val Trp Lys His Ser Ser Gly
 85 90 95
 Gly Ser Ser Lys Ala Leu Ser Thr Leu Ser Ala His Ser Thr Ala Val
 100 105 110
 Leu Leu Phe Phe Gly Pro Pro Met Phe Val Tyr Thr Trp Pro His Pro
 115 120 125
 Asn Ser Gln Met Asp Lys Phe Leu Ala Ile Phe Asp Ala Val Leu Thr
 130 135 140
 Pro Phe Leu Asn Pro Val Val Tyr Thr Phe Arg Asn Lys Glu Met Lys
 145 150 155 160
 Ala Ala Ile Lys Arg Val Cys Lys Gln Leu Val Ile Tyr Lys Lys Ile
 165 170 175
 Ser

<210> 1349

<211> 322

<212> PRT

<213> Unknown (H38g266 protein)

<220>

<223> Synthetic construct

<400> 1349

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Lys Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Leu Ala
 35 40 45
 Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys

```

65          70          75          80
Met Leu Val Ser Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
          85          90          95
Cys Leu Thr Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr
          100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
          115          120          125
Pro Leu His Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu
          130          135          140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
          145          150          155          160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
          165          170          175
Phe Phe Cys Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr
          180          185          190
Leu Leu Asn Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val
          195          200          205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
          210          215          220
Leu Met Gly Met Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr
          225          230          235          240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
          245          250          255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
          260          265          270
Thr Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Glu Arg Leu
          290          295          300
Leu Ser Arg Ala Asp Ser Cys Pro Leu Thr Asn Gln Gly Leu Arg Thr
          305          310          315          320
Lys Arg

```

<210> 1350

<211> 322

<212> PRT

<213> Unknown (H38g267 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1350

```

Tyr Thr Glu Pro Glu Asn Leu Thr Gly Val Leu Glu Phe Leu Leu Leu
1          5          10          15
Gly Leu Pro Asp Asp Pro Glu Leu Gln Pro Val Leu Phe Gly Leu Phe
          20          25          30
Leu Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
          35          40          45
Ala Val Ser Ser Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Ala Ser Thr Thr Val Pro
          65          70          75          80
Lys Met Ile Val Asp Ile Gln Ala His Ser Arg Leu Ile Ser Tyr Val
          85          90          95
Gly Cys Leu Thr Gln Met Ser Phe Leu Ile Phe Phe Ala Cys Met Glu
          100          105          110

```

```

Ser Leu Leu Leu Ile Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
    115                120                125
His Pro Leu His Tyr Gln Val Ile Met Ser Pro Arg Leu Cys Gly Phe
    130                135                140
Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
    145                150                155                160
Asn Leu Ile Val Leu Gln Leu Thr Cys Phe Asn Asp Val Glu Ile Ser
    165                170                175
Asn Phe Phe Cys Asp Pro Ser Xaa Leu Leu Lys Leu Ala Cys Ser Asp
    180                185                190
Thr Ser Ile Asn Asn Met Val Val Tyr Phe Ile Gly Ala Ile Phe Gly
    195                200                205
Phe Leu Pro Leu Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser
    210                215                220
Ser Ile Leu Arg Val Leu Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser
    225                230                235                240
Thr Cys Ser Ser His Leu Ser Val Val Cys Leu Leu Tyr Gly Thr Ala
    245                250                255
Leu Gly Gly Tyr Leu Ser Ser Ala Val Ser Leu Ser Ser Arg Lys Gly
    260                265                270
Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met Leu Asn Pro
    275                280                285
Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Gln Arg
    290                295                300
Leu His Gly Arg Ile Met Xaa Ser Pro Tyr Leu Leu His Leu Phe Cys
    305                310                315                320
Ser Ile

```

<210> 1351

<211> 308

<212> PRT

<213> Unknown (H38g268 protein)

<220>

<223> Synthetic construct

<400> 1351

```

Met Arg Gln Ile Asn Gln Thr Gln Val Thr Glu Phe Leu Leu Leu Gly
  1                5                10                15
Leu Ser Asp Gly Pro His Thr Glu Gln Leu Leu Phe Ile Val Leu Leu
    20                25                30
Gly Val Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Leu Ile Ser Leu
    35                40                45
Val His Val Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys
    50                55                60
Asn Leu Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln
    65                70                75                80
Ala Leu Val His Leu Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu
    85                90                95
Cys Ala Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys
    100                105                110
Ala Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn
    115                120                125
Pro Leu Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu
    130                135                140
Ala Thr Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr
    145                150                155                160
Thr Phe Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His
    165                170                175
Phe Phe Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr

```



```

      180      185      190
His Ala Ser Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu
      195      200      205
Ile Pro Val Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr
      210      215      220
Val Val Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr
225      230      235      240
Cys Gly Ser His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile
      245      250      255
Ile Thr Tyr Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val
      260      265      270
Ser Val Phe Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Leu Ile Tyr
      275      280      285
Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Lys Val Ala Thr
      290      295      300
Arg Asn Phe Pro
305

```

<210> 1352

<211> 321

<212> PRT

<213> Unknown (H38g269 protein)

<220>

<223> Synthetic construct

<400> 1352

```

Met Pro Ile Leu Met Ala Ile Gly Asn Trp Thr Glu Ile Ser Glu Phe
 1      5      10      15
Ile Leu Met Ser Phe Ser Ser Leu Pro Thr Glu Ile Gln Ser Leu Leu
      20      25      30
Phe Leu Thr Phe Leu Thr Ile Tyr Leu Val Thr Leu Lys Gly Asn Ser
      35      40      45
Leu Ile Ile Leu Val Thr Leu Ala Asp Pro Met Leu His Ser Pro Met
      50      55      60
Tyr Phe Phe Leu Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu
      65      70      75      80
Val Ile Val Pro Lys Met Leu Gly Thr Leu Leu Ala Gln Asp Thr Thr
      85      90      95
Ile Ser Phe Leu Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe
      100      105      110
Gly Val Ala Glu Cys Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr
      115      120      125
Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg
      130      135      140
Thr Arg Ala Lys Leu Ala Ala Ala Ser Trp Phe Pro Gly Phe Pro Val
      145      150      155      160
Ala Thr Val Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr
      165      170      175
Asn Lys Val Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Lys Leu
      180      185      190
Val Cys Ala Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr
      195      200      205
Ile Leu Val Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr
      210      215      220
Arg Ile Ala Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys His
      225      230      235      240
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
      245      250      255
Tyr Ile Ser Ser Ser Leu Thr Tyr Phe Trp Pro Lys Ser Asn Asn Ser
      260      265      270

```

Pro Glu Ser Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro
 275 280 285
 Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Ser Glu Val Lys Asn
 290 295 300
 Ala Leu Ser Arg Thr Phe His Lys Val Leu Ala Leu Arg Asn Cys Ile
 305 310 315 320
 Pro

<210> 1353

<211> 260

<212> PRT

<213> Unknown (H38g270 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(260)

<223> Xaa = Any Amino Acid

<400> 1353

Ala His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro
 1 5 10 15
 Gln Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met
 20 25 30
 Gly Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu
 35 40 45
 Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys
 50 55 60
 Lys Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly
 65 70 75 80
 Leu Val Ser Val Thr Trp Ser Cys Trp Gly Gly Gln Leu Leu Gly His
 85 90 95
 Val Ser Trp Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp
 100 105 110
 His Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser
 115 120 125
 Thr Val Ala Ile Glu Gly Thr Val Phe Val Leu Ala Val Gly Val Val
 130 135 140
 Leu Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg
 145 150 155 160
 Ala Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly
 165 170 175
 Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile
 180 185 190
 Ile Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly
 195 200 205
 Met Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro
 210 215 220
 Leu Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg
 225 230 235 240
 Leu Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu Xaa Arg His Leu His
 245 250 255
 Leu Thr Ser Leu
 260

<210> 1354

<211> 329

<212> PRT

<213> Unknown (H38g271 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1354

Glu Glu Ile Leu Xaa Ile Ile Ser Gln His Val His Thr Gly Cys Val
 1 5 10 15
 Gln Asn Xaa Glu Leu Gln Pro Ile Leu Phe Gly Leu Phe Leu Ser Met
 20 25 30
 Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Val Ser
 35 40 45
 Ser Asp Ser His Leu His Thr Pro Thr Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Leu Ala Asp Ile Gly Phe Pro Ser Thr Thr Val Pro Lys Met Ile
 65 70 75 80
 Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu
 85 90 95
 Thr Gln Ile Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu
 100 105 110
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 115 120 125
 Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 130 135 140
 Leu Ser Phe Phe Leu Ser Leu Leu Asp Phe Gln Leu His Asn Trp Ile
 145 150 155 160
 Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Ser Phe Phe
 165 170 175
 Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr
 180 185 190
 Asn Asn Ile Val Met Tyr Phe Leu Ala Ala Ile Leu Gly Phe Leu Pro
 195 200 205
 Ile Ser Gly Ile Phe Tyr Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
 210 215 220
 Lys Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Ala Leu Gly Gly
 245 250 255
 Tyr Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala
 260 265 270
 Ser Val Met Tyr Thr Val Val Ala Pro Met Leu Asn Pro Phe Ile Tyr
 275 280 285
 Ser Leu Arg Lys Arg Asp Ile Lys Ser Ala Leu Gln Gln Leu His Gly
 290 295 300
 Arg Ile Val Xaa Ser His Asp Leu Ile Ile Gly Ser Ile Leu Xaa Pro
 305 310 315 320
 Trp Val Gly Lys Gly Ser Lys Val Lys
 325

<210> 1355

<211> 321

<212> PRT

<213> Unknown (H38g272 protein)

<220>

<223> Synthetic construct

<400> 1355

```

Met Glu Ser Pro Asn His Thr Asp Val Asp Pro Ser Val Phe Phe Leu
 1          5          10          15
Leu Gly Ile Pro Gly Leu Glu Gln Phe His Leu Trp Leu Ser Leu Pro
          20          25          30
Val Cys Gly Leu Gly Thr Ala Thr Ile Val Gly Asn Ile Thr Ile Leu
          35          40          45
Val Val Val Ala Thr Glu Pro Val Leu His Lys Pro Val Tyr Leu Phe
          50          55          60
Leu Cys Met Leu Ser Thr Ile Asp Leu Ala Ala Ser Val Ser Thr Val
65          70          75          80
Pro Lys Leu Leu Ala Ile Phe Trp Cys Gly Ala Gly His Ile Ser Ala
          85          90          95
Ser Ala Cys Leu Ala Gln Met Phe Phe Ile His Ala Phe Cys Met Met
          100          105          110
Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Thr Ile Ile Ala
          130          135          140
His Ile Gly Val Ala Ala Val Val Arg Gly Ser Leu Leu Met Leu Pro
145          150          155          160
Cys Pro Phe Leu Ile Gly Arg Leu Asn Phe Cys Gln Ser His Val Ile
          165          170          175
Leu His Thr Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly
          180          185          190
Asp Thr Arg Pro Asn Arg Val Tyr Gly Leu Thr Ala Ala Leu Leu Val
          195          200          205
Ile Gly Val Asp Leu Phe Cys Ile Gly Leu Ser Tyr Ala Leu Ser Ala
          210          215          220
Gln Ala Val Leu Arg Leu Ser Ser His Glu Ala Arg Ser Lys Ala Leu
225          230          235          240
Gly Thr Cys Gly Ser His Val Cys Val Ile Leu Ile Ser Tyr Thr Pro
          245          250          255
Ala Leu Phe Ser Phe Phe Thr His Arg Phe Gly His His Val Pro Val
          260          265          270
His Ile His Ile Leu Leu Ala Asn Val Tyr Leu Leu Leu Pro Pro Ala
          275          280          285
Leu Asn Pro Val Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Lys Arg
          290          295          300
Val Val Arg Val Phe Gln Ser Gly Gln Gly Met Gly Ile Lys Ala Ser
305          310          315          320
Glu

```

<210> 1356

<211> 327

<212> PRT

<213> Unknown (H38g273 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1356

```

Met Thr Trp Ser Gly Gly Thr Ile Val Gly Glu Xaa Gly Glu Phe Val
 1          5          10          15
Leu Leu Gly Phe Pro Ala Pro Ala Pro Leu Gln Val Leu Leu Phe Ala
          20          25          30
Leu Leu Leu Leu Ala Tyr Val Leu Val Leu Thr Glu Asn Thr Leu Ile

```

```

      35              40              45
Ile Met Ala Ile Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe
  50              55              60
Phe Leu Ala Asn Met Ser Phe Leu Glu Ile Trp Tyr Val Thr Val Thr
  65              70              75              80
Ile Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly
      85              90              95
Gln Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu
      100              105              110
Gly Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp
      115              120              125
Arg Tyr Met Ala Ile Cys Tyr Pro Leu His Tyr Pro Val Ile Val Ser
      130              135              140
Gly Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe
      145              150              155              160
Gly Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Tyr Cys
      165              170              175
Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu
      180              185              190
Asn Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile
      195              200              205
Leu Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser
      210              215              220
Tyr Val Ala Ile Thr Gly Ala Val Met His Ile Pro Ser Ala Ala Gly
      225              230              235              240
Arg Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile
      245              250              255
Ile Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu
      260              265              270
Ser Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile
      275              280              285
Val Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val
      290              295              300
Lys Arg Ala Leu Cys Cys Thr Leu His Leu Tyr Gln His Gln Asp Pro
      305              310              315              320
Asp Pro Lys Lys Ala Ser Arg
      325

```

<210> 1357

<211> 312

<212> PRT

<213> Unknown (H38g274 protein)

<220>

<223> Synthetic construct

<400> 1357

```

Met Glu Ala Gly Asn Gln Thr Gly Phe Leu Glu Phe Ile Leu Leu Gly
  1              5              10              15
Leu Ser Glu Asp Pro Glu Leu Gln Pro Phe Ile Phe Gly Leu Phe Leu
      20              25              30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      35              40              45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50              55              60
Asn Leu Ser Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys
      65              70              75              80
Met Leu Val Asn Ile Gln Thr Glu Asn Lys Ala Ile Ser Tyr Met Asp
      85              90              95
Cys Leu Thr Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr
      100              105              110

```

Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His
 115 120 125
 Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys Gly Leu Leu
 130 135 140
 Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile
 145 150 155 160
 Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His
 165 170 175
 Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys Ser Asp Thr
 180 185 190
 Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val
 195 200 205
 Phe Pro Leu Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser
 210 215 220
 Ile Arg Lys Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Val His Phe Thr Ser Ala Val Thr His Ser Ser Gln Lys Ile Ser
 260 265 270
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Ser Leu
 290 295 300
 Leu Ser Arg Ala Ala Ser Cys Leu
 305 310

<210> 1358

<211> 320

<212> PRT

<213> Unknown (H38g275 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1358

Met Thr Ala Cys Asn Ala Ser Gln Gly His Pro Ser Phe Phe Ile Leu
 1 5 10 15
 Gln Gly Ile Pro Gly Met Glu Asp Lys His Arg Trp Ile Ser Ile Pro
 20 25 30
 Phe Ser Ser Met Tyr Phe Ile Met Val Leu Gly Asn Cys Thr Ile Leu
 35 40 45
 Leu Thr Ile Ser Thr Glu Arg Ser Leu His Lys Pro Met Phe Leu Leu
 50 55 60
 Leu Cys Leu Leu Ala Leu Thr Asp Leu Gly Met Ser Thr Thr Thr Ile
 65 70 75 80
 Pro Lys Val Leu Cys Ile Phe Trp Phe Gly Gln Ser Glu Ile Ser Tyr
 85 90 95
 Glu Gly Cys Leu Val Gln Leu Phe Phe Ile His Ser Ile Ser Ala Met
 100 105 110
 Gln Ser Ala Val Leu Met Thr Met Ala Phe Asp His Tyr Val Ala Ile
 115 120 125
 Cys Lys Pro Leu Arg Tyr Ala Thr Ile Leu Ser Asn Ser Cys Thr Gly
 130 135 140
 Leu Ile Gly Leu Val Ser Leu Val Arg Ala Ile Leu Phe Ile Leu Pro
 145 150 155 160
 Met Pro Ile Leu Leu Gln Gln Met Pro Tyr His Ala Asn Arg Val Ile

```

      165      170      175
Pro Thr Thr Ser Cys Glu His Met Ala Val Val Lys Met Val Cys Val
      180      185      190
Asp Thr Thr Val Asn Arg Ile Tyr Gly Leu Val Val Ala Leu Leu Val
      195      200      205
Ala Gly Tyr Asp Leu Ser Ala Ile Ala Ser Ser Tyr Val Leu Ile Ile
      210      215      220
Gln Ala Ile Met His Leu Ser Ser Lys Glu Ala His His Lys Ala Val
      225      230      235      240
Asn Thr Cys Thr Thr His Ile Cys Val Met Leu Ile Ser Tyr Thr Pro
      245      250      255
Ser Leu Phe Ser Phe Leu Ala His Arg Phe Gly Gln Gly Ile Pro Pro
      260      265      270
His Val His Ile Ile Leu Gly Asn Leu Tyr Phe Leu Val Pro Pro Met
      275      280      285
Leu Ser Pro Ile Ile Tyr Gly Val Lys Thr Lys Glu Phe Trp Asp Lys
      290      295      300
Val Thr Lys Xaa Val Ala Gly Lys Lys Asn Pro Gln Pro Leu Thr Met
      305      310      315      320

```

<210> 1359

<211> 316

<212> PRT

<213> Unknown (H38g276 protein)

<220>

<223> Synthetic construct

<400> 1359

```

Met Glu Leu Trp Asn Phe Thr Leu Gly Ser Gly Phe Ile Leu Val Gly
  1      5      10      15
Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Ile Thr
      20      25      30
Ile Leu Tyr Leu Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Leu Ala
      35      40      45
Ile Thr Met Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
      50      55      60
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
      65      70      75      80
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
      85      90      95
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Gly Ala Glu Asp
      100      105      110
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115      120      125
Pro Leu Thr Tyr Met Thr Leu Met Ser Ser Arg Ala Cys Trp Leu Met
      130      135      140
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Ile Tyr Thr
      145      150      155      160
Val Tyr Thr Met His Tyr Pro Phe Cys Arg Ala Gln Glu Ile Arg His
      165      170      175
Leu Leu Cys Glu Ile Pro His Leu Leu Lys Val Ala Cys Ala Asp Thr
      180      185      190
Ser Arg Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile
      195      200      205
Pro Ser Leu Ala Ala Ile Leu Ala Ser Tyr Thr Gln Ile Leu Leu Thr
      210      215      220
Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
      225      230      235      240
Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr
      245      250      255

```

Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
 290 295 300
 Leu Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu
 305 310 315

<210> 1360

<211> 312

<212> PRT

<213> Unknown (H38g277 protein)

<220>

<223> Synthetic construct

<400> 1360

Met Lys Ala Gly Asn Phe Ser Asp Thr Pro Glu Phe Phe Leu Leu Gly
 1 5 10 15
 Leu Ser Gly Asp Pro Glu Leu Gln Pro Ile Leu Phe Met Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Ala Thr Met Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Val Asn Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Ile Leu Ser Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Met Pro Lys
 65 70 75 80
 Met Leu Val Asn Ile Gln Ala Gln Ala Gln Ser Ile Asn Tyr Thr Gly
 85 90 95
 Cys Leu Thr Gln Ile Cys Phe Val Leu Val Phe Val Gly Leu Glu Asn
 100 105 110
 Gly Ile Leu Val Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Asn Val Ile Met Asn Pro Lys Leu Cys Gly Leu Leu
 130 135 140
 Leu Leu Leu Ser Phe Ile Val Ser Val Leu Asp Ala Leu Leu His Thr
 145 150 155 160
 Leu Met Val Leu Gln Leu Thr Phe Cys Ile Asp Leu Glu Ile Pro His
 165 170 175
 Phe Phe Cys Glu Leu Ala His Ile Leu Lys Leu Ala Cys Ser Asp Val
 180 185 190
 Leu Ile Asn Asn Ile Leu Val Tyr Leu Val Thr Ser Leu Leu Gly Val
 195 200 205
 Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr Arg Ile Val Ser Ser
 210 215 220
 Val Met Lys Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Ile
 225 230 235 240
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Gly Phe
 245 250 255
 Gly Val Tyr Leu Ser Ser Gly Ala Thr His Ser Ser Arg Lys Gly Ala
 260 265 270
 Ile Ala Ser Val Met Tyr Thr Val Thr Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Met Leu Lys Ala Leu Arg Lys Leu
 290 295 300
 Ile Ser Arg Ile Pro Ser Phe His
 305 310

<210> 1361

<211> 328

<212> PRT

<213> Unknown (H38g278 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1361

```

Lys Ile Ser Asn Ser Ser Lys Phe Gln Val Ser Glu Phe Ile Leu Leu
 1           5           10           15
Gly Phe Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro Leu
      20           25           30
Ala Leu Leu Tyr Leu Ser Ala Leu Ala Ala Asn Thr Leu Ile Leu Ile
      35           40           45
Ile Ile Trp Gln Asn Pro Ser Leu Gln Gln Pro Met Tyr Ile Phe Leu
      50           55           60
Gly Ile Leu Cys Met Val Asp Met Gly Leu Ala Thr Thr Ile Ile Pro
      65           70           75           80
Lys Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Val Ile Ser Leu Pro
      85           90           95
Glu Cys Phe Ala Gln Ile Tyr Ala Ile His Phe Phe Val Gly Met Glu
      100          105          110
Ser Gly Ile Leu Leu Cys Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
      115          120          125
His Pro Leu Arg Tyr Pro Ser Ile Val Thr Ser Ser Leu Ile Leu Lys
      130          135          140
Ala Thr Leu Phe Met Val Leu Arg Asn Gly Leu Phe Val Thr Pro Val
      145          150          155          160
Pro Val Leu Ala Ala Gln Arg Asp Tyr Cys Ser Lys Asn Glu Ile Glu
      165          170          175
His Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ala Cys Asp Asp
      180          185          190
Arg Arg Pro Asn Ser Ile Cys Gln Leu Val Leu Ala Trp Leu Gly Met
      195          200          205
Gly Ser Asp Leu Ser Leu Ile Ile Leu Ser Tyr Ile Leu Ile Leu Tyr
      210          215          220
Ser Val Leu Arg Leu Asn Ser Ala Glu Ala Ala Lys Ala Leu Ser
      225          230          235          240
Thr Cys Ser Ser His Leu Thr Leu Ile Leu Phe Phe Tyr Thr Ile Val
      245          250          255
Val Val Ile Ser Val Thr His Leu Thr Glu Met Lys Ala Thr Leu Ile
      260          265          270
Pro Val Leu Leu Asn Val Leu His Asn Ile Ile Pro Pro Ser Leu Asn
      275          280          285
Pro Thr Val Tyr Ala Leu Gln Thr Lys Glu Leu Arg Ala Ala Phe Gln
      290          295          300
Lys Val Leu Phe Ala Leu Thr Lys Glu Ile Arg Ser Xaa Arg Pro Ser
      305          310          315          320
Pro Xaa Cys Thr Xaa Thr Ser Ala
      325

```

<210> 1362

<211> 316

<212> PRT

<213> Unknown (H38g279 protein)

<220>

<223> Synthetic construct

<400> 1362

```

Met Glu Leu Arg Asn Ser Thr Leu Gly Ser Gly Phe Ile Leu Val Gly
1      5      10      15
Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Tyr Ala Thr Phe Thr
20      25      30
Ile Leu Tyr Met Leu Ala Leu Thr Ser Asn Gly Leu Leu Leu Leu Ala
35      40      45
Ile Thr Ile Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
50      55      60
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
65      70      75      80
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
85      90      95
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Ser Ala Glu Asp
100     105     110
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
115     120     125
Pro Leu Lys Tyr Met Thr Leu Met Ser Pro Arg Val Cys Trp Ile Met
130     135     140
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ile Ala Ile Gly His Thr
145     150     155     160
Met Tyr Thr Met His Leu Pro Phe Cys Val Ser Trp Glu Ile Arg His
165     170     175
Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
180     185     190
Ser Arg Tyr Glu Leu Ile Ile Tyr Val Thr Gly Val Thr Phe Leu Leu
195     200     205
Leu Pro Ile Ser Ala Ile Val Ala Ser Tyr Thr Leu Val Leu Phe Thr
210     215     220
Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
225     230     235     240
Cys Ser Ser His Leu Ile Val Val Gly Met Phe Tyr Gly Ala Ala Thr
245     250     255
Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
260     265     270
Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
275     280     285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
290     295     300
Leu Gly Lys Tyr Ile Leu Leu Ala His Ser Thr Leu
305     310     315

```

<210> 1363

<211> 299

<212> PRT

<213> Unknown (H38g280 protein)

<220>

<223> Synthetic construct

<400> 1363

```

Met Gly Phe Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro
1      5      10      15
Leu Ala Leu Leu Tyr Leu Leu Ala Leu Ser Ala Asn Ile Leu Ile Leu
20      25      30
Ile Ile Ile Asn Lys Glu Ala Ala Leu His Gln Pro Met Tyr Tyr Phe
35      40      45
Leu Gly Ile Leu Ala Met Ala Asp Ile Gly Leu Ala Thr Thr Ile Met
50      55      60
Pro Lys Ile Leu Ala Ile Leu Trp Phe Asn Ala Lys Thr Ile Ser Leu

```

```

65          70          75          80
Leu Glu Cys Phe Ala Gln Met Tyr Ala Ile His Cys Phe Val Ala Met
      85          90          95
Glu Ser Ser Thr Phe Val Cys Met Ala Ile Asp Arg Tyr Val Ala Ile
      100        105        110
Cys Arg Pro Leu Arg Tyr Pro Ser Ile Ile Thr Glu Ser Phe Val Phe
      115        120        125
Lys Ala Asn Gly Phe Met Ala Leu Arg Asn Ser Leu Cys Leu Ile Ser
      130        135        140
Val Pro Leu Leu Ala Ala Gln Arg His Tyr Cys Ser Gln Asn Gln Ile
      145        150        155        160
Glu His Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ser Cys Asp
      165        170        175
Asp Arg Arg Ile Asn Ser Ile Asn Gln Val Leu Leu Ala Trp Thr Leu
      180        185        190
Met Gly Ser Asp Leu Gly Leu Ile Ile Leu Ser Tyr Ala Leu Ile Leu
      195        200        205
Tyr Ser Val Leu Lys Leu Asn Ser Pro Glu Ala Ala Ser Lys Ala Leu
      210        215        220
Ser Thr Cys Thr Ser His Leu Ile Leu Ile Leu Phe Phe Tyr Thr Val
      225        230        235        240
Ile Ile Val Ile Ser Ile Thr Arg Ser Thr Gly Met Arg Val Pro Leu
      245        250        255
Ile Pro Val Leu Leu Asn Val Leu His Asn Val Ile Pro Pro Ala Leu
      260        265        270
Asn Pro Met Val Tyr Ala Leu Lys Asn Lys Glu Leu Arg Gln Gly Leu
      275        280        285
Tyr Lys Val Leu Arg Leu Gly Val Lys Gly Thr
      290        295

```

<210> 1364

<211> 327

<212> PRT

<213> Unknown (H38g281 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1364

```

Met Thr Trp Ser Gly Gly Thr Leu Val Gly Glu Xaa Gly Glu Phe Val
1          5          10          15
Leu Leu Gly Phe Pro Ala Pro Ala Pro Leu Gln Val Leu Ser Phe Ala
      20          25          30
Arg Xaa Ser Ala Ala Tyr Ala Leu Val Leu Thr Glu Asn Thr Leu Ile
      35          40          45
Ile Met Ala Ser Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe
      50          55          60
Val Leu Ala Asn Met Ser Ser Leu Glu Ile Trp Tyr Val Thr Val Thr
      65          70          75          80
Ile Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly
      85          90          95
Gln Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu
      100        105        110
Gly Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp
      115        120        125
Arg Tyr Met Ala Ile Cys Tyr Pro Leu His Tyr Pro Val Ile Val Ser
      130        135        140

```

Gly Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe
 145 150 155 160
 Gly Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Tyr Cys
 165 170 175
 Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu
 180 185 190
 Asn Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile
 195 200 205
 Leu Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser
 210 215 220
 Tyr Val Ala Ile Thr Gly Ala Val Met His Thr Ser Ser Ala Ala Gly
 225 230 235 240
 Arg Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile
 245 250 255
 Ile Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu
 260 265 270
 Ser Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile
 275 280 285
 Val Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val
 290 295 300
 Lys Arg Ala Leu Cys Cys Thr Leu His Leu Tyr Gln His Gln Asp Pro
 305 310 315 320
 Asp Pro Lys Lys Ala Ser Arg
 325

<210> 1365

<211> 333

<212> PRT

<213> Unknown (H38g282 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1365

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1 5 10 15
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35 40 45
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Val
 50 55 60
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
 130 135 140
 Leu Ala Val Ala Trp Thr Leu Val Val Ser His Ser Leu Phe Gln Leu
 145 150 155 160
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr

```

      180      185      190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
      195      200      205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr
      210      215      220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
225      230      235      240
Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
      245      250      255
Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
      260      265      270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
      275      280      285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
      290      295      300
Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
305      310      315      320
Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
      325      330

```

<210> 1366

<211> 280

<212> PRT

<213> Unknown (H38g283 protein)

<220>

<223> Synthetic construct

<400> 1366

```

Met Leu Leu Gly Asn Leu Ala Ile Ile Ser Phe Ile Cys Leu Asp Ser
 1      5      10      15
Arg Leu His Ser Pro Met Tyr Phe Phe Leu Cys Asn Phe Ser Leu Met
      20      25      30
Glu Met Val Val Thr Ser Thr Val Val His Arg Met Leu Ala Asp Leu
      35      40      45
Leu Ser Thr His Lys Thr Met Ser Leu Ala Lys Cys Leu Thr Gln Ser
50      55      60
Phe Phe Tyr Phe Ser Leu Gly Ser Ala Asn Phe Leu Ile Leu Met Val
65      70      75      80
Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro
      85      90      95
Thr Ile Thr Asn Gly Pro Val Cys Val Lys Leu Val Val Ala Cys Trp
      100      105      110
Val Val Gly Phe Leu Ser Ile Val Ser Pro Thr Leu Gln Lys Thr Arg
      115      120      125
Leu Trp Phe Cys Gly Pro Asn Ile Ile Gly His Tyr Phe Cys Asp Ser
130      135      140
Ala Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg His Ile Glu Arg
145      150      155      160
Met Asp Leu Phe Leu Ser Leu Leu Phe Val Leu Thr Thr Met Leu Leu
      165      170      175
Ile Ile Leu Ser Tyr Ile Leu Ile Val Ala Ala Val Leu His Ile Pro
      180      185      190
Ser Ser Ser Gly Cys Gln Lys Ala Phe Ser Thr Cys Ala Ser His Leu
      195      200      205
Thr Val Val Val Leu Gly Tyr Gly Ser Ala Ile Phe Ile Tyr Val Arg
      210      215      220
Pro Gly Lys Gly His Ser Thr Tyr Leu Asn Lys Ala Val Ala Met Val
225      230      235      240
Thr Ala Met Val Thr Pro Phe Leu Asn Pro Phe Ile Phe Thr Phe Arg
      245      250      255

```

Asn Glu Lys Val Lys Glu Val Ile Glu Asp Val Thr Lys Arg Ile Phe
 260 265 270
 Leu Gly Asp Pro Ala Ala Cys Arg
 275 280

<210> 1367
 <211> 313
 <212> PRT
 <213> Unknown (H38g284 protein)

<220>
 <223> Synthetic construct

<400> 1367
 Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly
 1 5 10 15
 Leu Ser Gln Thr Pro Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu
 20 25 30
 Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr
 35 40 45
 Ile Ser Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ala Phe Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Glu
 65 70 75 80
 Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Asp Gly
 85 90 95
 Cys Ile Ala Gln Leu Phe Phe Leu His Phe Ala Gly Ala Ser Glu Met
 100 105 110
 Phe Leu Leu Thr Val Met Ala Phe Asp Leu Tyr Thr Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ala Thr Ile Met Asn Gln Arg Leu Cys Cys Ile Leu
 130 135 140
 Val Ala Leu Ser Trp Arg Gly Gly Phe Ile His Ser Ile Ile Gln Val
 145 150 155 160
 Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser
 165 170 175
 Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr
 180 185 190
 Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val
 195 200 205
 Val Trp Leu Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu
 210 215 220
 Phe Lys Lys Leu Ser Gly Ser Gly Glu Asn Thr Asn Arg Ala Met Ser
 225 230 235 240
 Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser
 245 250 255
 Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val
 260 265 270
 Val Ser Val Phe Asn Thr Leu Ile Phe Pro Leu Arg Asn Pro Ile Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Leu Val
 290 295 300
 Thr Lys Tyr Ile Leu Cys Lys Glu Lys
 305 310

<210> 1368
 <211> 214
 <212> PRT
 <213> Unknown (H38g285 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(214)

<223> Xaa = Any Amino Acid

<400> 1368

```

Cys Leu Leu Xaa Leu Tyr Gln Val Cys Leu Leu Thr Arg Asp Pro Ile
 1           5           10           15
Leu Gln Asp Leu His Xaa Lys Pro Arg Ile Tyr Cys Ser Pro Cys Leu
 20           25           30
Xaa Val Tyr Ser Leu Gly Leu Asp Arg Xaa Xaa Val Phe Leu Thr Met
 35           40           45
Thr Gln Ser Val Leu Trp Asn Glu Pro Val Cys Phe Met Phe Ser Xaa
 50           55           60
Met Pro Phe Cys Leu Ser Xaa Ile Leu Pro Xaa Thr Tyr Tyr Glu Gln
 65           70           75           80
Val Val Met Leu Asn Leu Val Cys Ala Asp Ile Thr Tyr Ile Val His
 85           90           95
Thr Cys Gly Leu Phe Met Ala Phe Ser Val Asp Gly Phe Asp Ile Phe
 100          105          110
Gly Ile Ile Ile His Arg Tyr Gln Thr Leu Gln Ala Val Leu Xaa Leu
 115          120          125
Pro Ala Lys Glu Ser Val Pro Lys Val Phe Ser Ile Tyr Ala Phe His
 130          135          140
Ile Cys Val Thr Leu Tyr Leu Leu Met Ile Gly Phe Tyr Ser Phe Phe
 145          150          155          160
Ser Cys Cys Phe Ser Tyr His Thr Leu Thr Val Ile Pro Ile Ser Phe
 165          170          175
Ser Ser Phe Tyr Ser Leu Val Pro Ser Met Phe Asn Thr Ile Thr Cys
 180          185          190
Gly Val Lys Ser Lys His Ile Gln Glu Asn Met Val Gln Arg Phe Cys
 195          200          205
Gly Lys Ile Ser Cys His
 210

```

<210> 1369

<211> 330

<212> PRT

<213> Unknown (H38g286 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 1369

```

Met Cys Leu Leu Thr Leu Gln Val Thr Gly Pro Met Asn Val Ser Glu
 1           5           10           15
Pro Asn Ser Ser Phe Ala Leu Val Asn Glu Phe Ile Leu Gln Asp Leu
 20           25           30
Ser Phe Glu Trp Thr Ile Gln Ile Phe Leu Phe Ser Leu Phe Thr Thr
 35           40           45
Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala Ile Ala Cys Ala Leu
 50           55           60
Trp Cys Asp Arg Arg Arg His Thr Pro Met Tyr Met Phe Leu Gly Asn
 65           70           75           80
Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser Thr Val Pro Lys Met
 85           90           95

```

```

Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly Cys
      100      105      110
Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly Thr Ser Glu Cys Leu
      115      120      125
Ile Leu Thr Val Met Ala Phe Asp Gln Tyr Leu Val Ile Cys His Pro
      130      135      140
Leu His Tyr Pro Asn Ile Ile Met Thr Gly His Leu Cys Ala Lys Leu
145      150      155      160
Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe Leu Ile Pro Thr
      165      170      175
Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn Ile Asn Asp His
      180      185      190
Val Val Cys Asp Pro Gly Pro Leu Phe Ala Leu Ala Cys Val Ser Ala
      195      200      205
Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser Leu Val Ile Phe
      210      215      220
Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu Val Leu Lys Ala
225      230      235      240
Val Leu Gly Met Pro Ser Ser Thr Gly Lys His Lys Ala Phe Ser Thr
      245      250      255
Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met
      260      265      270
Val Met Cys Val Ser Pro Gly Leu Gly His Ser Met Gly Met Gln Lys
      275      280      285
Ile Lys Thr Leu Phe Tyr Ala Met Val Thr Pro Leu Phe Asn Pro Leu
      290      295      300
Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala Leu Arg Lys Val
305      310      315      320
Leu Gly Ser Ser Asn Ile Ile Xaa Ala Ile
      325      330

```

<210> 1370

<211> 310

<212> PRT

<213> Unknown (H38g287 protein)

<220>

<223> Synthetic construct

<400> 1370

```

Met Met Asp Asn His Ser Ser Ala Thr Glu Phe His Leu Leu Gly Phe
  1      5      10      15
Pro Gly Ser Gln Gly Leu His His Ile Leu Phe Ala Ile Phe Phe Phe
      20      25      30
Phe Tyr Leu Val Thr Leu Met Gly Asn Thr Val Ile Ile Val Ile Val
      35      40      45
Cys Val Asp Lys Arg Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His
      50      55      60
Leu Ser Thr Leu Glu Ile Leu Val Thr Thr Ile Ile Val Pro Met Met
      65      70      75      80
Leu Trp Gly Leu Leu Phe Leu Gly Cys Arg Gln Tyr Leu Ser Leu His
      85      90      95
Val Ser Leu Asn Phe Ser Cys Gly Thr Met Glu Phe Ala Leu Leu Gly
      100      105      110
Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg Tyr
      115      120      125
Asn Ile Ile Met Asn Ser Ser Thr Cys Ile Trp Val Val Ile Val Ser
      130      135      140
Trp Val Phe Gly Phe Leu Ser Glu Ile Trp Pro Ile Tyr Ala Thr Phe
145      150      155      160
Gln Phe Thr Phe Arg Lys Ser Asn Ser Leu Asp His Phe Tyr Cys Asp

```


<400>	1371														
Met	Ser	Asn	Thr	Asn	Gly	Ser	Ala	Ile	Thr	Glu	Phe	Ile	Leu	Leu	Gly
1				5					10					15	
Leu	Thr	Asp	Cys	Pro	Glu	Leu	Gln	Ser	Leu	Leu	Phe	Val	Leu	Phe	Leu
		20					25						30		
Val	Val	Tyr	Leu	Val	Thr	Leu	Leu	Gly	Asn	Leu	Gly	Met	Ile	Met	Leu
		35				40						45			
Met	Arg	Leu	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr
	50					55					60				
Asn	Leu	Ala	Phe	Val	Asp	Leu	Cys	Tyr	Thr	Ser	Asn	Ala	Thr	Pro	Gln
65					70					75					80
Met	Ser	Thr	Asn	Ile	Val	Ser	Glu	Lys	Thr	Ile	Ser	Phe	Ala	Gly	Cys
			85						90					95	
Phe	Thr	Gln	Cys	Tyr	Ile	Phe	Ile	Ala	Leu	Leu	Leu	Thr	Glu	Phe	Tyr
			100					105					110		
Met	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Tyr	Asp	Pro
	115					120						125			
Leu	Arg	Tyr	Ser	Val	Lys	Thr	Ser	Arg	Arg	Val	Cys	Ile	Cys	Leu	Ala
	130					135					140				
Thr	Phe	Pro	Tyr	Val	Tyr	Gly	Phe	Ser	Asp	Gly	Leu	Phe	Gln	Ala	Ile
145					150					155					160
Leu	Thr	Phe	Arg	Leu	Thr	Phe	Cys	Arg	Ser	Ser	Val	Ile	Asn	His	Phe
			165						170					175	
Tyr	Cys	Ala	Asp	Pro	Pro	Leu	Ile	Lys	Leu	Ser	Cys	Ser	Asp	Thr	Tyr
			180					185					190		
Val	Lys	Glu	His	Ala	Met	Phe	Ile	Ser	Ala	Gly	Phe	Asn	Leu	Ser	Ser
	195					200						205			
Ser	Leu	Thr	Ile	Val	Leu	Val	Ser	Tyr	Ala	Phe	Ile	Leu	Ala	Ala	Ile
	210					215					220				
Leu	Arg	Ile	Lys	Ser	Ala	Glu	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr	Cys
225					230					235					240
Gly	Ser	His	Met	Met	Ala	Val	Thr	Leu	Phe	Tyr	Gly	Thr	Leu	Phe	Cys
			245						250					255	

Met Tyr Ile Arg Pro Pro Thr Asp Lys Thr Val Glu Glu Ser Lys Ile
 260 265 270
 Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Val Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Leu Lys Asn Val Leu
 290 295 300
 Arg
 305

<210> 1372

<211> 313

<212> PRT

<213> Unknown (H38g289 protein)

<220>

<223> Synthetic construct

<400> 1372

Met Ala Asn Leu Ser Gln Pro Ser Glu Phe Val Leu Leu Gly Phe Ser
 1 5 10 15
 Ser Phe Gly Glu Leu Gln Ala Leu Leu Tyr Gly Pro Phe Leu Met Leu
 20 25 30
 Tyr Leu Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile
 35 40 45
 Ala Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe
 50 55 60
 Ser Leu Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu
 65 70 75 80
 Ser Asp Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met
 85 90 95
 Val Gln Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile
 100 105 110
 Leu Thr Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu
 115 120 125
 Arg Tyr Gly Thr Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly
 130 135 140
 Ala Ala Trp Ala Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser
 145 150 155 160
 Arg Ala His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe
 165 170 175
 Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu
 180 185 190
 Leu Glu Phe Trp Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser
 195 200 205
 Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu
 210 215 220
 Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu
 245 250 255
 Tyr Val Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val
 260 265 270
 Ala Leu Val Thr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu
 275 280 285
 Thr Phe Cys Asn Gln Thr Val Lys Thr Val Leu Gln Gly Gln Met Gln
 290 295 300
 Arg Leu Lys Gly Leu Cys Lys Ala Gln
 305 310

<210> 1373

<211> 316

<212> PRT

<213> Unknown (H38g290 protein)

<220>

<223> Synthetic construct

<400> 1373

```

Met Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile Leu
      20           25           30
Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
      35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
      65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
      85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
      100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
      115          120          125
Pro Leu His Cys Ser Thr Val Met Asn Pro Arg Ala Cys Tyr Ala Met
      130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
      145          150          155          160
Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
      165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
      180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
      195          200          205
Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys His
      210          215          220
Val Arg Arg Ala Ala Ser Glu Gly Lys Asn Lys Ala Met Ser Thr Cys
      225          230          235          240
Thr Thr Arg Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile Phe
      245          250          255
Ile Tyr Met Cys Pro Phe Arg Ala Leu Pro Ala Asp Lys Met Val Ser
      260          265          270
Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr Thr
      275          280          285
Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ser Arg
      290          295          300
His Val Val Cys Gln Val Asp Phe Ile Ile Arg Asn
      305          310          315

```

<210> 1374

<211> 345

<212> PRT

<213> Unknown (H38g291 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(345)

<223> Xaa = Any Amino Acid

<400> 1374

```

Met His Leu Pro Asn Ser Ser Glu Ile Ala Ile Thr Thr Phe Phe Leu
 1          5          10          15
Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Val Pro
          20          25          30
Ile Cys Leu Met Tyr Leu Val Ala Ile Leu Gly Asn Cys Thr Ile Leu
          35          40          45
Phe Val Ile Arg Thr Glu Pro Ser Leu His Ala Pro Met Tyr Tyr Phe
          50          55          60
Leu Ser Met Leu Ala Val Ser Asp Leu Gly Leu Ser Leu Ser Tyr Leu
65          70          75          80
Pro Thr Met Leu Arg Ile Phe Val Phe Asn Ala Thr Gly Ile Ser Ser
          85          90          95
Asn Ala Arg Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
          100          105          110
Glu Ser Ser Val Leu Leu Val Met Ser Phe Asp Arg Phe Leu Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ile Ser Glu Val Leu Val Ser Cys Ile Leu
130          135          140
Thr Ser Ala Arg Val Ala Lys Met Gly Leu Leu Phe Leu Ile Lys Arg
145          150          155          160
Glu Thr Thr Leu Asn Ser Leu Lys Glu Thr Thr Asn Ser Val Leu Leu
          165          170          175
Val Leu Pro Phe Pro Phe Thr Leu Thr Arg Leu Thr Tyr Cys Arg Lys
          180          185          190
Ser Leu Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Arg Lys Leu
195          200          205
Ala Cys Ser Asp Asn Thr Val Asn Phe Phe Tyr Gly Phe Phe Leu Ala
210          215          220
Leu Cys Met Met Ser Glu Ser Val Phe Ile Thr Val Ser Tyr Val Leu
225          230          235          240
Ile Leu Lys Thr Ile Met Gly Ile Gly Ser His Arg Glu Arg Leu Lys
          245          250          255
Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe Tyr
          260          265          270
Ala Pro Val Ile Ala Leu Ala Ser Met His Cys Phe Ala Ser Met Asn
          275          280          285
Cys Phe Gly Lys His Arg Ser Pro Leu Ala Met Ile Leu Ile Ala Asp
290          295          300
Val Phe Leu Leu Val Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val
305          310          315          320
Lys Thr Gln Gln Ile His Glu Lys Val Leu Gly Lys Leu Gly Leu Gln
          325          330          335
Gln Arg Cys Gln Xaa Thr Trp Tyr Lys
          340          345

```

<210> 1375

<211> 238

<212> PRT

<213> Unknown (H38g292 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(238)

<223> Xaa = Any Amino Acid

<400> 1375

```

Pro Leu Ile Xaa Pro Asp Pro Phe Ile Phe Thr Gln Leu Cys Ser Phe
 1          5          10          15
Leu Asn Lys Tyr Val Ala Ser Thr Arg Leu Asn Asp His Asn Ile Asp

```

	20		25		30										
Gln	Ala	Pro	Xaa	Ser	Arg	Ser	Ile	Ile	Leu	Asn	Leu	Cys	Leu	Ile	Ser
	35		40		45										
Phe	Gly	Ile	Lys	Gly	Met	Trp	Ser	Asn	Val	Asn	Ser	Cys	Phe	Leu	Ser
	50		55		60										
Ser	Leu	Pro	Arg	Glu	Lys	Glu	Leu	Gly	Leu	Lys	Ser	Glu	Gly	Asn	Tyr
65			70		75										80
Ser	Ser	Ala	Thr	Gln	Phe	Cys	Leu	Leu	Gly	Phe	Pro	Gly	Phe	Glu	Glu
			85		90										95
Leu	Pro	His	Phe	Leu	Leu	Val	Asn	Phe	Phe	Phe	His	Leu	Met	Arg	Leu
	100		105		110										
Met	Gly	Asn	Ala	Val	Ile	Tyr	Met	Val	Arg	Ile	Asp	Xaa	Ser	Leu	Gln
	115		120		125										
Ser	Pro	Gly	Asp	Phe	Phe	Leu	Ser	Gln	Leu	Phe	Ile	Phe	Ser	His	Ser
	130		135		140										
Leu	Leu	Met	Asp	Ile	Ser	Ile	Val	Ile	Ala	Ser	Leu	Ile	Gln	Ile	Asp
145			150		155										160
Ser	Tyr	Ser	Ser	Ile	Pro	Ser	Ala	Ser	Gly	Gln	Lys	Lys	Ser	Phe	Ser
			165		170										175
Thr	His	Ala	Ser	His	Phe	Thr	Cys	Val	Gly	Ile	Asp	Tyr	Asp	Ser	Cys
	180		185		190										
Leu	Phe	Leu	Tyr	Val	Lys	Pro	Lys	Gln	Ile	Trp	Ala	Ala	Glu	Xaa	Asn
	195		200		205										
Lys	Val	Val	Phe	Leu	Phe	Ile	Phe	Leu	Leu	Thr	Pro	Phe	Leu	Asn	Leu
	210		215		220										
Leu	Thr	Gly	Gln	Ile	Tyr	Xaa	Pro	Lys	Ser	Val	Leu	Gly	Gly		
225			230		235										

<210> 1376

<211> 311

<212> PRT

<213> Unknown (H38g293 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1376

Pro	Met	Lys	Val	Ala	Asn	Asn	Val	Thr	Glu	Phe	Ile	Phe	Leu	Gly	Leu
1			5					10					15		
Ser	Gln	Asp	Ser	Gly	Met	Gln	Leu	Met	Phe	Phe	Val	Leu	Phe	Leu	Leu
	20		25					30							
Phe	Tyr	Val	Val	Ile	Met	Val	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Met	Val
	35		40					45							
Phe	Ser	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	Asn
	50		55		60										
Leu	Ser	Phe	Val	Asp	Ile	Ala	Cys	Ser	Ser	Ala	Thr	Ala	Pro	Lys	Met
65			70		75										80
Ile	Glu	Asp	Phe	Val	Ser	Glu	Lys	Lys	Thr	Ile	Ser	Tyr	Trp	Gly	Cys
			85		90										95
Ile	Thr	Gln	Met	Phe	Thr	Phe	His	Phe	Phe	Gly	Cys	Ala	Glu	Ile	Phe
	100		105		110										
Val	Leu	Thr	Val	Met	Ala	Phe	Asp	Arg	Tyr	Ala	Ala	Ile	Cys	Gln	Pro
	115		120		125										
Leu	Arg	Tyr	Thr	Val	Ile	Met	Ser	Ala	Asn	Ala	Tyr	Thr	Val	Leu	Ala
	130		135		140										
Ser	Leu	Ser	Trp	Leu	Gly	Ala	Leu	Gly	His	Ser	Phe	Val	Gln	Thr	Leu
145			150		155										160

Leu Thr Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr
 165 170 175
 Phe Cys Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr
 180 185 190
 Leu Val Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly
 195 200 205
 Cys Phe Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu
 210 215 220
 Gln Lys Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile
 245 250 255
 Tyr Arg Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe
 260 265 270
 Tyr Thr Thr Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Glu Glu Val Lys Asn Ala Met Arg Arg Leu Trp Ser Ser Lys Ile
 290 295 300
 Ser Leu Lys Glu Lys Gln Arg
 305 310

<210> 1377

<211> 323

<212> PRT

<213> Unknown (H38g294 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1377

Met Glu Ile Leu Ser Asn Ser Thr Ser Lys Phe Pro Thr Phe Leu Leu
 1 5 10 15
 Thr Gly Ile Pro Gly Leu Glu Ser Ala His Val Trp Ile Ser Ile Pro
 20 25 30
 Phe Cys Cys Phe Tyr Ala Ile Ala Leu Ser Gly Asn Ser Val Ile Leu
 35 40 45
 Phe Val Ile Ile Thr Gln Gln Ser Leu His Glu Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ser Ala Thr Asp Leu Gly Leu Thr Val Ser Ser Leu
 65 70 75 80
 Ser Thr Thr Leu Gly Ile Leu Trp Phe Glu Ala Arg Glu Ile Ser Leu
 85 90 95
 Tyr Ser Cys Ile Val Gln Met Phe Phe Leu His Gly Phe Thr Phe Met
 100 105 110
 Glu Ser Gly Val Leu Val Ala Thr Ala Phe Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asp Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ser Arg Ile Ile
 130 135 140
 Gln Met Gly Leu Leu Met Ile Thr Arg Ala Ile Val Leu Ile Leu Pro
 145 150 155 160
 Leu Leu Leu Leu Leu Lys Pro Leu Tyr Phe Cys Arg Met Asn Ala Leu
 165 170 175
 Ser His Ser Tyr Cys Tyr His Pro Asp Val Ile Gln Leu Ala Cys Ser
 180 185 190
 Asp Ile Arg Ala Asn Ser Ile Cys Gly Leu Ile Asp Leu Ile Leu Thr
 195 200 205
 Thr Gly Ile Asp Thr Pro Cys Ile Val Leu Ser Tyr Ile Leu Ile Ile

```

      210              215              220
Arg Phe Val Leu Arg Ile Ala Ser Pro Glu Glu Trp His Lys Val Phe
225              230              235              240
Ser Thr Cys Val Ser His Val Gly Ala Val Ala Phe Phe Tyr Ile His
      245              250              255
Met Leu Ser Leu Ser Leu Val Tyr Arg Tyr Gly Arg Ser Ala Pro Arg
      260              265              270
Val Val His Ser Val Met Ala Asn Val Tyr Leu Leu Leu Pro Pro Val
      275              280              285
Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg Lys Ala
      290              295              300
Met Leu Ser Leu Leu Leu Thr Lys Xaa Thr Asp Ile Val Leu Phe Asp
305              310              315              320
Thr Asn Leu

```

<210> 1378

<211> 321

<212> PRT

<213> Unknown (H38g295 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1378

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Leu Leu Ser
      20              25              30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35              40              45
Ile Leu Ala Val Cys Ser Asp Ser Pro Leu His Thr Pro Arg Tyr Phe
      50              55              60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
      65              70              75              80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Thr Ser
      85              90              95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100              105              110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115              120              125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130              135              140
Val Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
      145              150              155              160
His Ser Trp Ile Val Leu Gln Phe Thr Ile Val Xaa Asn Leu Glu Ile
      165              170              175
Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser
      180              185              190
Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe
      195              200              205
Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile Ile
      210              215              220
Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe
      225              230              235              240
Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly Thr
      245              250              255

```

Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Gln Pro Pro Arg Asn
 260 265 270
 Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro M t Leu Asn
 275 280 285
 Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asn Ile Gln Ser Ala Leu Trp
 290 295 300
 Arg Leu His Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe
 305 310 315 320
 Ser

<210> 1379

<211> 325

<212> PRT

<213> Unknown (H38g296 protein)

<220>

<223> Synthetic construct

<400> 1379

Met Ala Ile Phe Asn Asn Thr Thr Ser Ser Ser Ser Asn Phe Leu Leu
 1 5 10 15
 Thr Ala Phe Pro Gly Leu Glu Cys Ala His Val Trp Ile Ser Ile Pro
 20 25 30
 Val Cys Cys Leu Tyr Thr Ile Ala Leu Leu Gly Asn Ser Met Ile Phe
 35 40 45
 Leu Val Ile Ile Thr Lys Arg Arg Leu His Lys Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Ala Val Asp Leu Cys Leu Thr Ile Thr Thr Leu
 65 70 75 80
 Pro Thr Val Leu Gly Val Leu Trp Phe His Ala Arg Glu Ile Ser Phe
 85 90 95
 Lys Ala Cys Phe Ile Gln Met Phe Phe Val His Ala Phe Ser Leu Leu
 100 105 110
 Glu Ser Ser Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Asn Tyr Ala Thr Ile Leu Thr Asp Arg Met Val Leu
 130 135 140
 Val Ile Gly Leu Val Ile Cys Ile Arg Pro Ala Val Phe Leu Leu Pro
 145 150 155 160
 Leu Leu Val Ala Ile Asn Thr Val Ser Phe His Gly Gly His Glu Leu
 165 170 175
 Ser His Pro Phe Cys Tyr His Pro Glu Val Ile Lys Tyr Thr Tyr Ser
 180 185 190
 Lys Pro Trp Ile Ser Ser Phe Trp Gly Leu Phe Leu Gln Leu Tyr Leu
 195 200 205
 Asn Gly Thr Asp Val Leu Phe Ile Leu Phe Ser Tyr Val Leu Ile Leu
 210 215 220
 Arg Thr Val Leu Gly Ile Val Ala Arg Lys Lys Gln Gln Lys Ala Leu
 225 230 235 240
 Ser Thr Cys Val Cys His Ile Cys Ala Val Thr Ile Phe Tyr Val Pro
 245 250 255
 Leu Ile Ser Leu Ser Leu Ala His Arg Leu Phe His Ser Thr Pro Arg
 260 265 270
 Val Leu Cys Ser Thr Leu Ala Asn Ile Tyr Leu Leu Leu Pro Pro Val
 275 280 285
 Leu Asn Pro Ile Ile Tyr Ser Leu Lys Thr Lys Thr Ile Arg Gln Ala
 290 295 300
 Met Phe Gln Leu Leu Gln Ser Lys Gly Ser Trp Gly Phe Asn Val Arg
 305 310 315 320
 Gly Leu Arg Gly Arg

325

<210> 1380
 <211> 315
 <212> PRT
 <213> Unknown (H38g297 protein)

<220>
 <223> Synthetic construct

<400> 1380
 Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1 5 10 15
 Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val
 20 25 30
 Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
 35 40 45
 Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
 65 70 75 80
 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
 85 90 95
 Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
 100 105 110
 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
 115 120 125
 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
 130 135 140
 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
 145 150 155 160
 Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
 165 170 175
 His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp
 180 185 190
 Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
 195 200 205
 Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala Arg Ile Leu Gly
 210 215 220
 Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
 225 230 235 240
 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
 245 250 255
 Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
 260 265 270
 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys
 290 295 300
 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
 305 310 315

<210> 1381
 <211> 323
 <212> PRT
 <213> Unknown (H38g298 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1381

```

Met Ser Pro Leu Asn Gln Thr Thr Glu Asn His Gln Ser Phe Phe Thr
 1          5          10          15
Leu Thr Gly Ile Pro Gly Met Pro Glu Lys Asp Leu Trp Met Ala Leu
 20          25          30
Pro Leu Cys Leu Leu Tyr Ser Thr Thr Ile Leu Gly Asn Val Thr Ile
 35          40          45
Leu Val Val Ile Lys Val Glu Gln Ser Leu His Glu Pro Met Tyr Tyr
 50          55          60
Phe Leu Ala Met Leu Ala Ala Thr Asp Leu Ser Leu Ser Leu Ser Ser
 65          70          75          80
Met Pro Thr Met Val Ser Val His Trp Phe Asn Trp Arg Ser Ile Thr
 85          90          95
Phe Asn Gly Cys Leu Ile Gln Met Phe Phe Ile His Thr Phe Gly Gly
100          105          110
Val Glu Ser Gly Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala
115          120          125
Ile Arg Phe Pro Leu His Tyr Ala Thr Ile Leu Thr His Ser Val Ile
130          135          140
Ser Lys Ile Ala Ala Ala Ile Leu Leu Arg Ser Val Gly Ala Val Leu
145          150          155          160
Pro Val Pro Phe Leu Ile Lys Arg Leu Pro Phe Cys His Ser Asn Val
165          170          175
Leu Ser His Ala Tyr Cys Leu His Gln Asp Ala Met Arg Leu Ala Cys
180          185          190
Ala Asp Thr Gly Val Asn Ser Ile Tyr Gly Leu Leu Ala Val Ile Phe
195          200          205
Ile Ile Val Leu Asp Ala Leu Ile Leu Leu Ala Ser Tyr Ile Leu Ile
210          215          220
Leu Gln Ala Val Leu Ser Ile Ala Ser Gln Glu Asp Arg Leu Lys Ala
225          230          235          240
Leu Asn Thr Cys Leu Ser His Met Ser Ala Val Leu Leu Phe Tyr Val
245          250          255
Pro Leu Ile Gly Met Thr Leu Ile His Arg Tyr Gly Lys His Leu Ser
260          265          270
Pro Leu Ile His Thr Phe Met Ala Asn Ile Tyr Leu Leu Pro Pro
275          280          285
Val Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Xaa Xaa
290          295          300
Gln Ile Val Gln Ala Phe Cys Gly Ala Arg Val Ser Pro Xaa Trp His
305          310          315          320
Leu Leu Phe

```

<210> 1382

<211> 312

<212> PRT

<213> Unknown (H38g299 protein)

<220>

<223> Synthetic construct

<400> 1382

```

Met Ser Val Leu Asn Asn Ser Glu Val Lys Leu Phe Leu Leu Ile Gly
 1          5          10          15
Ile Pro Gly Leu Glu His Ala His Ile Trp Phe Ser Ile Pro Ile Cys
 20          25          30
Leu Met Tyr Leu Leu Ala Ile Met Gly Asn Cys Thr Ile Leu Phe Ile

```

```

      35              40              45
Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala
  50              55              60
M t Leu Ala Val Ser Asp Met Gly Leu Ser Leu Ser Ser Leu Pro Thr
  65              70              75              80
Met Leu Arg Val Phe Leu Phe Asn Ala Met Gly Ile Ser Pro Asn Ala
      85              90              95
Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Val Met Glu Ser
      100              105              110
Ser Val Leu Leu Ile Met Ser Leu Asp Arg Phe Leu Ala Ile His Asn
      115              120              125
Pro Leu Arg Tyr Ser Ser Ile Leu Thr Ser Asn Arg Val Ala Lys Met
      130              135              140
Gly Leu Ile Leu Ala Ile Arg Ser Ile Leu Leu Val Ile Pro Phe Pro
  145              150              155              160
Phe Thr Leu Arg Arg Leu Lys Tyr Cys Gln Lys Asn Leu Leu Ser His
      165              170              175
Ser Tyr Cys Leu His Gln Asp Thr Met Lys Leu Ala Cys Ser Asp Asn
      180              185              190
Lys Thr Asn Val Ile Tyr Gly Phe Phe Ile Ala Leu Cys Thr Met Leu
      195              200              205
Asp Leu Ala Leu Ile Val Leu Ser Tyr Val Leu Ile Leu Lys Thr Ile
      210              215              220
Leu Ser Ile Ala Ser Leu Ala Glu Arg Leu Lys Ala Leu Asn Thr Cys
  225              230              235              240
Val Ser His Ile Cys Ala Val Leu Thr Phe Tyr Val Pro Ile Ile Thr
      245              250              255
Leu Ala Ala Met His His Phe Ala Lys His Lys Ser Pro Leu Val Val
      260              265              270
Ile Leu Ile Ala Asp Met Phe Leu Leu Val Pro Pro Leu Met Asn Pro
      275              280              285
Ile Val Tyr Cys Val Lys Thr Arg Gln Ile Trp Glu Lys Ile Leu Gly
      290              295              300
Lys Leu Leu Asn Val Cys Gly Arg
  305              310

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<210> 1383

<211> 308

<212> PRT

<213> Unknown (H38g300 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 1383

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Met Lys Ile Asn Asp Ser Ser Gly Glu Asp Phe Ile Leu Val Gly Phe
  1              5              10              15
Ser Glu Tyr Pro Gln Ala Glu Phe Ile Leu Ser Leu Phe Val Ser Gly
      20              25              30
Phe Tyr Thr Met Thr Phe Thr Gly Asn Thr Ala Ile Ile Leu Val Ser
      35              40              45
Leu Leu Asp Tyr Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Arg Lys
      50              55              60
Leu Ser Phe Leu Asp Met Cys Phe Thr Thr Cys Ile Val Leu Gln Met
  65              70              75              80
Leu Val Asn Ile Trp Gly Glu Ser Lys Lys Val Ser Tyr Val Gly Cys
      85              90              95

```

Met Val Gln Tyr Ser Val Ala Leu Ala Leu Gly Ser Thr Glu Cys Val
 100 105 110
 Leu Leu Ala Ile Met Ala Val Asp Arg Tyr Val Ala Val Arg Trp Pro
 115 120 125
 Leu His Tyr Val Thr Ile Met His Gln Gln Ile Cys His Phe Leu Ala
 130 135 140
 Ala Leu Ser Trp Phe Ser Gly Leu Ala Asn Ser Leu Phe His Ser Ser
 145 150 155 160
 Leu Thr Thr Ile Leu Pro Leu Cys Gly His Arg Arg Val Asp His Phe
 165 170 175
 Phe Cys Glu Val Leu Leu Ile Val Lys Leu Ser Cys Val Asp Thr Gly
 180 185 190
 Pro Thr Glu Leu Lys Met Leu Ile Ala Arg Val Ile Ile Leu Ala Leu
 195 200 205
 Pro Val Cys Thr Ile Leu Thr Ser Tyr Ala Cys Ile Ala Arg Ala Val
 210 215 220
 Leu Arg Leu Gln Ser Ala Glu Gly Gln Gln Lys Ala Phe Gly Thr Cys
 225 230 235 240
 Ala Ser His Leu Met Val Val Leu Leu Phe Tyr Gly Thr Ile Met Phe
 245 250 255
 Met Cys Leu Gln Leu Lys Ser Asn Tyr Ser Gln Ile Gln Gly Lys Leu
 260 265 270
 Leu Pro Leu Val Tyr Thr Ile Ala Ala Pro Thr Xaa Asn Pro Leu Ile
 275 280 285
 Tyr Ala Leu Arg Asn Lys Val Val Lys Arg Ala Ile Gly Lys Leu Ile
 290 295 300
 Trp Lys Asp Ser
 305

<210> 1384

<211> 317

<212> PRT

<213> Unknown (H38g301 protein)

<220>

<223> Synthetic construct

<400> 1384

Met Glu Ile Asp Asn Gln Thr Trp Val Arg Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Asp Trp Cys Thr Gln Ile Ser Leu Phe Ser Leu Phe Leu
 20 25 30
 Val Thr Tyr Leu Met Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
 35 40 45
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
 65 70 75 80
 Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
 85 90 95
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg His Val Ala Val Ser Asp
 115 120 125
 Arg Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
 130 135 140
 Ala Ile Thr Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Val Gln Thr
 145 150 155 160
 Ala Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asp His
 165 170 175
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr

180								185				190				
Ser	Ser	Asn	Glu	Ala	Ala	Ile	Met	Val	Ser	Ser	Ile	Val	Leu	Leu	Met	
195								200				205				
Thr	Pro	Phe	Cys	Leu	Val	Leu	Leu	Ser	Tyr	Ile	Arg	Ile	Ile	Ser	Thr	
210								215				220				
Ile	Leu	Lys	Ile	Gln	Ser	Arg	Glu	Gly	Arg	Lys	Lys	Ala	Phe	His	Thr	
225								230				235				
Cys	Ala	Ser	His	Leu	Thr	Val	Val	Ala	Leu	Cys	Tyr	Gly	Thr	Thr	Ile	
245								250				255				
Phe	Thr	Tyr	Ile	Gln	Pro	His	Ser	Gly	Pro	Ser	Val	Leu	Gln	Glu	Lys	
260								265				270				
Leu	Ile	Ser	Val	Phe	Tyr	Ala	Ile	Val	Met	Pro	Leu	Leu	Asn	Pro	Val	
275								280				285				
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Gly	Ala	Trp	His	Lys	Leu	
290								295				300				
Leu	Glu	Lys	Phe	Ser	Gly	Leu	Thr	Ser	Lys	Leu	Gly	Thr				
305								310				315				

<210> 1385

<211> 306

<212> PRT

<213> Unknown (H38g302 protein)

<220>

<223> Synthetic construct

<400> 1385

Met 1	Glu	Gly	Lys	Asn 5	Gln	Thr	Asn	Ile	Ser 10	Glu	Phe	Leu	Leu	Leu 15	Gly
Phe	Ser	Ser	Trp	Gln	Gln	Gln	Gln	Val	Leu	Leu	Phe	Ala	Leu	Phe	Leu
			20					25					30		
Cys	Leu	Tyr	Leu	Thr	Gly	Leu	Phe	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Ala
		35					40					45			
Ile	Gly	Ser	Asp	His	Cys	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala
	50					55					60				
Asn	Leu	Ser	Leu	Val	Asp	Leu	Cys	Leu	Pro	Ser	Ala	Thr	Val	Pro	Lys
65				70					75					80	
Met	Leu	Leu	Asn	Ile	Gln	Thr	Gln	Thr	Gln	Thr	Ile	Ser	Tyr	Pro	Gly
			85						90					95	
Cys	Leu	Ala	Gln	Met	Tyr	Phe	Cys	Met	Met	Phe	Ala	Asn	Met	Asp	Asn
			100					105					110		
Phe	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His
		115					120					125			
Pro	Leu	His	Tyr	Ser	Thr	Ile	Met	Ala	Leu	Arg	Leu	Cys	Ala	Ser	Leu
	130					135					140				
Val	Ala	Ala	Pro	Trp	Val	Ile	Ala	Ile	Leu	Asn	Pro	Leu	Leu	His	Thr
145				150					155					160	
Leu	Met	Met	Ala	His	Leu	His	Phe	Cys	Ser	Asp	Asn	Val	Ile	His	His
			165					170					175		
Phe	Phe	Cys	Asp	Ile	Asn	Ser	Leu	Leu	Pro	Leu	Ser	Cys	Ser	Asp	Thr
		180						185				190			
Ser	Leu	Asn	Gln	Leu	Ser	Val	Leu	Ala	Thr	Val	Gly	Leu	Ile	Phe	Val
		195					200					205			
Val	Pro	Ser	Val	Cys	Ile	Leu	Val	Ser	Tyr	Ile	Leu	Ile	Val	Ser	Ala
	210					215					220				
Val	Met	Lys	Val	Pro	Ser	Ala	Gln	Gly	Lys	Leu	Lys	Ala	Phe	Ser	Thr
225				230					235					240	
Cys	Gly	Ser	His	Leu	Ala	Leu	Val	Ile	Leu	Phe	Tyr	Gly	Ala	Asn	Thr
			245						250				255		
Gly	Val	Tyr	Met	Ser	Pro	Leu	Ser	Asn	His	Ser	Thr	Glu	Lys	Asp	Ser
		260						265				270			

Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr
 290 295 300
 Leu Ser
 305

<210> 1386

<211> 311

<212> PRT

<213> Unknown (H38g303 protein)

<220>

<223> Synthetic construct

<400> 1386

Met Gly Pro Arg Asn Gln Thr Ala Val Ser Glu Phe Leu Leu Met Lys
 1 5 10 15
 Val Thr Glu Asp Pro Glu Leu Lys Leu Ile Pro Phe Ser Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala
 35 40 45
 Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe
 50 55 60
 Asn Leu Ser Phe Thr Asp Ile Cys Leu Thr Thr Thr Thr Val Pro Lys
 65 70 75 80
 Ile Leu Val Asn Ile Gln Ala Gln Asn Gln Ser Ile Thr Tyr Thr Gly
 85 90 95
 Cys Leu Thr Gln Ile Cys Leu Val Leu Val Phe Ala Gly Leu Glu Ser
 100 105 110
 Cys Phe Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Thr Val Leu Met Asn Val His Phe Trp Gly Leu Leu
 130 135 140
 Ile Leu Leu Ser Met Phe Met Ser Thr Met Asp Ala Leu Val Gln Ser
 145 150 155 160
 Leu Met Val Leu Gln Leu Ser Phe Cys Lys Asn Val Glu Ile Pro Leu
 165 170 175
 Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser Ser Val Phe Gly Ala
 195 200 205
 Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser Gln Ile Val Thr Ser
 210 215 220
 Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe Tyr Gly Thr Ala Phe
 245 250 255
 Gly Val Tyr Ile Ser Ser Ala Val Ala Glu Ser Ser Arg Ile Thr Ala
 260 265 270
 Val Ala Ser Val Met Tyr Thr Val Val Pro Gln Met Met Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Lys Ala Leu Arg Lys Leu
 290 295 300
 Ile Gly Arg Leu Phe Pro Phe
 305 310

<210> 1387

<211> 313

<212> PRT

<213> Unknown (H38g304 protein)

<220>

<223> Synthetic construct

<400> 1387

```

Met Glu Ala Arg Asn Gln Thr Ala Ile Ser Lys Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ile Glu Asp Pro Glu Leu Gln Pro Val Leu Phe Ser Leu Phe Leu
      20           25           30
Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala
      35           40           45
Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50           55           60
Asn Leu Ser Phe Leu Asp Ile Cys Leu Ser Thr Thr Thr Ile Pro Lys
65           70           75           80
Met Leu Val Asn Ile Gln Ala Gln Asn Arg Ser Ile Thr Tyr Ser Gly
      85           90           95
Cys Leu Thr Gln Ile Cys Phe Val Leu Phe Phe Ala Gly Leu Glu Asn
      100          105          110
Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu Arg Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu
      130          135          140
Ile Leu Leu Ser Leu Leu Thr Ser Val Val Asn Ala Leu Leu Leu Ser
145          150          155          160
Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Leu
      165          170          175
Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu Thr Cys Ser Asp Thr
      180          185          190
Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala Cys Ile Phe Gly Gly
      195          200          205
Val Pro Leu Ser Gly Ile Ile Leu Ser Tyr Thr Gln Ile Thr Ser Cys
      210          215          220
Val Leu Arg Met Pro Ser Ala Ser Gly Lys His Lys Ala Val Ser Thr
225          230          235          240
Cys Gly Ser His Leu Ser Ile Val Leu Leu Phe Tyr Gly Ala Gly Leu
      245          250          255
Gly Val Tyr Ile Ser Ser Val Val Thr Asp Ser Pro Arg Lys Ala Ala
      260          265          270
Val Ala Ser Val Met Tyr Ser Val Phe Pro Gln Met Val Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Thr Leu Arg Lys Phe
      290          295          300
Ile Gly Arg Ile Pro Ser Leu Leu Trp
305          310

```

<210> 1388

<211> 313

<212> PRT

<213> Unknown (H38g305 protein)

<220>

<223> Synthetic construct

<400> 1388

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Met Glu Pro Arg Asn Gln Thr Ser Ala Ser Gln Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Glu Lys Pro Glu Gln Glu Thr Leu Leu Phe Ser Leu Phe Phe
      20           25           30
Cys Met Tyr Leu Val Met Val Val Gly Asn Leu Leu Ile Ile Leu Ala
      35           40           45

```

Ile Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Phe Cys Leu Ala Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Ser Leu Gln Thr Gly Ser Lys Ala Ile Ser Tyr Pro Cys
 85 90 95
 Cys Leu Ile Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser
 100 105 110
 Val Ile Ile Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Ala Lys Ile Met Ser Leu Arg Leu Cys Arg Leu Leu
 130 135 140
 Val Gly Ala Leu Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile
 145 150 155 160
 Leu Leu Met Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His
 165 170 175
 Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr
 180 185 190
 Ser Val Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala
 195 200 205
 Thr Pro Phe Val Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Val Ala
 210 215 220
 Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile
 245 250 255
 Gly Val Tyr Leu Cys Pro Ser Ser Val Leu Thr Thr Val Lys Glu Lys
 260 265 270
 Ala Ser Ala Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Leu Lys Gly Ala Leu Arg Lys Leu
 290 295 300
 Val Asn Arg Lys Ile Thr Ser Ser Ser
 305 310

<210> 1389

<211> 98

<212> PRT

<213> Unknown (H38g306 protein)

<220>

<223> Synthetic construct

<400> 1389

Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu
 1 5 10 15
 Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
 20 25 30
 Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu
 35 40 45
 Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe Leu
 50 55 60
 Ala Met Leu Ala Ala Ile Asp Gln Leu Ser Ile Ser Ser Ala Leu Pro
 65 70 75 80
 Pro Gly Gln Thr Val Phe Trp Phe Thr Asp Gln Lys Asn Lys Pro Phe
 85 90 95
 Ala Gly

<210> 1390

<211> 320

<212> PRT

<213> Unknown (H38g307 protein)

<220>

<223> Synthetic construct

<400> 1390

```

Met Pro Ser Ala Ser Ala Met Ile Ile Phe Asn Leu Ser Ser Tyr Asn
1           5           10           15
Pro Gly Pro Phe Ile Leu Val Gly Ile Pro Gly Leu Glu Gln Phe His
20           25           30
Val Trp Ile Gly Ile Pro Phe Cys Ile Ile Tyr Ile Val Ala Val Val
35           40           45
Gly Asn Cys Ile Leu Leu Tyr Leu Ile Val Val Glu His Ser Leu His
50           55           60
Glu Pro Met Phe Phe Phe Leu Ser Met Leu Ala Met Thr Asp Leu Ile
65           70           75           80
Leu Ser Thr Ala Gly Val Pro Lys Ala Leu Ser Ile Phe Trp Leu Gly
85           90           95
Ala Arg Glu Ile Thr Phe Pro Gly Cys Leu Thr Gln Met Phe Phe Leu
100          105          110
His Tyr Asn Phe Val Leu Asp Ser Ala Ile Leu Met Ala Met Ala Phe
115          120          125
Asp His Tyr Val Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr Ile Leu
130          135          140
Thr Pro Lys Thr Ile Ile Lys Ser Ala Met Gly Ile Ser Phe Arg Ser
145          150          155          160
Phe Cys Ile Ile Leu Pro Asp Val Phe Leu Leu Thr Cys Leu Pro Phe
165          170          175
Cys Arg Thr Arg Ile Ile Pro His Thr Tyr Cys Glu His Ile Gly Val
180          185          190
Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Phe Trp Tyr Gly Phe
195          200          205
Cys Val Pro Ile Met Thr Val Ile Ser Asp Val Ile Leu Ile Ala Val
210          215          220
Ser Tyr Ala His Ile Leu Cys Ala Val Phe Gly Leu Pro Ser Gln Glu
225          230          235          240
Ala Cys Gln Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys Val Ile
245          250          255
Leu Met Phe Tyr Thr Pro Ala Phe Phe Ser Ile Leu Ala His Arg Phe
260          265          270
Gly His Asn Val Ser Arg Thr Phe His Ile Met Phe Ala Asn Leu Tyr
275          280          285
Ile Val Ile Pro Pro Ala Leu Asn Pro Met Val Tyr Gly Val Lys Thr
290          295          300
Lys Gln Ile Arg Asp Lys Val Ile Leu Leu Phe Ser Lys Gly Thr Gly
305          310          315          320

```

<210> 1391

<211> 312

<212> PRT

<213> Unknown (H38g308 protein)

<220>

<223> Synthetic construct

<400> 1391

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Met Ser Gly Thr Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
1           5           10           15
Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu
20           25           30

```

Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ser
 35 40 45
 Val Ser Ile Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Ala Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn
 100 105 110
 Phe Leu Leu Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His
 115 120 125
 Pro Leu His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu
 130 135 140
 Val Ala Gly Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His
 165 170 175
 Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
 180 185 190
 His Leu Asn Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile
 195 200 205
 Thr Pro Phe Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr
 210 215 220
 Val Leu Lys Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile
 245 250 255
 Ala Val Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr
 260 265 270
 Met Ala Thr Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Leu Lys Gly Ala Leu Lys Lys Val
 290 295 300
 Val Gly Arg Val Val Phe Ser Val
 305 310

<210> 1392

<211> 254

<212> PRT

<213> Unknown (H38g309 protein)

<220>

<223> Synthetic construct

<400> 1392

Met Tyr Phe Phe Leu Arg Gln Leu Ser Val Val Glu Leu Phe Tyr Thr
 1 5 10 15
 Thr Asp Ile Val Pro Arg Thr Leu Ala Asn Leu Gly Ser Pro His Pro
 20 25 30
 Gln Ala Ile Ser Phe Gln Gly Cys Ala Ala His Met Tyr Val Phe Ile
 35 40 45
 Val Leu Gly Ile Ser Glu Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp
 50 55 60
 Arg Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser
 65 70 75 80
 Pro Arg Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile
 85 90 95
 Ile Thr Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg
 100 105 110
 Ser His Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu

```

      115              120              125
Arg Leu Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr
 130              135              140
Ala Thr Ile Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser
145              150              155              160
Tyr Ile Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser
      165              170              175
Arg Arg Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser
      180              185              190
Leu Phe Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly
      195              200              205
Ser Ser Val Thr Thr Asp Arg Val Leu Ser Leu Phe Tyr Thr Val Ile
      210              215              220
Thr Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Val
225              230              235              240
Arg Arg Ala Leu Arg His Leu Val Lys Arg Gln Arg Pro Ser
      245              250

```

<210> 1393

<211> 333

<212> PRT

<213> Unknown (H38g310 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1393

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Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1              5              10              15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
      20              25              30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
      35              40              45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Val
      50              55              60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
65              70              75              80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
      85              90              95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
      100              105              110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
      115              120              125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
      130              135              140
Leu Ala Val Ala Trp Thr Leu Val Val Ser His Ser Leu Phe Gln Leu
145              150              155              160
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
      165              170              175
Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr
      180              185              190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
      195              200              205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr
      210              215              220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
225              230              235              240

```

Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
 245 250 255
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
 290 295 300
 Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
 305 310 315 320
 Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
 325 330

<210> 1394

<211> 311

<212> PRT

<213> Unknown (H38g311 protein)

<220>

<223> Synthetic construct

<400> 1394

Met Glu Glu Tyr Asn Thr Ser Ser Thr Asp Phe Thr Phe Met Gly Leu
 1 5 10 15
 Phe Asn Arg Lys Glu Thr Ser Gly Leu Ile Phe Ala Ile Ile Ser Ile
 20 25 30
 Ile Phe Phe Thr Ala Leu Met Ala Asn Gly Val Met Ile Phe Leu Ile
 35 40 45
 Gln Thr Asp Leu Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser His
 50 55 60
 Leu Ser Leu Ile Asp Met Met Tyr Ile Ser Thr Ile Val Pro Lys Met
 65 70 75 80
 Leu Val Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly Cys
 85 90 95
 Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe Phe
 100 105 110
 Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115 120 125
 Leu Arg Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile Ile
 130 135 140
 Ala Gly Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr Pro
 145 150 155 160
 Ile Thr Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His Phe
 165 170 175
 Phe Cys Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Ala
 180 185 190
 Leu Tyr Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu Ile
 195 200 205
 Pro Phe Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr Val
 210 215 220
 Gln Cys Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys
 225 230 235 240
 Ser Ser His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr
 245 250 255
 Thr Tyr Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys Val
 260 265 270
 Leu Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Lys Arg Ala Leu
 290 295 300
 Gly Arg Phe Lys Gly Pro Gln

305

310

<210> 1395

<211> 295

<212> PRT

<213> Unknown (H38g312 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(295)

<223> Xaa = Any Amino Acid

<400> 1395

```

Ile Gln Cys Lys Gly Xaa Xaa Lys Xaa Ile Lys Thr Phe Ser Val Thr
 1           5           10           15
Pro Ile Leu Asn Gly Asn Arg Glu Ile Ala Arg Phe Leu Ser Asn Leu
      20           25           30
Ser Leu Ala Gly Ile Gly Phe Pro Ser Thr Ile Val Ser Lys Met Ile
      35           40           45
Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu
      50           55           60
Thr Gln Val Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu
65           70           75           80
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Asp Ile Cys His Pro Leu
      85           90           95
Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
      100          105          110
Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile
      115          120          125
Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe
      130          135          140
Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr
145          150          155          160
Asn Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro
      165          170          175
Ile Ser Gly Thr Phe Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
      180          185          190
Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly
      195          200          205
Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Gly Phe Gly Gly
      210          215          220
Asp Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala
225          230          235          240
Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
      245          250          255
Ser Arg Asn Arg Glu Ile Lys Ser Ala Leu Arg Gln Leu His Cys Arg
      260          265          270
Ile Val Xaa Ser His Phe Leu Ile Ile Cys Ser Ile Pro Ser Val Val
      275          280          285
Xaa Val Arg Lys Gly Ser Lys
      290          295

```

<210> 1396

<211> 314

<212> PRT

<213> Unknown (H38g313 protein)

<220>

<223> Synthetic construct

<400> 1396

```

Met Thr Leu Gly Ser Leu Gly Asn Ser Ser Ser Val Ser Ala Thr
 1              5              10              15
Phe Leu Leu Ser Gly Ile Pro Gly Leu Glu Arg Met His Ile Trp Ile
      20              25              30
Ser Ile Pro Leu Cys Phe Met Tyr Leu Val Ser Ile Pro Gly Asn Cys
      35              40              45
Thr Ile Leu Phe Ile Ile Lys Thr Glu Arg Ser Leu His Glu Pro Met
      50              55              60
Tyr Leu Phe Leu Ser Met Leu Ala Leu Ile Asp Leu Gly Leu Ser Leu
65              70              75              80
Cys Thr Leu Pro Thr Val Leu Gly Ile Phe Trp Val Gly Ala Arg Glu
      85              90              95
Ile Ser His Asp Ala Cys Phe Ala Gln Leu Phe Phe Ile His Cys Phe
      100              105              110
Ser Phe Leu Glu Ser Ser Val Leu Leu Ser Met Ala Phe Asp Arg Phe
      115              120              125
Val Ala Ile Cys His Pro Leu His Tyr Val Ser Ile Leu Thr Asn Thr
      130              135              140
Val Ile Gly Arg Ile Gly Leu Val Ser Leu Gly Arg Ser Val Ala Leu
145              150              155              160
Ile Phe Pro Leu Pro Phe Met Leu Lys Arg Phe Pro Tyr Cys Gly Ser
      165              170              175
Pro Val Leu Ser His Ser Tyr Cys Leu His Gln Glu Val Met Lys Leu
      180              185              190
Ala Cys Ala Asp Met Lys Ala Asn Ser Ile Tyr Gly Met Phe Val Ile
      195              200              205
Val Ser Thr Val Gly Ile Asp Ser Leu Leu Ile Leu Phe Ser Tyr Ala
      210              215              220
Leu Ile Leu Arg Thr Val Leu Ser Ile Ala Ser Arg Ala Glu Arg Phe
225              230              235              240
Lys Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Leu Phe
      245              250              255
Tyr Thr Pro Met Ile Gly Leu Ser Val Ile His Arg Phe Gly Lys Gln
      260              265              270
Ala Pro His Leu Val Gln Val Val Met Gly Phe Met Tyr Leu Leu Phe
      275              280              285
Pro Pro Val Met Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
      290              295              300
Arg Asp Arg Val Thr His Ala Phe Cys Tyr
305              310

```

<210> 1397

<211> 330

<212> PRT

<213> Unknown (H38g314 protein)

<220>

<223> Synthetic construct

<400> 1397

```

Met Gly Leu Phe Arg Gln Ser Lys His Pro Met Ala Asn Ile Thr Trp
 1              5              10              15
Met Ala Asn His Thr Gly Trp Ser Asp Phe Ile Leu Leu Gly Leu Phe
      20              25              30
Arg Gln Ser Lys His Pro Ala Leu Cys Val Val Ile Phe Val Val
      35              40              45
Phe Leu Met Ala Leu Ser Gly Asn Ala Val Leu Ile Leu Leu Ile His
      50              55              60
Cys Asp Ala His Leu His Thr Pro Met Tyr Phe Phe Ile Ser Gln Leu

```

```

65          70          75          80
Ser Leu Met Asp Met Ala Tyr Ile Ser Val Thr Val Pro Lys Met Leu
          85          90
Leu Asp Gln Val Met Gly Val Asn Lys Ile Ser Ala Pro Glu Cys Gly
          100          105          110
Met Gln Met Phe Phe Tyr Val Thr Leu Ala Gly Ser Glu Phe Phe Leu
          115          120          125
Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
          130          135          140
Arg Tyr Pro Val Leu Met Asn His Arg Val Cys Leu Phe Leu Ser Ser
          145          150          155          160
Gly Cys Trp Phe Leu Gly Ser Val Asp Gly Phe Thr Phe Thr Pro Ile
          165          170          175
Thr Met Thr Phe Pro Phe Arg Gly Ser Arg Glu Ile His His Phe Phe
          180          185          190
Cys Glu Val Pro Ala Val Leu Asn Leu Ser Cys Ser Asp Thr Ser Leu
          195          200          205
Tyr Glu Ile Phe Met Tyr Leu Cys Cys Val Leu Met Leu Leu Ile Pro
          210          215          220
Val Val Ile Ile Ser Ser Ser Tyr Leu Leu Ile Leu Leu Thr Ile His
          225          230          235          240
Gly Met Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys Ser
          245          250          255
Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ala Ala Ile Tyr Thr
          260          265          270
Tyr Met Leu Pro Ser Ser Tyr His Thr Pro Glu Lys Asp Met Met Val
          275          280          285
Ser Val Phe Tyr Thr Ile Leu Thr Pro Val Val Asn Pro Leu Ile Tyr
          290          295          300
Ser Leu Arg Asn Lys Asp Val Met Gly Ala Leu Lys Lys Met Leu Thr
          305          310          315          320
Val Glu Pro Ala Phe Gln Lys Ala Met Glu
          325          330

```

<210> 1398

<211> 197

<212> PRT

<213> Unknown (H38g315 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(197)

<223> Xaa = Any Amino Acid

<400> 1398

```

Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn Pro Leu Leu
1          5          10          15
Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu Ala Ile Gly
          20          25          30
Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr Thr Asn Thr
          35          40          45
Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe Phe Cys Asp
          50          55          60
Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr Met His Asp
65          70          75          80
Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile Cys Leu Leu
          85          90          95
Ser Val Leu Leu Ser Tyr Val Phe Ile Met Ala Ala Ile Leu Arg Thr
          100          105          110

```

Gly Ser Val Glu Gly Arg Arg Arg Gly Phe Ser Thr Cys Ala Ser His
 115 120 125
 Leu Thr Val Val Thr Met Tyr His Gly Thr Leu Ile Phe Ile Tyr Leu
 130 135 140
 Arg Pro Ser Thr Gly His Ser Leu Asp Ile Asp Lys Val Thr Ser Val
 145 150 155 160
 Phe Tyr Thr Leu Ile Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
 165 170 175
 Arg Asn Lys Asp Val Lys Asn Ala Phe Arg Lys Val Ile Gly Arg Lys
 180 185 190
 Leu Leu Pro Xaa Gly
 195

<210> 1399

<211> 313

<212> PRT

<213> Unknown (H38g316 protein)

<220>

<223> Synthetic construct

<400> 1399

Met Met Thr Leu Lys Asn Cys Thr Val Phe Thr Asp Phe Ile Phe Leu
 1 5 10 15
 Gly Leu Ser Gly Thr Gln Asp Ile Gln Gln Gly Leu Phe Val Leu Phe
 20 25 30
 Phe Leu Ile Tyr Gly Ile Thr Val Ile Val Asn Leu Gly Met Ile Leu
 35 40 45
 Leu Ile Lys Met Asp Leu Arg Leu His Thr Pro Val Tyr Tyr Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Cys Asp Val Cys Tyr Ser Ser Ser Val Ser Pro
 65 70 75 80
 Arg Met Leu Ala Asp Phe Leu Ser Asp Gln Lys Trp Ile Pro Tyr Asn
 85 90 95
 Leu Cys Ala Ile Gln Met Tyr Leu Phe Gly Val Phe Ala Asp Val Glu
 100 105 110
 Cys Leu Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Thr Ile Thr Met Pro Arg Arg Ile Cys Thr Gln
 130 135 140
 Leu Val Ala Leu Ala Tyr Val Val Gly Leu Val Asp Ser Ala Ile His
 145 150 155 160
 Thr Cys Cys Thr Phe Arg Leu Ser Phe Cys Asn Ser Asn Val Ile Asn
 165 170 175
 His Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Asn Pro Thr Ile
 180 185 190
 Asn Ser Ile Asn Glu Ile Val Met Phe Thr Phe Val Gly Cys Val Ala
 195 200 205
 Gly Cys Ser Ile Val Thr Val Phe Leu Ser Tyr Ser Tyr Ile Ile Ile
 210 215 220
 Thr Ile Leu Lys Met Ser Ser Ala Glu Gly Arg Arg Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Thr Ser His Leu Met Ala Val Ala Val Phe His Gly Thr Leu
 245 250 255
 Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser Met Glu Thr Asp
 260 265 270
 Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Arg Asp Val Lys Gly Ala Leu Lys Lys
 290 295 300
 Ala Ile Ser Thr Lys Leu Tyr Ser Val

305

310

<210> 1400

<211> 323

<212> PRT

<213> Unknown (H38g317 protein)

<220>

<223> Synthetic construct

<400> 1400

```

Met Ser Thr Leu Pro Thr Gln Ile Ala Pro Asn Ser Ser Thr Ser Met
 1          5          10          15
Ala Pro Thr Phe Leu Leu Val Gly Met Pro Gly Leu Ser Gly Ala Pro
 20          25          30
Ser Trp Trp Thr Leu Pro Leu Ile Ala Val Tyr Leu Leu Ser Ala Leu
 35          40          45
Gly Asn Gly Thr Ile Leu Trp Ile Ile Ala Leu Gln Pro Ala Leu His
 50          55          60
Arg Pro Met His Phe Phe Leu Phe Leu Leu Ser Val Ser Asp Ile Gly
 65          70          75          80
Leu Val Thr Ala Leu Met Pro Thr Leu Leu Gly Ile Ala Leu Ala Gly
 85          90          95
Ala His Thr Val Pro Ala Ser Ala Cys Leu Leu Gln Met Val Phe Ile
 100         105         110
His Val Phe Ser Val Met Glu Ser Ser Val Leu Leu Ala Met Ser Ile
 115         120         125
Asp Arg Ala Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Ala Leu Leu
 130         135         140
Thr Asn Gly Val Ile Ser Lys Ile Ser Leu Ala Ile Ser Phe Arg Cys
 145         150         155         160
Leu Gly Leu His Leu Pro Leu Pro Phe Leu Leu Ala Tyr Met Pro Tyr
 165         170         175
Cys Leu Pro Gln Val Leu Thr His Ser Tyr Cys Leu His Pro Asp Val
 180         185         190
Ala Arg Leu Ala Cys Pro Glu Ala Trp Gly Ala Ala Tyr Ser Leu Phe
 195         200         205
Val Val Leu Ser Ala Met Gly Leu Asp Pro Leu Leu Ile Phe Phe Ser
 210         215         220
Tyr Gly Leu Ile Gly Lys Val Leu Gln Gly Val Glu Ser Arg Glu Asp
 225         230         235         240
Arg Trp Lys Ala Gly Gln Thr Cys Ala Ala His Leu Ser Ala Val Leu
 245         250         255
Leu Phe Tyr Ile Pro Met Ile Leu Leu Ala Leu Ile Asn His Pro Glu
 260         265         270
Leu Pro Ile Thr Gln His Thr His Thr Leu Leu Ser Tyr Val His Phe
 275         280         285
Leu Leu Pro Pro Leu Ile Asn Pro Ile Leu Tyr Ser Val Lys Met Lys
 290         295         300
Glu Ile Arg Lys Arg Ile Leu Asn Arg Leu Gln Pro Arg Lys Val Gly
 305         310         315         320
Gly Ala Gln

```

<210> 1401

<211> 128

<212> PRT

<213> Unknown (H38g318 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(128)

<223> Xaa = Any Amino Acid

<400> 1401

```

Ser Arg Ser Asp Thr Gln Val Asn Glu Leu Val Leu Phe Thr Val Phe
 1           5           10           15
Gly Phe Ile Glu Leu Ser Thr Ile Ser Gly Val Phe Ile Ser Tyr Cys
          20           25           30
Tyr Ile Ile Leu Ser Val Leu Glu Ile His Ser Ala Glu Gly Arg Phe
          35           40           45
Lys Ala Leu Ser Thr Cys Thr Ser His Leu Ser Ala Val Ala Ile Phe
          50           55           60
Gln Gly Thr Leu Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser
65           70           75           80
Leu Asp Gln Asp Lys Met Thr Ser Leu Phe Tyr Thr Leu Val Val Pro
          85           90           95
Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu
          100          105          110
Ala Leu Lys Lys Leu Lys Asn Lys Ile Leu Phe Xaa Gly Asn Ser Lys
          115          120          125

```

<210> 1402

<211> 316

<212> PRT

<213> Unknown (H38g319 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1402

```

Met Phe Leu Leu Asn Thr Ser Glu Val Glu Val Ser Thr Phe Leu Leu
 1           5           10           15
Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Ile Pro
          20           25           30
Ile Cys Leu Met Tyr Leu Met Ala Ile Leu Gly Asn Cys Thr Ile Leu
          35           40           45
Phe Val Ile Arg Thr Glu His Ser Leu Gln Glu Pro Met Tyr Tyr Phe
          50           55           60
Leu Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser Phe Ser Ser Leu
65           70           75           80
Pro Thr Met Leu Arg Ile Phe Leu Phe Asn Asn Met Gly Ile Ser Ala
          85           90           95
Asp Thr Cys Ile Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
          100          105          110
Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp His Leu Val Ala Ile.
          115          120          125
Cys Asn Pro Leu Arg Tyr Ser Ser Ile Leu Thr Ser Phe Arg Val Leu
          130          135          140
Gln Ile Gly Leu Ala Phe Ala Ile Lys Ser Ile Leu Leu Val Leu Pro
145          150          155          160
Pro Phe Thr Leu Lys Arg Leu Arg Tyr Cys Asn Lys His Leu Leu Ser
          165          170          175
His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser Asp
          180          185          190
Asn Arg Val Asn Phe Tyr Tyr Gly Leu Phe Val Ala Leu Cys Met Met

```

	195		200		205										
Ser	Asp	Ser	Val	Phe	Ile	Ala	Ile	Ser	Tyr	Met	L u	Phe	Ile	Leu	Lys
	210				215						220				
Thr	Val	Leu	Gly	Ile	Ala	Ser	His	Gly	Glu	Cys	Leu	Glu	Ala	Leu	Asp
225				230					235						240
Thr	Cys	Val	Ser	His	Ile	Cys	Ala	Val	Leu	Val	Phe	Tyr	Val	Pro	Ile
			245						250					255	
Ile	Thr	Leu	Ala	Thr	Met	Arg	Arg	Phe	Ala	Lys	His	Lys	Ser	Pro	Leu
		260						265					270		
Ala	Met	Ile	Leu	Ile	Ala	Asp	Ala	Phe	Leu	Leu	Val	Pro	Pro	Leu	Met
	275					280						285			
Asn	Pro	Ile	Val	Tyr	Cys	Val	Lys	Thr	Arg	Gln	Ile	Arg	Val	Lys	Val
	290					295					300				
Leu	Glu	Lys	Leu	Ala	Leu	Lys	Pro	Lys	Xaa	Trp	Gly				
305					310						315				

<210> 1403

<211> 314

<212> PRT

<213> Unknown (H38g320 protein)

<220>

<223> Synthetic construct

<400> 1403

Met	Met	Ala	Ser	Glu	Arg	Asn	Gln	Ser	Ser	Thr	Pro	Thr	Phe	Ile	Leu
1				5				10						15	
Leu	Gly	Phe	Ser	Glu	Tyr	Pro	Glu	Ile	Gln	Val	Pro	Leu	Phe	Leu	Val
			20				25						30		
Phe	Leu	Phe	Val	Tyr	Thr	Val	Thr	Val	Val	Gly	Asn	Leu	Gly	Met	Ile
	35					40					45				
Ile	Ile	Ile	Arg	Leu	Asn	Ser	Lys	Leu	His	Thr	Ile	Met	Cys	Phe	Phe
	50				55					60					
Leu	Ser	His	Leu	Ser	Leu	Thr	Asp	Phe	Cys	Phe	Ser	Thr	Val	Val	Thr
65					70				75					80	
Pro	Lys	Leu	Leu	Glu	Asn	Leu	Val	Val	Glu	Tyr	Arg	Thr	Ile	Ser	Phe
			85					90					95		
Ser	Gly	Cys	Ile	Met	Gln	Phe	Cys	Phe	Ala	Cys	Ile	Phe	Gly	Val	Thr
	100					105						110			
Glu	Thr	Phe	Met	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Val
	115					120					125				
Cys	Lys	Pro	Leu	Leu	Tyr	Thr	Thr	Ile	Met	Ser	Gln	Lys	Leu	Cys	Ala
	130				135					140					
Leu	Leu	Val	Ala	Gly	Ser	Tyr	Thr	Trp	Gly	Ile	Val	Cys	Ser	Leu	Ile
145				150					155					160	
Leu	Thr	Tyr	Phe	Leu	Leu	Asp	Leu	Ser	Phe	Cys	Glu	Ser	Thr	Phe	Ile
			165				170						175		
Asn	Asn	Phe	Ile	Cys	Asp	His	Ser	Val	Ile	Val	Ser	Ala	Ser	Tyr	Ser
	180						185					190			
Asp	Pro	Tyr	Ile	Ser	Gln	Arg	Leu	Cys	Phe	Ile	Ile	Ala	Ile	Phe	Asn
	195					200						205			
Glu	Val	Ser	Ser	Leu	Ile	Ile	Ile	Leu	Thr	Ser	Tyr	Met	Leu	Ile	Phe
	210				215						220				
Thr	Thr	Ile	Met	Lys	Met	Arg	Ser	Ala	Ser	Gly	Arg	Gln	Lys	Thr	Phe
225				230					235					240	
Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Ala	Ile	Thr	Ile	Phe	His	Gly	Thr
			245					250					255		
Ile	Leu	Phe	Leu	Tyr	Cys	Val	Pro	Asn	Pro	Lys	Thr	Ser	Ser	Leu	Ile
	260					265					270				
Val	Thr	Val	Ala	Ser	Val	Phe	Tyr	Thr	Val	Ala	Ile	Pro	Met	Leu	Asn
	275					280					285				

Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Ile Asn Asn Met Phe Glu
 290 295 300
 Lys Leu Val Val Thr Lys Leu Ile Tyr His
 305 310

<210> 1404

<211> 322

<212> PRT

<213> Unknown (H38g321 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1404

His Thr Glu Pro Arg Asn His Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
 35 40 45
 Ile Leu Ala Val Arg Ser Asp Ser Pro Leu His Asn Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
 65 70 75 80
 Val Ala Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
 100 105 110
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
 115 120 125
 Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130 135 140
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
 145 150 155 160
 Leu His Ser Ser Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
 165 170 175
 Ile Ser His Phe Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys
 180 185 190
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
 210 215 220
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly
 245 250 255
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg
 260 265 270
 Asn Gly Val Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
 275 280 285
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
 290 295 300
 Arg Arg Leu Leu Ser Arg Thr Val Glu Phe His Asp Leu Phe His Ser
 305 310 315 320
 Phe Ser

<210> 1405
 <211> 330
 <212> PRT
 <213> Unknown (H38g322 protein)

<220>
 <223> Synthetic construct

<400> 1405
 Met Ser Val Leu Asn Asn Thr Ile Ala Glu Pro Leu Ile Phe Leu Leu
 1 5 10 15
 Met Gly Ile Pro Gly Leu Lys Ala Thr Gln Tyr Trp Ile Ser Ile Pro
 20 25 30
 Phe Cys Leu Leu Tyr Val Val Ala Val Ser Gly Asn Ser Met Ile Leu
 35 40 45
 Phe Val Val Leu Cys Glu Arg Ser Leu His Lys Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ser Ala Thr Asp Leu Ser Leu Ser Leu Cys Thr Leu
 65 70 75 80
 Ser Thr Thr Leu Gly Val Phe Trp Phe Glu Ala Arg Glu Ile Asn Leu
 85 90 95
 Asn Ala Cys Ile Ala Gln Met Phe Phe Leu His Gly Phe Thr Phe Met
 100 105 110
 Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Arg Ile Ala
 130 135 140
 Lys Ile Gly Met Ser Met Leu Ile Arg Asn Val Ala Val Met Leu Pro
 145 150 155 160
 Val Met Leu Phe Val Lys Arg Leu Ser Phe Cys Ser Ser Met Val Leu
 165 170 175
 Ser His Ser Tyr Cys Tyr His Val Asp Leu Ile Gln Leu Ser Cys Thr
 180 185 190
 Asp Asn Arg Ile Asn Ser Ile Leu Gly Leu Phe Ala Leu Leu Ser Thr
 195 200 205
 Thr Gly Phe Asp Cys Pro Cys Ile Leu Leu Ser Tyr Ile Leu Ile Ile
 210 215 220
 Arg Ser Val Leu Ser Ile Ala Ser Ser Glu Glu Arg Arg Lys Ala Phe
 225 230 235 240
 Asn Thr Cys Thr Ser His Ile Ser Ala Val Ser Ile Phe Tyr Leu Pro
 245 250 255
 Leu Ile Ser Leu Ser Leu Val His Arg Tyr Gly His Ser Ala Pro Pro
 260 265 270
 Phe Val His Ile Ile Met Ala Asn Val Phe Leu Leu Ile Pro Pro Val
 275 280 285
 Leu Asn Pro Ile Ile Tyr Ser Val Lys Ile Lys Gln Ile Gln Lys Ala
 290 295 300
 Ile Ile Lys Val Leu Ile Gln Lys His Ser Lys Ser Asn His Gln Leu
 305 310 315 320
 Phe Leu Ile Arg Asp Lys Ala Ile Tyr Glu
 325 330

<210> 1406
 <211> 314
 <212> PRT
 <213> Unknown (H38g323 protein)

<220>
 <223> Synthetic construct

<400> 1406

```

Met Met Met Val Leu Arg Asn Leu Ser Met Glu Pro Thr Phe Ala Leu
 1      5      10      15
Leu Gly Phe Thr Asp Tyr Pro Lys Leu Gln Ile Pro Leu Phe Leu Val
 20      25      30
Phe Leu Leu Met Tyr Val Ile Thr Val Val Gly Asn Leu Gly Met Ile
 35      40      45
Ile Ile Ile Lys Ile Asn Pro Lys Phe His Thr Pro Met Tyr Phe Phe
 50      55      60
Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Val Thr
 65      70      75      80
Pro Lys Leu Leu Glu Asn Leu Val Met Ala Asp Lys Ser Ile Phe Tyr
 85      90      95
Phe Ser Cys Met Met Gln Tyr Phe Leu Ser Cys Thr Ala Val Val Thr
 100      105      110
Glu Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile
 115      120      125
Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ala
 130      135      140
Leu Leu Val Ala Gly Ser Tyr Leu Trp Gly Met Phe Gly Pro Leu Val
 145      150      155      160
Leu Leu Cys Tyr Ala Leu Arg Leu Asn Phe Ser Gly Pro Asn Val Ile
 165      170      175
Asn His Phe Phe Cys Glu Tyr Thr Ala Leu Ile Ser Val Ser Gly Ser
 180      185      190
Asp Ile Leu Ile Pro His Leu Leu Leu Phe Ser Phe Ala Thr Phe Asn
 195      200      205
Glu Met Cys Thr Leu Leu Ile Ile Leu Thr Ser Tyr Val Phe Ile Phe
 210      215      220
Val Thr Val Leu Lys Ile Arg Ser Val Ser Gly Arg His Lys Ala Phe
 225      230      235      240
Ser Thr Trp Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
 245      250      255
Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg Gln Thr
 260      265      270
Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Asn Pro Met Leu Asn
 275      280      285
Pro Pro Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Trp
 290      295      300
Lys Leu Ile His Thr Gln Val Pro Phe His
305      310

```

<210> 1407

<211> 314

<212> PRT

<213> Unknown (H38g324 protein)

<220>

<223> Synthetic construct

<400> 1407

```

Met Val Leu Ala Ser Gly Asn Ser Ser Ser His Pro Val Ser Phe Ile
 1      5      10      15
Leu Leu Gly Ile Pro Gly Leu Glu Ser Phe Gln Leu Trp Ile Ala Phe
 20      25      30
Pro Phe Cys Ala Thr Tyr Ala Val Ala Val Val Gly Asn Ile Thr Leu
 35      40      45
Leu His Val Ile Arg Ile Asp His Thr Leu His Glu Pro Met Tyr Leu
 50      55      60
Phe Leu Ala Met Leu Ala Ile Thr Asp Leu Val Leu Ser Ser Ser Thr
 65      70      75      80
Gln Pro Lys Met Leu Ala Ile Phe Trp Phe His Ala His Glu Ile Gln

```

```

      85      90      95
Tyr His Ala Cys Leu Ile Gln Val Phe Phe Ile His Ala Phe Ser Ser
      100      105      110
Val Glu Ser Gly Val Leu Met Ala Met Ala Leu Asp Cys Tyr Val Ala
      115      120      125
Thr Cys Phe Pro Leu Arg His Ser Ser Ile Leu Thr Pro Ser Val Val
      130      135      140
Ile Lys Leu Gly Thr Ile Val Met Leu Arg Gly Leu Leu Trp Val Ser
      145      150      155
Pro Phe Cys Phe Met Val Ser Arg Met Pro Phe Cys Gln His Gln Ala
      165      170      175
Ile Pro Gln Ser Tyr Cys Glu His Met Ala Val Leu Lys Leu Val Cys
      180      185      190
Ala Asp Thr Ser Ile Ser Arg Gly Tyr Gly Leu Phe Val Ala Phe Ser
      195      200      205
Val Ala Gly Phe Asp Met Ile Val Ile Gly Met Ser Tyr Val Met Ile
      210      215      220
Leu Arg Ala Val Leu Gln Leu Pro Ser Gly Glu Ala Arg Leu Lys Ala
      225      230      235
Phe Ser Thr Arg Ala Ser His Ile Cys Val Ile Leu Ala Leu Tyr Ile
      245      250      255
Pro Ala Leu Phe Ser Phe Leu Thr Tyr Arg Phe Gly His Asp Val Pro
      260      265      270
Arg Val Val His Ile Leu Phe Ala Asn Leu Tyr Leu Leu Ile Pro Pro
      275      280      285
Met Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gly Asp
      290      295      300
Arg Val Ile Gln Gly Cys Cys Gly Asn Ile
      305      310

```

<210> 1408

<211> 287

<212> PRT

<213> Unknown (H38g325 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(287)

<223> Xaa = Any Amino Acid

<400> 1408

```

Tyr Ile Leu Leu Asp Ile Tyr Ile Cys Leu Asn Asn Thr His Val Xaa
  1           5           10           15
Leu Cys Val Glu Ser Gln Arg Gln Phe Lys Ile Ser Phe Tyr Phe Ser
      20      25      30
Phe Phe Leu Leu Ala Ile Thr Xaa Phe Xaa Xaa Xaa Ile Leu Ile Ile
      35      40      45
Met Lys Thr Xaa Gln Tyr Phe Leu Lys His Lys His Leu Lys Lys Lys
      50      55      60
Phe Ser Xaa Cys Leu Val Tyr Ile Leu Thr Tyr Ile Leu Ser Leu Xaa
      65      70      75      80
Ser Lys Phe Phe Ala Leu Cys Xaa Ile Phe Ala Asp Lys Ala Phe Gln
      85      90      95
Glu Gln Val Ser Gly Asn Xaa Xaa Ser Arg Ser Xaa Glu Ser Pro Val
      100      105      110
His Tyr Thr Leu Thr Met Ser Gln Lys Phe Cys Ser Ile His Pro Ala
      115      120      125
Gly Cys Tyr Asp Gln Gly Ile Xaa Ser Ile Pro Gly His Ser Phe Ser
      130      135      140

```

```

His Cys Ile Ala Tyr Cys Gly His Asn Val Val Asn Ile Phe Xaa Asn
145          150          155          160
Lys Tyr Ser Val Ala Ile Ser Asp Ser Cys Ser Ser Trp Ile Ala
          165          170          175
Asp Phe Cys Leu Phe Val Cys Phe Ala Leu Val Asn Phe Asp Xaa Leu
          180          185          190
Arg Asn Leu Arg Val Leu Leu Leu Ser Phe His Phe Gln Leu Val Xaa
          195          200          205
Lys Ala Leu Ser Ala Ser Ala His Gln Pro Ser Pro Pro Ile Ser His
          210          215          220
Ile Ser Thr Ile Phe Leu Thr Leu Val Pro Asn Ser Lys Asn Ser Gln
225          230          235          240
Ala Thr Val Lys Ala His Ser Val Cys Tyr Ala Met Leu Ile Pro Met
          245          250          255
Leu Asn Ser Gln Thr Cys Ser Met Arg Tyr Lys Asn Val Asn Glu Ser
          260          265          270
Leu Gln Lys Leu Met Asp Phe Lys Ile Phe Xaa His Xaa Lys Gln
          275          280          285

```

<210> 1409

<211> 323

<212> PRT

<213> Unknown (H38g326 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1409

```

Ser His Thr Glu Pro Xaa Asn Leu Thr Ser Val Ser Glu Phe Leu Leu
1      5      10      15
Gln Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu
20     25     30
Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile
35     40     45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe
50     55     60
Leu Ser Asn Leu Ser Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val
65     70     75     80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Xaa
85     90     95
Ala Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile
100    105    110
Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile
115    120    125
Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val
130    135    140
Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
145    150    155    160
His Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile
165    170    175
Ser Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser
180    185    190
Asp Gly Ile Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Leu Phe
195    200    205
Ser Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val
210    215    220
Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe

```



```

225          230          235          240
Ser Ile Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr
          245          250          255
Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Gly Asn
          260          265          270
Gly Val Val Ala Ser Val Met Tyr Ala Val Gly Thr Pro Met Leu Asn
          275          280          285
Ser Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp
          290          295          300
Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Leu
305          310          315          320
Phe Leu Cys

```

<210> 1410
 <211> 317
 <212> PRT
 <213> Unknown (H38g327 protein)

<220>
 <223> Synthetic construct

```

<400> 1410
Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met
 1          5          10          15
Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu
          20          25          30
Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile
          35          40          45
Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe
          50          55          60
Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val
65          70          75          80
Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile
          85          90          95
Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly
          100          105          110
Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
          115          120          125
Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr
          130          135          140
Cys Ile Arg Leu Ala Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro
145          150          155          160
Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn
          165          170          175
Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser
          180          185          190
Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu
          195          200          205
Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn
          210          215          220
Ile Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys
225          230          235          240
Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr
          245          250          255
Gly Thr Leu Phe Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile
          260          265          270
Asn Phe Asn Lys Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met
          275          280          285
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala
290          295          300

```

Leu Gly Arg Val Phe Ser Leu Asn Phe Trp Lys Gly Gln
 305 310 315

<210> 1411

<211> 312

<212> PRT

<213> Unknown (H38g328 protein)

<220>

<223> Synthetic construct

<400> 1411

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1 5 10 15
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35 40 45
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Val Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
 130 135 140
 Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
 145 150 155 160
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
 195 200 205
 Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr
 210 215 220
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
 245 250 255
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
 290 295 300
 Leu Val Ile Tyr Lys Lys Ile Ser
 305 310

<210> 1412

<211> 223

<212> PRT

<213> Unknown (H38g329 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(223)

<223> Xaa = Any Amino Acid

<400> 1412

```

Val Arg His Pro Leu Arg Cys Gly Lys Xaa Glu Pro Ala Pro Leu Pro
1      5      10      15
Pro Leu Ala Leu Arg Asn Pro Ile Met Thr Ser Cys Phe Cys Gly Phe
20      25      30
Leu Val Leu Phe Phe Phe Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln
35      40      45
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp Ala Glu
50      55      60
Ile Pro Ser Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
65      70      75      80
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Leu Pro Ala Ala Ile
85      90      95
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
100     105     110
Val Ser Ser Ile Leu Arg Val Ser Ser Arg Gly Lys Tyr Lys Ala
115     120     125
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
130     135     140
Thr Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
145     150     155     160
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Ser Met Leu
165     170     175
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu
180     185     190
Arg Gln Pro His Gly Ser Thr Val Gln Phe Gln Tyr Leu Leu Ile Cys
195     200     205
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
210     215     220

```

<210> 1413

<211> 280

<212> PRT

<213> Unknown (H38g330 protein)

<220>

<223> Synthetic construct

<400> 1413

```

Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu Ala Val
1      5      10      15
Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu Ser Asn
20      25      30
Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met
35      40      45
Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys
50      55      60
Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu Asp Met
65      70      75      80
Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro
85      90      95
Leu His Tyr Pro Val Ile Met Asn Pro His Leu Gly Val Phe Leu Val
100     105     110
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp
115     120     125
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
130     135     140

```

Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Val
 145 150 155 160
 Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Met Phe Gly Phe Leu
 165 170 175
 Pro Ile Ser Gly Ile Leu Leu Ser Tyr Ala Asn Asn Val Pro Ser Ile
 180 185 190
 Leu Arg Ile Ser Ser Ser Asp Arg Lys Ser Lys Ala Phe Ser Thr Cys
 195 200 205
 Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
 210 215 220
 Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val
 225 230 235 240
 Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile
 245 250 255
 Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu Arg
 260 265 270
 Ser Arg Thr Val Glu Ser His Asp
 275 280

<210> 1414

<211> 308

<212> PRT

<213> Unknown (H38g331 protein)

<220>

<223> Synthetic construct

<400> 1414

Met Glu Thr Gln Asn Leu Thr Val Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr Gln Ser Gln Asp Ala Gln Leu Leu Val Phe Val Leu Val Leu
 20 25 30
 Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
 35 40 45
 Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ala Leu Leu Asp Ala Ser Tyr Ser Phe Ile Val Val Pro Arg
 65 70 75 80
 Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Ser
 85 90 95
 Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Ala Gly Glu Met
 100 105 110
 Phe Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ser Thr Ile Met Asn Pro Arg Ala Cys Tyr Ala Leu
 130 135 140
 Ser Leu Val Leu Trp Leu Gly Gly Phe Ile His Ser Ile Val Gln Val
 145 150 155 160
 Ala Leu Ile Leu His Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
 165 170 175
 Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asn Thr
 180 185 190
 Phe Val Val Glu Leu Leu Met Val Ser Asn Ser Gly Leu Leu Ser Leu
 195 200 205
 Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
 210 215 220
 Ile Arg Glu His Ser Ser Glu Gly Lys Ser Lys Ala Ile Ser Thr Cys
 225 230 235 240
 Thr Thr His Ile Ile Ile Phe Leu Met Phe Gly Pro Ala Ile Phe
 245 250 255
 Ile Tyr Thr Cys Pro Phe Gln Ala Phe Pro Ala Asp Lys Val Val Ser

260 265 270
 Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Val Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Glu Val Lys Ala Ser Met Arg Lys Leu Leu Ser Gln
 290 295 300
 His Met Phe Cys
 305

<210> 1415
 <211> 154
 <212> PRT
 <213> Unknown (H38g332 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(154)
 <223> Xaa = Any Amino Acid

<400> 1415
 Gly Met Arg Lys Glu Gln Ala Val Cys Gly Ser His Arg Met Ile Glu
 1 5 10 15
 Met Met Cys Gly Pro Xaa Val Arg Leu Pro Gly Ser Asn Ala Gly Ser
 20 25 30
 Leu Leu Phe Thr His Leu Ile Leu Ala Cys Gly Ser Leu Leu Ile
 35 40 45
 Pro Phe His Leu Gly Leu Val Ala Ser His Thr Ser Ile Phe Leu Thr
 50 55 60
 Val Leu His Met Lys Ser Pro Xaa Ser Arg Asn Lys Ala Leu Ala Asn
 65 70 75 80
 Cys Ser Ser His Leu Ser Val Gly Leu Tyr Leu Gly Thr Val Cys Leu
 85 90 95
 Ile Tyr Val Thr Gln Gly Phe Ser His Ile Pro Glu Gln Lys Gln Ala
 100 105 110
 Val Ser Val Phe Cys Thr Val Leu Thr Pro Met Leu Asn Pro Leu Ile
 115 120 125
 Tyr Ile Leu Arg Asn Lys Asp Val Val Arg Ala Leu Gln Lys Val Leu
 130 135 140
 Gly Thr His Gln Val Ser Lys Gln Asn Thr
 145 150

<210> 1416
 <211> 324
 <212> PRT
 <213> Unknown (H38g333 protein)

<220>
 <223> Synthetic construct

<400> 1416
 Met Ser Phe Phe Val Asp Leu Arg Pro Met Asn Arg Ser Ala Thr
 1 5 10 15
 His Ile Val Thr Glu Phe Ile Leu Leu Gly Phe Pro Gly Cys Trp Lys
 20 25 30
 Ile Gln Ile Phe Leu Phe Ser Leu Phe Leu Val Ile Tyr Val Leu Thr
 35 40 45
 Leu Leu Gly Asn Gly Ala Ile Ile Tyr Ala Val Arg Cys Asn Pro Leu
 50 55 60
 Leu His Thr Pro Met Tyr Phe Leu Leu Gly Asn Phe Ala Phe Leu Glu
 65 70 75 80

```

<400> 1417
Met Ala Asn Ile Thr Arg Met Ala Asn His Thr Gly Lys Leu Asp Phe
 1          5          10          15
Ile Leu Met Gly Leu Phe Arg Arg Ser Lys His Pro Ala Leu Leu Ser
          20          25          30
Val Val Ile Phe Val Val Phe Leu Lys Ala Leu Ser Gly Asn Ala Val
          35          40          45
Leu Ile Leu Leu Ile His Cys Asp Ala His Leu His Ser Pro Met Tyr
          50          55          60
Phe Phe Ile Ser Gln Leu Ser Leu Met Asp Met Ala Tyr Ile Ser Val
65          70          75          80
Thr Val Pro Lys Met Leu Leu Asp Gln Val Met Gly Val Asn Lys Val
          85          90          95
Ser Ala Pro Glu Cys Gly Met Gln Met Phe Leu Tyr Leu Thr Leu Ala
          100          105          110
Gly Ser Glu Phe Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val
          115          120          125
Ala Ile Cys His Pro Leu Arg Tyr Pro Val Leu Met Asn His Arg Val
          130          135          140
Cys Leu Phe Leu Ala Ser Gly Cys Trp Phe Leu Gly Ser Val Asp Gly

```

```

145          150          155          160
Phe Met Leu Thr Pro Ile Thr Met Ser Phe Pro Phe Cys Arg Ser Trp
          165          170          175
Glu Ile His His Phe Phe Cys Glu Val Pro Ala Val Thr Ile Leu Ser
          180          185          190
Cys Ser Asp Thr Ser Leu Tyr Glu Thr Leu Met Tyr Leu Cys Cys Val
          195          200          205
Leu Met Leu Leu Ile Pro Val Thr Ile Ile Ser Ser Ser Tyr Leu Leu
          210          215          220
Ile Leu Leu Thr Val His Arg Met Asn Ser Ala Glu Gly Arg Lys Lys
225          230          235          240
Ala Phe Ala Thr Cys Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr
          245          250          255
Gly Ala Ala Val Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr Pro
          260          265          270
Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Val
          275          280          285
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Met Gly Ala
290          295          300
Leu Lys Lys Met Leu Thr Val Arg Phe Val Leu
305          310          315

```

<210> 1418

<211> 253

<212> PRT

<213> Unknown (H38g335 protein)

<220> .

<223> Synthetic construct

<221> VARIANT

<222> (1)...(253)

<223> Xaa = Any Amino Acid

<400> 1418

```

Ser His Leu Ser Val Ile Asp Thr Leu Tyr Ile Ser Thr Ile Val Pro
 1          5          10          15
Lys Met Leu Val Asp Tyr Leu Met Gly Glu Gly Thr Ile Ser Phe Ile
          20          25          30
Ala Cys Thr Ala Gln Cys Phe Leu Tyr Met Gly Phe Met Gly Ala Glu
          35          40          45
Phe Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          50          55          60
Asn Pro Leu Arg Tyr Pro Val Leu Ile Ser Trp Arg Val Cys Trp Met
65          70          75          80
Ile Leu Ala Ser Ser Trp Phe Gly Gly Ala Leu Asp Ser Phe Leu Leu
          85          90          95
Thr Pro Ile Thr Met Ser Leu Pro Phe Cys Ala Ser His Gln Ile Asn
          100          105          110
His Phe Phe Cys Glu Ala Pro Thr Met Leu Arg Leu Ala Cys Gly Asp
          115          120          125
Lys Thr Thr Tyr Glu Thr Val Met Tyr Val Cys Cys Val Ala Met Leu
          130          135          140
Leu Ile Pro Phe Ser Val Val Thr Ala Ser Tyr Thr Arg Ile Leu Ile
145          150          155          160
Thr Val His Gln Met Thr Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala
          165          170          175
Thr Cys Ser Ser His Met Met Val Val Thr Leu Phe Tyr Gly Ala Ala
          180          185          190
Leu Tyr Thr Tyr Thr Leu Pro Gln Ser Tyr His Thr Pro Ile Lys Asp
          195          200          205

```

Lys Val Phe Ser Ala Phe Tyr Thr Ile Leu Thr Pro Leu Leu Asn Pro
 210 215 220
 Leu Ile Tyr Ser Leu Arg Asn Arg Asp Val Met Gly Ala Leu Lys Arg
 225 230 235 240
 Val Val Ala Arg Cys Xaa Gly Thr Cys Gly Val Met Arg
 245 250

<210> 1419

<211> 285

<212> PRT

<213> Unknown (H38g336 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(285)

<223> Xaa = Any Amino Acid

<400> 1419

Val Phe Ser Arg Thr Arg Val Arg Leu Asn Cys Lys Arg Ile Phe Trp
 1 5 10 15
 Leu Thr Pro Val Phe Phe Leu Ser Pro Ser Cys Pro Ser Pro Ile Ala
 20 25 30
 Val Ser Lys Ser Ala Val Ser Phe Val Ser Gln Ser Arg Arg Ile Arg
 35 40 45
 Phe Leu Gly Cys Asp Ile Gln Thr Tyr Val Phe Leu Ala Pro Gly Gly
 50 55 60
 Thr Glu Ala Leu Leu Phe Gly Phe Met Ser Tyr Asp Arg Tyr Val Ala
 65 70 75 80
 Ile Cys His Pro Leu His Tyr Pro Met Leu Met Ser Lys Lys Ile Cys
 85 90 95
 Cys Leu Met Val Ala Cys Ala Trp Ala Ser Gly Ser Ile Asn Ala Phe
 100 105 110
 Ile His Thr Leu Tyr Val Phe Gln Leu Pro Phe Cys Arg Ser Arg Leu
 115 120 125
 Ile Asn His Phe Phe Cys Glu Val Pro Ala Leu Leu Ser Leu Val Cys
 130 135 140
 Gln Asp Thr Ser Gln Tyr Glu Tyr Thr Val Leu Leu Ser Gly Leu Ile
 145 150 155 160
 Ile Leu Leu Leu Pro Phe Leu Ala Ile Leu Ala Ser Tyr Ala Arg Val
 165 170 175
 Leu Ile Val Val Phe Gln Met Ser Ser Gly Lys Gly Gln Ala Lys Ala
 180 185 190
 Val Ser Thr Cys Ser Ser His Leu Ile Val Ala Ser Leu Phe Tyr Ala
 195 200 205
 Thr Thr Leu Phe Thr Tyr Thr Arg Pro His Ser Leu Arg Ser Pro Ser
 210 215 220
 Arg Asp Lys Ala Val Ala Val Phe Tyr Thr Ile Val Thr Pro Leu Leu
 225 230 235 240
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Val
 245 250 255
 Arg Arg Leu Leu Gly Tyr Trp Ile Cys Cys Arg Lys Tyr Asp Phe Arg
 260 265 270
 Ser Leu Tyr Xaa Leu Ser Ile Asn Asn Ile Lys Ser Cys
 275 280 285

<210> 1420

<211> 271

<212> PRT

<213> Unknown (H38g337 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(271)

<223> Xaa = Any Amino Acid

<400> 1420

```

Arg Arg Asp Ile Phe Tyr Phe Ala Phe Ile Cys Ser Tyr Ser Xaa Leu
 1           5           10           15
Thr Leu Arg Ser Phe Val Tyr Leu Phe Ile Arg Pro Ser Ile His Pro
 20           25           30
Ser Ile His Ser Ala Ile Leu Leu Phe Asn Ser Asp Leu Leu Asn Ser
 35           40           45
Leu Leu Cys Ser Ser Ile Phe Asp Met Pro His Asp Val Gln Gln Xaa
 50           55           60
Leu Leu Leu Lys Ser Xaa Phe Leu Val Ser His Cys Phe Ser Leu Val
 65           70           75           80
Leu Tyr Leu Leu Leu Leu Xaa Leu Arg Thr Glu Lys Ser Ile Glu Lys
 85           90           95
Ile Leu Leu Pro Gly Tyr Gly Thr Leu Leu Ser Met Ala Ile Ser Tyr
100           105           110
Cys Leu Cys Val Phe Gly Leu Ser Asn Pro Ala Ala Cys Val Tyr Ala
115           120           125
Gln Xaa Cys Ser Trp Asn Lys Met Val Trp Phe Leu Phe Gln Glu Val
130           135           140
Leu Pro Ser Leu Phe Xaa Leu Arg Ile Gly Leu Pro Arg Cys Ile Thr
145           150           155           160
Ser Leu Thr Leu Tyr Ser Cys Asp Phe Phe Leu Met Ile Gly Gln Ile
165           170           175
Cys Thr Lys Lys Ser Lys Ile Ile Tyr Tyr Ile Met Pro Phe Leu Leu
180           185           190
Leu Phe Met Pro Asp Xaa Ile Phe Leu Val Leu Gln Cys Pro Leu Leu
195           200           205
Ile Ser Ile Asn Lys Xaa Pro Phe Pro Asn Leu Leu Lys Ser Pro Cys
210           215           220
Gly Ile Gly His Leu Ser Val Asp Ser Ile Ser Ser Pro Ser Phe Phe
225           230           235           240
Cys Leu Pro Val Cys Pro Ser Ile Tyr Pro Ser Thr Xaa Leu Phe Val
245           250           255
Arg Ser Thr Met Ile Xaa Xaa Ile Pro Thr Tyr Cys Asp Pro Ile
260           265           270

```

<210> 1421

<211> 310

<212> PRT

<213> Unknown (H38g338 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1421

```

Met Ser Leu Ala Glu Gly Asn Gln Ser Ser Gly Ala Val Phe Thr Leu
 1           5           10           15
Leu Gly Phe Ser Glu Tyr Ala Asp Leu Gln Val Pro Leu Phe Leu Val
 20           25           30

```

```

Phe Leu Thr Ile Tyr Thr Ile Thr Val Leu Gly Asn Leu Gly Met Ile
    35                40                45
Met Ile Ile Arg Ile Asn Pro Lys Leu His Thr Arg Met Tyr Phe Phe
    50                55                60
Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Val Thr
    65                70                75                80
Pro Lys Leu Leu Glu Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe
    85                90                95
Thr Gly Cys Ile Met Gln Phe Phe Leu Ala Cys Ile Cys Ala Val Ala
    100               105               110
Glu Thr Phe Met Leu Ala Val Met Ala Tyr Asp Xaa Tyr Val Ala Val
    115               120               125
Cys Asn Pro Leu Leu Tyr Thr Val Val Arg Ser Gln Lys Leu Cys Ala
    130               135               140
Ser Leu Val Ala Gly Pro Tyr Thr Trp Gly Ile Ile Ser Ser Leu Thr
    145               150               155               160
Leu Thr Tyr Phe Leu Leu Ser Leu Ser Phe Cys Gly Ser Asn Ile Ile
    165               170               175
Asn Asn Phe Val Cys Glu His Ser Val Ile Ile Ser Val Ser Cys Ser
    180               185               190
Asp Pro Tyr Ile Ser Gln Met Leu Cys Phe Val Ile Ala Ile Phe Asn
    195               200               205
Glu Val Ser Ser Leu Gly Val Ile Leu Thr Thr Tyr Ile Phe Ile Phe
    210               215               220
Ile Ala Val Ile Lys Met Pro Ser Ala Val Gly His Gln Lys Ala Phe
    225               230               235               240
Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
    245               250               255
Val Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Trp Leu Ile
    260               265               270
Val Lys Val Gly Ser Val Phe Tyr Thr Val Ile Ile Pro Thr Leu Asn
    275               280               285
Pro Leu Thr Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Met Phe Glu
    290               295               300
Ser Xaa Xaa Ile Thr Gln
    305                310

```

<210> 1422

<211> 217

<212> PRT

<213> Unknown (H38g339 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(217)

<223> Xaa = Any Amino Acid

<400> 1422

```

Phe Leu Val Leu Phe Ala Cys Ile Glu Asp Met Phe Leu Thr Val Met
    1                5                10                15
Ala Tyr Asp Cys Phe Ile Ala Ile Cys His Pro Leu His Tyr Pro Val
    20               25               30
Ile Val Asn Pro His Leu Cys Val Phe Phe Ile Leu Val Ser Phe Phe
    35               40               45
Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu Gln Phe
    50               55               60
Thr Ile Ile Lys Asn Val Glu Val Ser Asn Phe Val Cys Asp Pro Ser
    65               70               75               80
Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Ser Ile Phe

```


Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Asn Lys Ala Leu Arg Lys Val
 290 295 300
 Met Gly Ser Lys Ile His Ser
 305 310

<210> 1424

<211> 321

<212> PRT

<213> Unknown (H38g341 protein)

<220>

<223> Synthetic construct

<400> 1424

Met Phe Leu Thr Glu Arg Asn Thr Thr Ser Glu Ala Thr Phe Thr Leu
 1 5 10 15
 Leu Gly Phe Ser Asp Tyr Leu Glu Leu Gln Ile Pro Leu Phe Phe Val
 20 25 30
 Phe Leu Ala Val Tyr Gly Phe Ser Val Val Gly Asn Leu Gly Met Ile
 35 40 45
 Val Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Asn His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala
 65 70 75 80
 Pro Met Met Leu Val Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe
 85 90 95
 Ser Gly Cys Leu Val Gln Phe Phe Phe Phe Cys Thr Phe Val Val Thr
 100 105 110
 Glu Leu Ile Leu Phe Ala Val Met Ala Tyr Asp His Phe Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Leu Tyr Thr Val Ala Ile Ser Gln Lys Leu Cys Ala
 130 135 140
 Met Leu Val Val Val Leu Tyr Ala Trp Gly Val Ala Cys Ser Leu Thr
 145 150 155 160
 Leu Ala Cys Ser Ala Leu Lys Leu Ser Phe His Gly Phe Asn Thr Ile
 165 170 175
 Asn His Phe Phe Cys Glu Leu Ser Ser Leu Ile Ser Leu Ser Tyr Pro
 180 185 190
 Asp Ser Tyr Leu Ser Gln Leu Leu Leu Phe Thr Val Ala Thr Phe Asn
 195 200 205
 Glu Ile Ser Thr Leu Leu Ile Ile Leu Thr Ser Tyr Ala Phe Ile Ile
 210 215 220
 Val Thr Thr Leu Lys Met Pro Ser Ala Ser Gly His Arg Lys Val Phe
 225 230 235 240
 Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
 245 250 255
 Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr
 260 265 270
 Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Leu Leu Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ile Arg
 290 295 300
 Lys Ile Ile Asn Thr Lys Tyr Phe His Ile Lys His Arg His Trp Tyr
 305 310 315 320
 Pro

<210> 1425

<211> 101

<212> PRT

<213> Unknown (H38g342 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(101)

<223> Xaa = Any Amino Acid

<400> 1425

Cys	Cys	Pro	Leu	His	His	His	Tyr	Leu	Pro	Arg	Gln	Ser	Leu	Asp	Gln
1				5					10					15	
Leu	Thr	Tyr	Leu	Ile	Ala	Leu	Ile	Phe	Asn	Phe	Leu	Phe	Val	Phe	Gly
			20					25					30		
Leu	Gln	Ser	Ser	Phe	Ile	Phe	Leu	Lys	Ala	Xaa	Gln	Cys	Phe	Pro	Lys
		35					40					45			
Asp	Ile	His	Tyr	Ile	Phe	Val	Lys	Ala	Arg	Arg	Ala	Ser	Gly	Tyr	Leu
	50					55					60				
Thr	Tyr	His	Ile	Ala	Gly	Asn	Arg	Ser	Xaa	Thr	Val	Phe	Phe	Leu	Val
65				70					75					80	
Cys	Asn	Cys	His	Tyr	Tyr	Gly	Asp	Asp	Ile	Gly	Xaa	Val	Xaa	Ile	Phe
				85					90					95	
Tyr	Val	Asn	Ile	Leu											
				100											

<210> 1426

<211> 319

<212> PRT

<213> Unknown (H38g343 protein)

<220>

<223> Synthetic construct

<400> 1426

Met	Pro	Val	Gly	Lys	Leu	Val	Phe	Asn	Gln	Ser	Glu	Pro	Thr	Glu	Phe
1				5					10					15	
Val	Phe	Arg	Ala	Phe	Thr	Thr	Ala	Thr	Glu	Phe	Gln	Val	Leu	Leu	Phe
			20					25					30		
Leu	Leu	Phe	Leu	Leu	Leu	Tyr	Leu	Met	Ile	Leu	Cys	Gly	Asn	Thr	Ala
		35					40					45			
Ile	Ile	Trp	Val	Val	Cys	Thr	His	Ser	Thr	Leu	Arg	Thr	Pro	Met	Tyr
	50				55					60					
Phe	Phe	Leu	Ser	Asn	Leu	Ser	Phe	Leu	Glu	Leu	Cys	Tyr	Thr	Thr	Val
65				70					75					80	
Val	Val	Pro	Leu	Met	Leu	Ser	Asn	Ile	Leu	Gly	Ala	Gln	Lys	Pro	Ile
				85					90					95	
Ser	Leu	Ala	Gly	Cys	Gly	Ala	Gln	Met	Phe	Phe	Phe	Val	Thr	Leu	Gly
		100					105						110		
Ser	Thr	Asp	Cys	Phe	Leu	Leu	Ala	Ile	Met	Ala	Tyr	Asp	Arg	Tyr	Val
	115						120					125			
Ala	Ile	Cys	His	Pro	Leu	His	Tyr	Thr	Leu	Ile	Met	Thr	Arg	Glu	Leu
	130					135					140				
Cys	Thr	Gln	Met	Leu	Gly	Gly	Ala	Leu	Gly	Leu	Ala	Leu	Phe	Pro	Ser
145				150					155					160	
Leu	Gln	Leu	Thr	Ala	Leu	Ile	Phe	Thr	Leu	Pro	Phe	Cys	Gly	His	His
			165					170						175	
Gln	Glu	Ile	Asn	His	Phe	Leu	Cys	Asp	Val	Pro	Pro	Val	Leu	Arg	Leu
		180						185					190		
Ala	Cys	Ala	Asp	Ile	Arg	Val	His	Gln	Ala	Val	Leu	Tyr	Val	Val	Ser
		195					200					205			

```

Ile Leu Val Leu Thr Ile Pro Phe Leu Leu Ile Cys Val Ser Tyr Val
  210                215                220
Phe Ile Thr Cys Ala Ile Leu Ser Ile Arg Ser Ala Glu Gly Arg Arg
225                230                235                240
Arg Ala Phe Ser Thr Cys Ser Phe His Leu Thr Val Val Leu Leu Gln
                245                250                255
Tyr Gly Cys Cys Ser Leu Val Tyr Leu Arg Pro Arg Ser Ser Thr Ser
                260                265                270
Glu Asp Glu Asp Ser Gln Ile Ala Leu Val Tyr Thr Phe Val Thr Pro
                275                280                285
Leu Leu Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly
                290                295                300
Ala Leu Arg Ser Ala Ile Ile Arg Lys Ala Ala Ser Asp Ala Asn
305                310                315

```

<210> 1427
 <211> 208
 <212> PRT
 <213> Unknown (H38g344 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(208)
 <223> Xaa = Any Amino Acid

```

<400> 1427
Met Glu Leu Glu Asn Gly Thr Val Lys Thr Gly Phe Phe Leu Leu Gly
  1                5                10                15
Phe Ser Asp His Leu Glu Leu Gln Ser Leu Leu Phe Ala Glu Phe Phe
                20                25                30
Ser Ile Tyr Ser Val Thr Leu Met Gly Asn Leu Gly Met Ile Leu Leu
                35                40                45
Ile Thr Ile Ser Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Cys
                50                55                60
Val Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Ile Ala Pro Lys
65                70                75                80
Leu Leu Val Asn Leu Val Ser Glu Lys Lys Thr Ile Ser Tyr Asn Gly
                85                90                95
Cys Val Ala Gln Leu Tyr Phe Phe Cys Ser Leu Val Asp Thr Glu Ser
                100                105                110
Phe Leu Leu Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn
                115                120                125
Pro Leu Leu Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu
                130                135                140
Ala Ile Gly Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr
145                150                155                160
Thr Asn Thr Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe
                165                170                175
Phe Cys Asp Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr
                180                185                190
Met His Asp Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile
195                200                205

```

<210> 1428
 <211> 321
 <212> PRT
 <213> Unknown (H38g345 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1428

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Pro Gly Leu Ser
 20           25           30
Leu Ser Met Tyr Leu Leu Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
 35           40           45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50           55           60
Ser Asn Pro Ser Trp Ala Asp Ile Ala Phe Thr Ser Ala Thr Val Pro
 65           70           75           80
Lys Met Ile Val Asp Met Gln Ser His Arg Val Ile Ser Tyr Ala Ser
 85           90           95
Cys Leu Thr Gln Met Ser Phe Phe Ala Leu Phe Ala Cys Ile Glu Asp
 100          105          110
Met Leu Leu Ile Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His
 115          120          125
Ser Pro His Tyr Pro Val Ile Met Asn Pro Arg Leu Gly Val Phe Phe
 130          135          140
Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser
 145          150          155          160
Trp Thr Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn
 165          170          175
Phe Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180          185          190
Val Ile Asp Ser Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Arg Phe
 195          200          205
Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Ser Asn Ile Val Pro Ser
 210          215          220
Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Ser Lys Ala Phe Ser Thr
 225          230          235          240
Cys Arg Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245          250          255
Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Gly Asp Gly Val
 260          265          270
Val Val Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275          280          285
Ile Tyr Cys Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu
 290          295          300
Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu
 305          310          315          320
Cys

```

<210> 1429

<211> 310

<212> PRT

<213> Unknown (H38g346 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1429

Glu Lys Asn Leu Ile Ser Met Asn Gly Phe Met Asn Phe Thr Asp Tyr
 1 5 10 15
 Pro Glu Leu Glu Met Pro Leu Phe Leu Val Phe Leu Ser Cys Phe Leu
 20 25 30
 Ala Ile Ile Leu Arg Asn Met Glu Trp Val Ile Leu Thr Gln Val Asn
 35 40 45
 Val His Leu Phe Thr Pro Ile Tyr Phe Phe Leu Thr Asn Val Thr Leu
 50 55 60
 Trp Asp Thr Ser Val Ile Met Pro Gln Ile Leu Ala Ile Leu Ala Thr
 65 70 75 80
 Gly Lys Thr Thr Ile Ser Tyr Val Pro Leu Ile Lys Ala Met Arg Ser
 85 90 95
 Phe Phe Phe Ile Cys Val Gly Thr Xaa Cys Phe Leu Pro Thr Ala Met
 100 105 110
 Thr Ile Ser Ser His Cys Pro Thr Leu Gln Ala Met Asn Phe Lys Thr
 115 120 125
 Cys Trp Gly Phe Phe Leu Val Gly Ile Cys Cys Cys Thr Cys Trp Val
 130 135 140
 Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly Leu Ser Gly Ala
 145 150 155 160
 Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe Cys Asp Asp Asn
 165 170 175
 Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys Leu Ile Xaa Asn
 180 185 190
 Thr Ser Gly Asn Ser Lys Ile Ile Ile Val Ile Leu Thr Ala Phe Met
 195 200 205
 Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile
 210 215 220
 Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Arg Ser Gln Xaa Phe Tyr
 225 230 235 240
 Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr Phe Phe Gly Ile
 245 250 255
 Pro Ile Phe Arg His Val Lys Tyr Leu Arg Xaa Ile Thr Asp Arg Arg
 260 265 270
 Gln Val Gly Ile Met Thr Cys Thr Ile Phe Ile Pro Met Leu Glu Leu
 275 280 285
 Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val Ala Phe Lys Lys Ala
 290 295 300
 Ile Gly Asn Phe Trp Val
 305 310

<210> 1430

<211> 336

<212> PRT

<213> Unknown (H38g347 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 1430

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Arg
 1 5 10 15
 Gly Thr Ser Glu Asp Pro Glu Trp Gln Leu Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu


```

      35              40              45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50              55              60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Ala
 65              70              75              80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85              90              95
Gly Cys Leu Thr Gln Met Ser Pro Phe Ala Ile Phe Gly Val Met Glu
      100              105              110
Glu Asn Thr Leu Leu Ser Val Met Ala Ser Asp Arg Phe Val Ala Ile
      115              120              125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
      130              135              140
Phe Leu Val Leu Leu Ser Phe Phe Phe Phe Cys Cys Leu Leu Asp Ala
 145              150              155              160
Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
      165              170              175
Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
      180              185              190
Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala
      195              200              205
Ile Phe Gly Phe Leu Pro Ile Ser Gly Ser Leu Phe Ser Tyr Tyr Lys
      210              215              220
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Xaa
 225              230              235              240
Ala Phe Ser Ser Cys Trp Ser His Leu Ser Val Val Cys Xaa Phe Tyr
      245              250              255
Gly Thr Gly Val Gly Gly Tyr Leu Ser Xaa Asp Val Ser Ser Ser Pro
      260              265              270
Arg Lys Val Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met
      275              280              285
Leu Asn Pro Phe Val Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val
      290              295              300
Leu Arg Trp Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Leu Ile
 305              310              315              320
Cys Ser Ile Pro Phe Val Val Xaa Val Lys Lys Gly Ser Lys Val Lys
      325              330              335

```

<210> 1431

<211> 325

<212> PRT

<213> Unknown (H38g348 protein)

<220>

<223> Synthetic construct

<400> 1431

```

Met Lys Thr Phe Ser Ser Phe Leu Gln Ile Gly Arg Asn Met His Gln
 1              5              10              15
Gly Asn Gln Thr Thr Ile Thr Glu Phe Ile Leu Leu Gly Phe Phe Lys
      20              25              30
Gln Asp Glu His Gln Asn Leu Leu Phe Val Leu Phe Leu Gly Met Tyr
      35              40              45
Leu Val Thr Val Ile Gly Asn Gly Leu Ile Ile Val Ala Ile Ser Leu
      50              55              60
Asp Thr Tyr Leu His Thr Pro Met Tyr Leu Phe Leu Ala Asn Leu Ser
 65              70              75              80
Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val
      85              90              95
Asn Ile Gln Thr Lys Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr
      100              105              110

```

Gln Met Tyr Phe Ser Ile Val Phe Val Val Ile Asp Asn Leu Leu Leu
 115 120 125
 Gly Thr Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro Leu Asn
 130 135 140
 Tyr Thr Ile Leu Met Arg Pro Arg Phe Gly Ile Leu Leu Thr Val Ile
 145 150 155 160
 Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu
 165 170 175
 Ile Gln Leu Leu Phe Cys Asn His Asn Thr Leu Pro His Phe Phe Cys
 180 185 190
 Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Leu Ile Asn
 195 200 205
 Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe
 210 215 220
 Thr Leu Ser Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Arg
 225 230 235 240
 Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
 245 250 255
 His Leu Thr Val Val Leu Leu Phe Tyr Gly Thr Ile Val Gly Val Tyr
 260 265 270
 Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala
 275 280 285
 Val Leu Phe Thr Val Val Thr Pro Met Ile Asn Pro Phe Ile Tyr Ser
 290 295 300
 Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg Lys Leu Ile Asn Arg
 305 310 315 320
 Lys Ile Ser Ser Leu
 325

<210> 1432

<211> 256

<212> PRT

<213> Unknown (H38g349 protein)

<220>

<223> Synthetic construct

<400> 1432

Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Asp Thr Cys Tyr Ser
 1 5 10 15
 Asn Val Phe Thr Pro Lys Leu Leu Glu Ile Leu Val Val Glu Asp Arg
 20 25 30
 Thr Ile Ser Phe Lys Gly Cys Met Val Gln Phe Phe Phe Gly Cys Ala
 35 40 45
 Phe Val Ile Thr Glu Met Phe Met Leu Ala Val Met Ala Tyr Asp Leu
 50 55 60
 Phe Met Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro
 65 70 75 80
 Lys Leu Cys Ala Leu Leu Val Ala Gly Thr Tyr Thr Trp Gly Gly Leu
 85 90 95
 Cys Ser Leu Thr Leu Thr Tyr Ser Leu Leu Val Leu Ser Tyr Cys Gly
 100 105 110
 Ser Asn Ile Ile Asn His Phe Gly Cys Glu Tyr Ser Ala Ile Leu Ser
 115 120 125
 Leu Ser Cys Ser Asp Pro Tyr Phe Asn Gln Met Ala Cys Leu Val Ile
 130 135 140
 Ser Ile Phe Ser Glu Ala Cys Ser Leu Leu Ala Ile Leu Ala Phe Tyr
 145 150 155 160
 Val Phe Ile Val Ala Thr Val Ile Lys Met Leu Ser Thr Gly Gly Pro
 165 170 175
 Gln Lys Ala Ile Ser Thr Cys Ala Ser His Leu Thr Thr Val Ser Ile

<400> 1433															
Met	Ala	Glu	Ser	Gly	Thr	Thr	Val	Thr	Glu	Phe	Phe	Leu	Arg	Gly	Phe
1				5					10					15	
Arg	Leu	Lys	Ala	Glu	Leu	Gln	Ile	Gly	Leu	Phe	Phe	Val	Phe	Leu	Val
			20					25					30		
Ile	Phe	Leu	Ile	Thr	Met	Gly	Gly	Asn	Leu	Gly	Met	Ile	Val	Leu	Met
		35				40						45			
Leu	Ile	Gln	Thr	Asp	Pro	Arg	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	His	Leu	Ser	Phe	Leu	Asp	Ile	Cys	Tyr	Ser	Ser	Val	Ile	Gly	Pro
65					70					75				80	
Gln	Leu	Leu	Glu	Thr	Leu	Ala	Thr	Asp	Lys	Met	Ile	Ile	Thr	Tyr	Glu
				85					90					95	
Arg	Cys	Ala	Ser	Gln	Phe	Phe	Phe	Phe	Thr	Leu	Cys	Ala	Ser	Ile	Glu
			100					105					110		
Cys	Phe	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Val	Cys
	115					120						125			
Asn	Pro	Leu	Leu	Tyr	Ala	Ile	Val	Met	Thr	Pro	Lys	Thr	Arg	Leu	Ala
	130					135					140				
Leu	Leu	Ala	Gly	Ala	Tyr	Ser	Gly	Ala	Ile	Val	Asn	Ser	Val	Ile	Cys
145				150						155				160	
Thr	Gly	Cys	Thr	Phe	Ser	Ile	Ser	Phe	Ser	Lys	Ser	Asn	His	Val	Asp
				165					170					175	
Phe	Phe	Phe	Cys	Asp	Leu	Pro	Pro	Leu	Lys	Leu	Ala	Cys	Ser	Glu	
			180					185					190		
Thr	Arg	Pro	Arg	Glu	Trp	Val	Ile	Tyr	Leu	Ser	Ala	Phe	Leu	Val	Ile
	195					200						205			
Thr	Thr	Ser	Ile	Ser	Val	Ile	Leu	Thr	Ser	Tyr	Leu	Phe	Ile	Ile	Gln
	210					215					220				
Ser	Val	Leu	Lys	Ile	Arg	Thr	Ala	Gly	Gly	Arg	Ala	Lys	Thr	Phe	Ser
225					230					235				240	
Thr	Cys	Ala	Ser	His	Met	Thr	Ala	Leu	Thr	Leu	Phe	Phe	Gly	Thr	Leu
				245					250					255	
Ile	Phe	Ile	Tyr	Leu	Lys	Gly	Asn	Met	Gly	Glu	Ser	Leu	Glu	Glu	Asp
			260					265					270		
Lys	Ile	Val	Ser	Ile	Phe	Tyr	Thr	Val	Val	Ile	Pro	Met	Leu	Asn	Pro
	275						280					285			
Met	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Met	Lys	Glu	Ala	Leu	Lys	Lys
	290					295					300				

Val Phe Asn Arg Ile Arg Val Ser Gln Ala Glu Xaa Leu Leu
 305 310 315

<210> 1434

<211> 313

<212> PRT

<213> Unknown (H38g351 protein)

<220>

<223> Synthetic construct

<400> 1434

Met Leu Leu Thr Asp Arg Asn Thr Ser Gly Thr Thr Phe Thr Leu Leu
 1 5 10 15
 Gly Phe Ser Asp Tyr Pro Glu Leu Gln Val Pro Leu Phe Leu Val Phe
 20 25 30
 Leu Ala Ile Tyr Asn Val Thr Val Leu Gly Asn Ile Gly Leu Ile Val
 35 40 45
 Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Gln Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala Pro
 65 70 75 80
 Lys Met Leu Val Asn Leu Val Val Lys Asp Arg Thr Ile Ser Phe Leu
 85 90 95
 Gly Cys Val Val Gln Phe Phe Phe Phe Cys Thr Phe Val Val Thr Glu
 100 105 110
 Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Thr Val Asp Met Ser Gln Lys Leu Cys Val Leu
 130 135 140
 Leu Val Val Gly Ser Tyr Ala Trp Gly Val Ser Cys Ser Leu Glu Leu
 145 150 155 160
 Thr Cys Ser Ala Leu Lys Leu Cys Phe His Gly Phe Asn Thr Ile Asn
 165 170 175
 His Phe Phe Cys Glu Phe Ser Ser Leu Leu Ser Leu Ser Cys Ser Asp
 180 185 190
 Thr Tyr Ile Asn Gln Trp Leu Leu Phe Phe Leu Ala Thr Phe Asn Glu
 195 200 205
 Ile Ser Thr Leu Leu Ile Val Leu Thr Ser Tyr Ala Phe Ile Val Val
 210 215 220
 Thr Ile Leu Lys Met Arg Ser Val Ser Gly Arg Arg Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile
 245 250 255
 Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr Val
 260 265 270
 Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Thr Val Thr Glu
 290 295 300
 Ile Leu Asp Thr Lys Val Phe Ser Tyr
 305 310

<210> 1435

<211> 312

<212> PRT

<213> Unknown (H38g352 protein)

<220>

<223> Synthetic construct

<400> 1435

```

Met Ala Glu Arg Asn Tyr Thr Val Val Thr Glu Phe Phe Leu Thr Ala
 1           5           10           15
Phe Thr Glu His Leu Gln Trp Arg Val Pro Leu Phe Leu Ile Phe Leu
           20           25           30
Ser Phe Tyr Leu Ala Thr Met Leu Gly Asn Thr Gly Met Ile Leu Leu
           35           40           45
Ile Arg Gly Asp Arg Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
           50           55           60
His Leu Ser Leu Val Asp Ile Cys Tyr Ser Ser Ala Ile Ile Pro Gln
           65           70           75           80
Met Leu Ala Val Leu Trp Glu His Gly Thr Thr Ile Ser Gln Ala Arg
           85           90           95
Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Ala Ser Ile Asp Cys
           100          105          110
Tyr Leu Leu Ala Ile Met Ala Tyr Asp Arg Tyr Thr Ala Val Cys Gln
           115          120          125
Pro Leu Leu Tyr Val Thr Ile Ile Thr Glu Lys Asp Arg Leu Gly Leu
           130          135          140
Val Thr Gly Ala Tyr Val Ala Gly Phe Phe Ser Ala Phe Val Arg Thr
           145          150          155          160
Val Thr Ala Phe Thr Leu Ser Phe Cys Gly Asn Asn Glu Ile Asn Phe
           165          170          175
Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Gly Asp Ser
           180          185          190
Tyr Thr Gln Glu Val Val Ile Ile Val Phe Ala Leu Phe Val Met Pro
           195          200          205
Ala Cys Ile Leu Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala
           210          215          220
Ile Leu Gln Ile His Ser Ala Gly Gly Arg Ala Lys Thr Phe Ser Thr
           225          230          235          240
Cys Ala Ser His Leu Thr Ala Val Ala Leu Phe Phe Gly Thr Leu Ile
           245          250          255
Phe Met Tyr Leu Arg Asp Asn Thr Gly Gln Ser Ser Glu Gly Asp Arg
           260          265          270
Val Val Ser Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu
           275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Thr Arg Lys Ala
           290          295          300
Leu Ser Lys Ser Lys Pro Ala Arg
           305          310

```

<210> 1436

<211> 254

<212> PRT

<213> Unknown (H38g353 protein)

<220>

<223> Synthetic construct

<400> 1436

```

Met Tyr Tyr Phe Leu Ser Met Leu Ser Ala Thr Asp Leu Gly Leu Ser
 1           5           10           15
Ile Ser Thr Leu Val Thr Met Leu Ser Ile Phe Trp Phe Asn Val Arg
           20           25           30
Glu Ile Ser Phe Asn Ala Cys Leu Ser His Met Phe Phe Ile Lys Phe
           35           40           45
Phe Thr Val Met Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg
           50           55           60
Phe Val Ala Val Ser Asn Pro Leu Arg Tyr Ala Met Ile Leu Thr Asp
           65           70           75           80

```

```

Ser Arg Ile Ala Gln Ile Gly Val Ala Ser Val Ile Arg Gly Leu Leu
      85                      90                      95
Met Leu Thr Pro Met Val Ala Leu Leu Ile Arg Leu Ser Tyr Cys His
      100                      105                      110
Ser Gln Val Leu His His Ser Tyr Cys Tyr His Pro Asp Val Met Lys
      115                      120                      125
Leu Ser Cys Thr Asp Thr Arg Ile Asn Ser Ala Val Gly Leu Thr Ala
      130                      135                      140
Met Phe Ser Thr Val Gly Val Asp Leu Leu Leu Ile Leu Leu Ser Tyr
      145                      150                      155                      160
Val Leu Ile Ile Arg Thr Val Leu Ser Val Ala Ser Pro Glu Glu Arg
      165                      170                      175
Lys Glu Thr Phe Ser Thr Cys Val Ser His Ile Val Ala Phe Ala Ile
      180                      185                      190
Tyr Tyr Ile Pro Leu Ile Ser Leu Ser Ile Val His Arg Phe Gly Lys
      195                      200                      205
Gln Ala Pro Ala Tyr Val His Thr Met Ile Ala Asn Thr Tyr Leu Leu
      210                      215                      220
Ile Ser Pro Leu Met Asn Pro Val Ile Tyr Ser Val Lys Thr Lys Gln
      225                      230                      235                      240
Ile Arg Arg Ala Val Ile Lys Ile Leu His Ser Lys Glu Thr
      245                      250

```

<210> 1437

<211> 188

<212> PRT

<213> Unknown (H38g354 protein)

<220>

<223> Synthetic construct

<400> 1437

```

Met Asp Trp Glu Asn Cys Ser Ser Leu Thr Asp Phe Phe Leu Leu Gly
  1                      5                      10                      15
Ile Thr Asn Asn Pro Glu Met Lys Val Thr Leu Phe Ala Val Phe Leu
      20                      25                      30
Ala Val Tyr Ile Ile Asn Phe Ser Ala Asn Leu Gly Met Ile Val Leu
      35                      40                      45
Ile Arg Met Asp Tyr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50                      55                      60
His Leu Ser Phe Cys Asp Leu Cys Tyr Ser Thr Ala Thr Gly Pro Lys
      65                      70                      75                      80
Met Leu Val Asp Leu Leu Ala Lys Asn Lys Ser Ile Pro Phe Tyr Gly
      85                      90                      95
Cys Ala Leu Gln Phe Leu Val Phe Cys Ile Phe Ala Asp Ser Glu Cys
      100                      105                      110
Leu Leu Leu Ser Val Met Ala Phe Asp Arg Tyr Lys Ala Ile Ile Asn
      115                      120                      125
Pro Leu Leu Tyr Thr Val Asn Met Ser Ser Arg Val Cys Tyr Leu Leu
      130                      135                      140
Leu Thr Gly Val Tyr Leu Val Gly Ile Ala Asp Ala Leu Ile His Met
      145                      150                      155                      160
Thr Leu Ala Phe Arg Leu Cys Phe Cys Gly Ser Asn Glu Ile Asn His
      165                      170                      175
Phe Phe Cys Asp Ile Pro Pro Leu Leu Leu Leu Ser
      180                      185

```

<210> 1438

<211> 326

<212> PRT

<213> Unknown (H38g355 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1438

```

Leu Asn Phe Ile Ile Phe Phe Arg Xaa Thr Ser Tyr Ile Glu Pro Met
 1           5           10           15
Ala Lys Arg Asn Leu Ser Thr Val Thr Glu Phe Ile Leu Val Val Phe
      20           25           30
Thr Asp His Pro Glu Leu Ala Val Pro Leu Phe Leu Val Phe Leu Ser
      35           40           45
Phe Tyr Leu Val Thr Phe Leu Gly Asn Gly Gly Met Ile Ile Leu Ile
      50           55           60
Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser His
      65           70           75           80
Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln Ile
      85           90           95
Leu Ala Thr Leu Ala Thr Asp Lys Thr Val Ile Ser Tyr Gly Cys Arg
      100          105          110
Ala Val Gln Phe Ser Phe Phe Thr Ile Cys Ala Gly Thr Glu Cys Tyr
      115          120          125
Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Ser Asn Pro
      130          135          140
Leu His Cys Asn Met Thr Met Thr Pro Gly Thr Cys Arg Val Phe Leu
      145          150          155          160
Ala Ser Ala Phe Ile Cys Gly Val Ser Gly Ala Ile Leu His Thr Thr
      165          170          175
Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe Phe
      180          185          190
Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met Thr
      195          200          205
Gln Thr Glu Ile Val Ile Leu Leu Cys Ala Lys Cys Met Phe Leu Ala
      210          215          220
Asn Val Met Val Ile Leu Ile Cys Tyr Met Leu Ile Ile Arg Ala Ile
      225          230          235          240
Leu Arg Val Lys Ser Ala Gly Gly Xaa Ala Lys Thr Phe Ser Thr Cys
      245          250          255
Thr Ser His Leu Thr Thr Val Val Leu Phe Phe Gly Thr Leu Ala Phe
      260          265          270
Met Tyr Gln Arg Ser Asn Ser Ala Lys Ser Ser Glu Glu Asp Lys Ile
      275          280          285
Val Ser Val Phe Tyr Thr Val Ile Ile Pro Met Leu Asn Pro Leu Ile
      290          295          300
Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Phe Gly Lys Leu Val
      305          310          315          320
Gly Lys Phe Gln Phe Pro
      325

```

<210> 1439

<211> 328

<212> PRT

<213> Unknown (H38g356 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1439

```

Met L u Pro Ser Gln Thr Tyr Val Asn Ile Ser Phe Phe Gln Pro Pro
 1          5          10          15
Ala Leu Leu Met Ile Gly Ile Pro Gly Leu Glu Ala Val His Gly Trp
      20          25          30
Leu Ala Ile Pro Phe Ser Ser Met Tyr Thr Val Ala Leu Pro Gly Asn
      35          40          45
Cys Leu Ile Leu Leu Ala Val Lys Arg Asn Pro Ser Leu His Gln Pro
      50          55          60
Met Cys Tyr Phe Leu Ser Met Leu Ala Leu Pro Lys Ala Gly Leu Thr
      65          70          75          80
Leu Ser Thr Leu Pro Ile Thr Leu Ala Val Leu Trp Phe Asp His Arg
      85          90          95
Leu Met Gly Phe Asn Ala Cys Leu Val Gln Met Phe Phe Leu His Ser
      100          105          110
Ser Val Val Glu Ser Ser Val Leu Leu Ala Ile Ser Phe Asp His Phe
      115          120          125
Val Ala Ile Ser Asn Pro Leu His Tyr Ala Ala Val Leu Thr Asn Ser
      130          135          140
Val Ile Ile Arg Ile Gly Leu Ala Ile Val Ala Arg Ser Tyr Leu Val
      145          150          155          160
Pro Leu Pro Val Pro Phe Pro Val Lys Ser Leu Asn Phe Cys Pro Gly
      165          170          175
Asp Asn Ile Pro Ser His Ser Phe Cys Phe His Pro Asp Val Met Arg
      180          185          190
Arg Ala Cys Ala Asp Ile Thr Ile Asn Ile Cys Tyr Gly Val Tyr Val
      195          200          205
Val Val Ser Thr Gly Gly Leu Asp Ser Leu Leu Ile Phe Leu Ser Tyr
      210          215          220
Thr Phe Ile Leu His Thr Val Met Gly Leu Ala Ala Pro Arg Glu Arg
      225          230          235          240
Ile Trp Ala Leu Asn Thr Cys Val Ser His Ile Pro Ala Val Phe Val
      245          250          255
Phe Phe Ile Pro Gly Ile Thr Val Ser Met Ile His His Phe Gly Arg
      260          265          270
His Leu Pro His Ile Val His Ala Leu Val Thr Tyr Val Tyr Leu Val
      275          280          285
Met Pro Ser Val Leu His Pro Ile Ile Tyr Ser Met Lys Ser Lys Pro
      290          295          300
Ile Arg Glu Ala Ile Leu Arg Met Leu Met Gly Arg Ser Gln Gly Xaa
      305          310          315          320
Xaa Asn Tyr Lys Ile Leu Xaa Gly
      325

```

<210> 1440

<211> 311

<212> PRT

<213> Unknown (H38g357 protein)

<220>

<223> Synthetic construct

<400> 1440

```

Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu
      20          25          30
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu

```



```

      35      40      45
Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
  50      55      60
His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys
  65      70      75      80
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly
      85      90      95
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val
      100      105      110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
      115      120      125
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu
      130      135      140
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu
  145      150      155      160
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His
      165      170      175
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile
      180      185      190
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser
      195      200      205
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr
      210      215      220
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
  225      230      235      240
Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu
      245      250      255
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys
      260      265      270
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Val
      290      295      300
Met Gly Ser Lys Ile His Ser
  305      310

```

<210> 1441

<211> 209

<212> PRT

<213> Unknown (H38g358 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(209)

<223> Xaa = Any Amino Acid

<400> 1441

```

Cys His Pro Pro Leu Arg Trp Gly Ser Xaa Glu Pro Ala Glu Glu Glu
  1      5      10      15
Gly Leu Ala Leu Ser Ser Arg Phe Phe Phe Leu Ser Val Leu Asp
      20      25      30
Ala Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp
      35      40      45
Ala Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu
      50      55      60
Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala
  65      70      75      80
Val Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr
      85      90      95

```

Lys Ile Val Ser Ser Ile Leu Ser Val Ser Ser Ser Arg Gly Gln Tyr
 100 105 110
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe
 115 120 125
 Tyr Gly Thr Gly Val Gly Gly Tyr Phe Ser Ser Asp Val Ser Ser Ser
 130 135 140
 Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Pro
 145 150 155 160
 Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg His Ile Lys Ser
 165 170 175
 Val Leu Arg Arg Pro His Ser Ser Thr Val Gln Ser Pro Cys Leu Leu
 180 185 190
 Asn Cys Ser Ile Pro Phe Val Val Trp Val Asn Lys Gly Ser Lys Val
 195 200 205
 Lys

<210> 1442

<211> 212

<212> PRT

<213> Unknown (H38g359 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1442

Ile Xaa Leu Lys Leu Ile Phe Gly Asn Pro Arg Xaa Xaa Xaa Ile Phe
 1 5 10 15
 Arg Cys Val Tyr Asp Tyr Leu Trp Asp Cys Gln Pro Leu Leu Tyr Asp
 20 25 30
 Thr Ile Thr Thr Leu Lys Met Ser Gly Arg Ser Trp Xaa Leu His Ile
 35 40 45
 Val Glu Gly Leu Thr Asn Val Ile Gln Cys Ile His Phe Thr Cys Ser
 50 55 60
 Leu Ser Phe Cys Gly Thr Ser Ser Ile Gly Phe Thr Leu Cys Asp Leu
 65 70 75 80
 Pro Leu Leu Leu Thr Leu Asn Cys Gly Asp Ser Phe Leu Gln Gln Leu
 85 90 95
 Leu Ile Phe His Phe Ala Leu Tyr Met Ile Leu Thr Arg Leu Val Leu
 100 105 110
 Ile Leu Phe Ser Asp Leu Phe Ile Ser Lys Ala Ile Xaa Thr Pro Ala
 115 120 125
 Asn Gln Val Ser Arg Gln Arg Phe Leu Asn Leu Phe Leu Pro Leu Pro
 130 135 140
 His Ala Glu Leu Gln Phe Gly Xaa Leu Leu Arg Leu Gln Leu Xaa Ser
 145 150 155 160
 Met Cys Ala Ala Val Gly Lys Ser Leu Thr Gly Glu Arg Ala Val Thr
 165 170 175
 Met Phe Xaa Thr Glu Xaa Thr Pro Gly Xaa Pro Phe Gln Phe Tyr Ser
 180 185 190
 Leu Arg Asn Lys Lys Ala Lys Glu Ala Leu Arg Lys Gly Leu Asn Lys
 195 200 205
 Ala Lys Leu Phe
 210

<210> 1443

<211> 315

<212> PRT

<213> Unknown (H38g360 protein)

<220>

<223> Synthetic construct

<400> 1443

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
 1          5          10          15
Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
      20          25          30
Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
 35          40          45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 50          55          60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
 65          70          75          80
Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
      85          90          95
Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
      100          105          110
Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
      115          120          125
Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
      130          135          140
Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
      145          150          155          160
Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
      165          170          175
Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
      180          185          190
Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
      195          200          205
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
      210          215          220
Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
      225          230          235          240
Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
      245          250          255
Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
      260          265          270
Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
      275          280          285
Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
      290          295          300
Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln
      305          310          315

```

<210> 1444

<211> 278

<212> PRT

<213> Unknown (H38g361 protein)

<220>

<223> Synthetic construct

<400> 1444

```

Met Tyr Ala Leu Ala Thr Leu Gly Asn Leu Thr Ile Val Leu Ile Ile
 1          5          10          15
Arg Val Glu Arg Arg Leu His Glu Pro Met Tyr Leu Phe Leu Ala Met
      20          25          30

```

Leu Ser Thr Ile Asp Leu Val Leu Ser Ser Ile Thr Met Pro Lys Met
 35 40 45
 Ala Ser Leu Phe Leu Met Gly Ile Gln Glu Ile Glu Phe Asn Ile Cys
 50 55 60
 Leu Ala Gln Met Phe Leu Ile His Ala Leu Ser Ala Val Glu Ser Ala
 65 70 75 80
 Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro
 85 90 95
 Leu Arg His Ala Ser Val Leu Thr Gly Cys Thr Val Ala Lys Ile Gly
 100 105 110
 Leu Ser Ala Leu Thr Arg Gly Phe Val Phe Phe Phe Pro Leu Pro Phe
 115 120 125
 Ile Leu Lys Trp Leu Ser Tyr Cys Gln Thr His Thr Val Thr His Ser
 130 135 140
 Phe Cys Leu His Gln Asp Ile Met Lys Leu Ser Cys Thr Asp Thr Arg
 145 150 155 160
 Val Asn Val Val Tyr Gly Leu Phe Ile Ile Leu Ser Val Met Gly Val
 165 170 175
 Asp Ser Leu Phe Ile Gly Phe Ser Tyr Ile Leu Ile Leu Trp Ala Val
 180 185 190
 Leu Glu Leu Ser Ser Arg Arg Ala Ala Leu Lys Ala Phe Asn Thr Cys
 195 200 205
 Ile Ser His Leu Cys Ala Val Leu Val Phe Tyr Val Pro Leu Ile Gly
 210 215 220
 Leu Ser Val Val His Arg Leu Gly Gly Pro Thr Ser Leu Leu His Val
 225 230 235 240
 Val Met Ala Asn Thr Tyr Leu Leu Leu Pro Pro Val Val Asn Pro Leu
 245 250 255
 Val Tyr Gly Ala Lys Thr Lys Glu Ile Cys Ser Arg Val Leu Cys Met
 260 265 270
 Phe Ser Gln Gly Gly Lys
 275

<210> 1445

<211> 319

<212> PRT

<213> Unknown (H38g362 protein)

<220>

<223> Synthetic construct

<400> 1445

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe
 1 5 10 15
 Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala
 20 25 30
 Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Leu
 35 40 45
 Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr
 50 55 60
 Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser
 65 70 75 80
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile
 85 90 95
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr
 100 105 110
 Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val
 130 135 140
 Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met

```

145          150          155          160
Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn
          165          170          175
Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala
          180          185          190
Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser
          195          200          205
Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu
          210          215          220
Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys
225          230          235          240
Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr
          245          250          255
Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile
          260          265          270
Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile
          275          280          285
Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu
290          295          300
Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His
305          310          315

```

<210> 1446

<211> 322

<212> PRT

<213> Unknown (H38g363 protein)

<220>

<223> Synthetic construct

<400> 1446

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
 1          5          10          15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
          20          25          30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
          35          40          45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
65          70          75          80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
          85          90          95
His Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
          100          105          110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
          130          135          140
Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
          165          170          175
Phe Phe Cys Asp Leu Pro Leu Ala Thr Lys Leu Ala Cys Ile Asp Thr
          180          185          190
Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser Gly Phe Leu Ser Leu
          195          200          205
Ser Ser Phe Leu Leu Leu Val Val Ser Tyr Thr Val Ile Leu Val Thr
210          215          220
Val Arg Asn Arg Ser Ser Val Ser Met Val Lys Ala His Ser Thr Leu
225          230          235          240

```

```

Thr Ala His Ile Thr Val Val Thr Leu Phe Phe Gly Ser Cys Ile Phe
      245      250      255
Ile Tyr Val Trp Pro Phe Ser Ser Tyr Ser Val Asp Lys Val Leu Ala
      260      265      270
Val Phe Tyr Thr Ile Phe Thr Ser Ile Leu Asn Pro Val Ile Tyr Met
      275      280      285
Leu Arg Asn Lys Glu Val Lys Ala Ala Met Ser Lys Leu Lys Ser Arg
      290      295      300
Tyr Gln Lys Leu Gly Gln Val Ser Val Val Ile Arg Asn Val Leu Phe
      305      310      315      320
Leu Glu

```

<210> 1447

<211> 322

<212> PRT

<213> Unknown (H38g364 protein)

<220>

<223> Synthetic construct

<400> 1447

```

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe
  1      5      10      15
Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala
      20      25      30
Ile Ser Leu Ser Ala Met Tyr Ile Ile Ala Leu Leu Gly Asn Thr Ile
      35      40      45
Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr
      50      55      60
Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser
      65      70      75      80
Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile
      85      90      95
Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr
      100      105      110
Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val
      115      120      125
Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val
      130      135      140
Met Leu Gly Met Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile
      145      150      155      160
Thr Pro Leu Ser Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn
      165      170      175
Val Val Val His Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala
      180      185      190
Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser
      195      200      205
Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu
      210      215      220
Ile Leu Lys Ala Val Phe Gly Leu Ser Ser Lys Thr Ala Gln Leu Lys
      225      230      235      240
Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr
      245      250      255
Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Val
      260      265      270
Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile
      275      280      285
Pro Ala Thr Leu Asn Pro Ile Tyr Gly Met Arg Thr Lys Gln L u
      290      295      300
Arg Glu Arg Ile Trp Ser Tyr Leu Met His Val Leu Phe Asp His Ser

```

305
Asn Leu

310

315

320

<210> 1448
<211> 314
<212> PRT
<213> Unknown (H38g365 protein)

<220>
<223> Synthetic construct

<400> 1448
Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
1 5 10 15
Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser
20 25 30
Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
35 40 45
Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser
50 55 60
Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
65 70 75 80
Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly Cys
85 90 95
Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
100 105 110
Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
115 120 125
Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
130 135 140
Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
145 150 155 160
Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
165 170 175
Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
180 185 190
Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu
195 200 205
Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile
210 215 220
Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
225 230 235 240
Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
245 250 255
Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser
260 265 270
Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
275 280 285
Leu Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Lys Leu Asn Ile
290 295 300
Gln Tyr Phe Ser Leu Gly Lys Thr Ala Pro
305 310

<210> 1449
<211> 317
<212> PRT
<213> Unknown (H38g366 protein)

<220>
<223> Synthetic construct

<400> 1449

```

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu
1      5      10
Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro
20      25      30
Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu
35      40      45
Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe
50      55      60
Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile
65      70      75      80
Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu
85      90      95
Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val
100     105     110
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
115     120     125
Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly
130     135     140
Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro
145     150     155     160
Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val
165     170     175
Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys
180     185     190
Gly Asp Ser Arg Val Asn Asn Val Tyr Gly Leu Ser Ile Gly Phe Leu
195     200     205
Val Leu Ile Leu Asp Ser Val Ala Ile Ala Ala Ser Tyr Val Met Ile
210     215     220
Phe Arg Ala Val Met Gly Leu Ala Thr Pro Glu Ala Arg Leu Lys Thr
225     230     235     240
Leu Gly Thr Cys Ala Ser His Leu Cys Ala Ile Leu Ile Phe Tyr Val
245     250     255
Pro Ile Ala Val Ser Ser Leu Ile His Arg Phe Gly Gln Cys Val Pro
260     265     270
Pro Pro Val His Thr Leu Leu Ala Asn Phe Tyr Leu Leu Ile Pro Pro
275     280     285
Ile Leu Asn Pro Ile Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu
290     295     300
Ser Leu Leu Gln Ile Pro Arg Ile Glu Met Lys Ile Arg
305     310     315

```

<210> 1450

<211> 101

<212> PRT

<213> Unknown (H38g367 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(101)

<223> Xaa = Any Amino Acid

<400> 1450

```

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val
1      5      10      15
Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr
20      25      30
Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr

```



```

          35          40          45
Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Ile Leu
  50          55          60
Glu Gly Xaa Phe Ile His Phe Trp His His Val Tyr Ser Ile Leu Lys
65          70          75          80
Ile Pro Arg Met Lys Lys Lys Asn Leu Gln Ile Ile Pro Leu Ile Gly
          85          90          95
Cys Cys Leu Ala Glu
          100

```

<210> 1451
 <211> 169
 <212> PRT
 <213> Unknown (H38g368 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(169)
 <223> Xaa = Any Amino Acid

```

<400> 1451
Asn Ser Glu Ser Lys His Phe Leu Leu Leu Lys Leu Cys Ser Met Phe
  1          5          10          15
Ala Val Thr Phe Leu Ser Leu Ile Leu Ser Gly Lys Gly Leu Gln Phe
          20          25          30
Pro Phe Tyr Phe Ser Glu Cys Asn Cys Lys Val Ser Asp Val Phe Thr
          35          40          45
Val Glu Thr Arg Glu Gln Glu Ala Pro Met Lys Thr Thr Gly Phe Tyr
          50          55          60
Gly Gly Ile Met Val Trp Xaa Val Glu Ala Cys Tyr Ser Ser Cys Ile
65          70          75          80
Ser Leu Gly Ser Asn Pro Asp Tyr Thr Ala Tyr Gly Ala Leu Thr Ala
          85          90          95
Arg Xaa Pro Gln Glu Phe Leu Cys Trp Xaa Asn Arg Phe Ile Ile Met
          100          105          110
Pro Val Asn Leu Lys Met Leu Xaa Val Lys Thr Ile Trp Cys Phe Ser
          115          120          125
Arg Thr Gln Xaa Ser Leu Thr Val Ile Thr Ile Phe Pro Leu Pro Thr
          130          135          140
Phe Asn Lys Xaa Ile Ile Tyr Ile Tyr Xaa Thr Lys Glu Ile Xaa Ser
145          150          155          160
Cys Phe Ser Glu Thr Thr Gln Phe Tyr
          165

```

<210> 1452
 <211> 279
 <212> PRT
 <213> Unknown (H38g369 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(279)
 <223> Xaa = Any Amino Acid

```

<400> 1452
Leu Pro Pro Leu Phe Phe Arg Val Phe Val Ile Leu Phe Val Ser Leu
  1          5          10          15

```

Leu Phe Val Lys Leu Cys Ile Leu Phe Leu Ile Ile Leu Leu Val Lys
 20 25 30
 Phe Leu Leu Lys Thr Lys Ile Ala Met Thr Tyr Phe Thr Tyr Leu Ser
 35 40 45
 Asn Tyr Lys Leu Lys Ala Xaa Asn Ser Ile Asp Phe His Ile His Met
 50 55 60
 Phe Val Tyr Val Tyr Ile Met Asn Lys Leu Val His Leu Lys Tyr Glu
 65 70 75 80
 Thr Leu Thr Ser Leu Pro Phe Phe Trp Asn Ser Leu Gly Cys Leu Asp
 85 90
 Thr Ser Xaa Phe Cys Phe Thr Phe Tyr Val Thr Tyr Ser Ser Leu Ile
 100 105 110
 Val Ile Asn Met Leu Tyr Phe Leu Ala Val Leu Ala Lys Ser Ser Phe
 115 120 125
 Ile Leu Cys Phe Asn Ser Leu Ser Val Asn Cys Asp Thr Phe Cys Val
 130 135 140
 Trp Leu Ser Cys Phe Gly Ile Val Tyr Leu Asp Val His Pro Ile Ala
 145 150 155 160
 His Cys Leu Phe Leu Lys Arg Leu Phe Lys Cys Tyr Val Phe Leu Xaa
 165 170 175
 Ser Leu Val Phe Cys Phe Met His Ala Leu Leu Pro Xaa Thr Leu Lys
 180 185 190
 Asn Thr Cys Phe Asp Val Leu Phe Ile Phe Ile Cys Glu Lys Ser Leu
 195 200 205
 Leu Ala Asn Met Ser Phe Val Thr Ile Val Ser Ser Leu Ile Leu Leu
 210 215 220
 Thr Asn Xaa Glu Ile Ile Ser Phe Ser Ser Val Ile Leu Cys Gly Thr
 225 230 235 240
 Ile His Leu Asn Leu Ser Ser Phe Phe Leu His Arg Phe Phe Ile Phe
 245 250 255
 Phe Phe Cys Leu Lys Ser Ala Asn Ile Tyr Leu Asn Val Asp Leu Leu
 260 265 270
 Ser Ile Ile Leu Thr Leu Val
 275

<210> 1453

<211> 154

<212> PRT

<213> Unknown (H38g370 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(154)

<223> Xaa = Any Amino Acid

<400> 1453

Cys Thr Met Cys Val Trp Leu Leu Ala Xaa Asp Arg Gln Ile His Ile
 1 5 10 15
 His Ser His Ser Asn Lys Pro Lys Gln Val Thr His Pro Met Cys Phe
 20 25 30
 Trp Asp Lys Asp Val His Ser Ser Trp Ala Trp Gly Cys Gly Tyr Arg
 35 40 45
 Lys Gly Asn Lys Phe Phe Leu Ser Tyr Asp Thr Leu Cys Pro Pro Lys
 50 55 60
 Val Ile His Pro Phe Arg Xaa Gln Leu Phe Leu Ser Ser Ser Asp Ile
 65 70 75 80
 Ile Asn Asp Pro His Ile Asp Lys His Asp Ser Thr Leu Ile Thr Leu
 85 90 95
 Xaa Ala Phe Tyr Thr Ile Phe Tyr Lys Pro Thr Met Leu His Leu Phe

```

          100          105          110
Ser Glu Ile Leu Ser Met Ile Tyr Phe Met Gly Thr Lys Lys Asn Glu
          115          120          125
Xaa Lys Pro Arg Lys Lys Asp Cys Glu Ser His Xaa Lys Gly Leu Glu
          130          135          140
Xaa Met Gly Gln Ile Ile Ile Leu Phe Tyr
145          150

```

<210> 1454
 <211> 186
 <212> PRT
 <213> Unknown (H38g371 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(186)
 <223> Xaa = Any Amino Acid

```

<400> 1454
Pro Ala His Pro Arg Ser Pro His His Pro Leu Phe Pro Pro Tyr Ile
  1          5          10          15
Tyr Leu Lys Asn Phe Phe Pro Thr Ile Phe Pro Gln Asn Leu Leu Ser
          20          25          30
Leu Leu Phe Thr Thr Val Phe Pro Pro Pro Thr Pro Asn Ile Phe
          35          40          45
Ser Pro Pro Ser Phe Pro His Cys Leu Phe Cys Asn Thr Phe Ser Cys
          50          55          60
Ser Leu Ile Leu Tyr Phe Pro Leu Ala Leu Thr Thr Leu Phe Thr Pro
          65          70          75          80
Pro Ser Thr Pro Lys Leu Phe Ser Pro Ser Tyr Arg Ser Ser His Thr
          85          90          95
Ala Val Ser Val Ala Ala Thr Asn Arg Ser Glu Ala Ser Cys Ala Cys
          100          105          110
Arg Ser His Ser Leu Gln His Ala Ala Val Ala Ser Pro Cys Pro Gly
          115          120          125
Pro Leu Ser Arg Glu Arg Ser Ser Pro Ala Arg Arg His Ala Xaa Ala
          130          135          140
Xaa Asn Gly Leu Thr Pro Leu Leu Ala Pro Phe Ile Tyr Xaa Gly Tyr
          145          150          155          160
Ala Tyr Glu Val Pro Gly Leu Leu Phe Gln Asp Trp Val Arg Glu Asn
          165          170          175
Ala Glu Ala Tyr Ser Asp Trp Thr Leu Leu
          180          185

```

<210> 1455
 <211> 142
 <212> PRT
 <213> Unknown (H38g372 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(142)
 <223> Xaa = Any Amino Acid

```

<400> 1455
Tyr Ile Glu Met Asp Asn Tyr Phe Leu Thr Xaa Leu Xaa Arg Tyr Leu
  1          5          10          15

```

```

Leu Phe Phe His Phe Ile Ile Ser Thr Gln Tyr Phe Gly Ile Lys Lys
      20      25      30
Phe Ile Leu Thr Ser Leu Leu Ala Tyr Cys Phe Trp Met Phe Ser Ile
      35      40      45
Thr Lys Phe Leu Thr Tyr Gly Leu Lys Trp Leu Leu Ile Pro Asp Cys
      50      55      60
Xaa Ser Trp Tyr Gln His Ala Xaa Phe Asn Pro Xaa Gln Ile Leu Phe
65      70      75      80
Leu Gln Asn Ser Xaa Ser Trp Leu Glu Val Tyr Phe Tyr Leu Phe Leu
      85      90      95
Leu Phe Ala Val Pro Phe Asp Lys Ile Ile Phe Leu Ser Xaa Lys Met
      100     105     110
Tyr Leu Asn Lys Xaa Ile Ile Ser Val Leu Val Gly Thr Arg Trp Thr
      115     120     125
Phe Gln Arg Cys Val His Thr Leu Cys Ile Leu Ser Leu Phe
      130     135     140

```

<210> 1456
 <211> 82
 <212> PRT
 <213> Unknown (H38g373 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(82)
 <223> Xaa = Any Amino Acid

```

<400> 1456
Asn Val Phe Arg Xaa Phe Leu Asp Phe Cys Arg Asp Ser Asp Ile His
 1      5      10
Arg Ala Tyr Leu Cys Ile Leu Ser Ser Xaa Leu Arg Phe Ser Val Leu
      20      25      30
Gly Ile Phe Xaa Gly Arg Ala Met Asn Ile Leu Ile Gly Leu Thr Lys
      35      40      45
Val Leu Lys Cys Pro Ile Leu Cys Val Val Phe Asn His Thr Cys Ile
      50      55      60
Leu Ile Thr Thr Leu Ala Val Ile Ala Tyr Arg Phe Arg Gln Ser Gly
65      70      75      80
Tyr Ser

```

<210> 1457
 <211> 207
 <212> PRT
 <213> Unknown (H38g374 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(207)
 <223> Xaa = Any Amino Acid

```

<400> 1457
Glu Ile Ile Leu Ile Gly Ile Ser Leu Lys Leu Tyr Leu Val Val Phe
 1      5      10
Thr Ile Ile Lys Ile Lys Xaa His Ser Ile Gly Leu Ser Ser Asn Lys
      20      25      30
Asn Met Arg Leu Pro Ser Asp Phe Phe Leu Ser Gln Ala Ile Tyr Tyr

```

<210> 1458
<211> 313
<212> PRT
<213> Unknown (H38g375 protein)

<220>
<223> Synthetic construct

Met 1	Arg	Asn	Leu	Ser 5	Gly	Gly	His	Val	Glu 10	Glu	Phe	Val	Leu	Val 15	Gly
Phe	Pro	Thr	Thr 20	Pro	Pro	Leu	Gln	Leu 25	Leu	Leu	Phe	Val	Leu 30	Phe	Phe
Ala	Ile	Tyr 35	Leu	Leu	Thr	Leu	Leu 40	Glu	Asn	Ala	Leu	Ile 45	Val	Phe	Thr
Ile	Trp 50	Leu	Ala	Pro	Ser	Leu 55	His	Arg	Pro	Met	Tyr 60	Phe	Phe	Leu	Gly
His 65	Leu	Ser	Phe	Leu	Glu 70	Leu	Trp	Tyr	Ile	Asn 75	Val	Thr	Ile	Pro	Arg
Leu	Leu	Ala	Ala 85	Phe	Leu	Thr	Gln	Asp 90	Gly	Arg	Val	Ser	Tyr 95	Val	Gly
Cys	Met	Thr	Gln 100	Leu	Tyr	Phe	Phe 105	Ile	Ala	Leu	Ala	Cys	Thr 110	Glu	Cys
Val	Leu 115	Leu	Ala	Val	Met	Ala	Tyr 120	Asp	Arg	Tyr	Leu	Ala 125	Ile	Cys	Gly
Pro	Leu 130	Leu	Tyr	Pro	Ser	Leu 135	Met	Pro	Ser	Ser	Leu 140	Ala	Thr	Arg	Leu
Ala 145	Ala	Ala	Ser	Trp	Gly 150	Ser	Gly	Phe	Phe	Ser	Ser 155	Met	Met	Lys	Leu
Leu	Phe	Ile	Ser 165	Gln	Leu	Ser	Tyr	Cys 170	Gly	Pro	Asn	Ile	Ile 175	Asn	His
Phe	Phe	Cys 180	Asp	Ile	Ser	Pro	Leu 185	Leu	Asn	Leu	Thr	Cys 190	Ser	Asp	Lys
Glu	Gln 195	Ala	Glu	Leu	Val	Asp	Phe 200	Leu	Leu	Ala	Leu 205	Val	Met	Ile	Leu
Leu	Pro 210	Leu	Leu	Ala	Val	Val 215	Ser	Ser	Tyr	Thr	Ala 220	Ile	Ile	Ala	Ala
Ile 225	Leu	Arg	Ile	Pro	Thr 230	Ser	Arg	Gly	Arg	His 235	Lys	Ala	Phe	Ser	Thr 240

```
<210> 1459
<211> 322
<212> PRT
<213> Unknown (H38g376 protein)
```

<220>
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(322)
<223> Xaa = Any Amino Acid
```

745

290 295 300
 Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Leu His Pro
 305 310 315 320
 Phe Ser

<210> 1460
 <211> 186
 <212> PRT
 <213> Unknown (H38g377 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(186)
 <223> Xaa = Any Amino Acid

<400> 1460
 Pro Val Pro Gln His Leu Phe Phe Phe Leu Lys Val Thr Gly His Leu
 1 5 10 15
 Leu Thr Xaa Ile Arg Asn Leu Xaa Phe Val Pro Asp Phe Ser Phe Ser
 20 25 30
 Leu Ala Leu His Ile Tyr Gln Xaa Tyr Xaa Phe Xaa Thr Asn Leu Asn
 35 40 45
 Glu Leu His Leu Cys Pro Ser Leu Ile Ser Pro Pro Ser Leu Ser Val
 50 55 60
 His Xaa Leu Arg Leu His His Val Asn Tyr Tyr His Gly Met Leu Thr
 65 70 75 80
 Glu Leu Leu Leu Pro Met Val Pro Cys His Asn Ser Ser Phe Ile Trp
 85 90 95
 Leu Pro Ile Asn Phe Xaa Lys Phe Ile Cys Ile Cys Tyr Phe Ser Gly
 100 105 110
 Xaa Lys Leu Pro Met His Val Glu Asp Gly Met Gln Thr Ala Leu His
 115 120 125
 Ala Cys Pro Leu Leu Met Gln Leu Leu Leu Ser Ile Pro His Ser Tyr
 130 135 140
 Pro Leu Leu Leu Asp Asn Ser Phe Leu Phe Leu Arg Leu His Pro Arg
 145 150 155 160
 Ser Lys Leu Ser Tyr Phe Leu His Ile Leu Leu Ser Xaa Pro Phe Thr
 165 170 175
 Tyr Val Asn His Leu Leu Pro Phe Leu Leu
 180 185

<210> 1461
 <211> 336
 <212> PRT
 <213> Unknown (H38g378 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(336)
 <223> Xaa = Any Amino Acid

<400> 1461
 Ser Arg Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Gly Ser Ser Glu Asp Pro Glu Arg Gln Pro Val Leu Thr Gly Leu Phe
 20 25 30

```

Leu Ser Thr Cys Leu Val Met Ala Leu Gly Asn Leu Leu Ile Ile Leu
  35                      40                      45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
  50                      55                      60
Ser Asn Leu Ser Leu Pro Asp Ile Ser Phe Thr Ser Thr Thr Val Pro
  65                      70                      75                      80
Lys Met Thr Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
                      85                      90                      95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
                      100                      105                      110
Asp Asn Ile Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Lys
                      115                      120                      125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
                      130                      135                      140
Phe Leu Leu Leu Leu Ser Phe Phe Ser Ser Leu Ser Leu Leu Asp Ala
  145                      150                      155                      160
Gln Leu Tyr Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
                      165                      170                      175
Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
                      180                      185                      190
Cys Cys Asp Thr Phe Asn Asn Asn Ile Ile Leu Tyr Phe Pro Asp Ala
                      195                      200                      205
Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys
                      210                      215                      220
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
  225                      230                      235                      240
Ala Phe Ser Thr Tyr Gly Ser His Leu Ser Asp Val Ser Xaa Phe Tyr
                      245                      250                      255
Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro
                      260                      265                      270
Arg Lys Thr Ala Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met
                      275                      280                      285
Met Asn Pro Phe Ile Tyr Ser Pro Arg Asn Arg Asp Met Lys Ser Val
                      290                      295                      300
Leu Arg Arg Pro His Gly Ser Thr Phe Xaa Ser Gln Tyr Leu Leu Ile
  305                      310                      315                      320
Cys Ser Ile Pro Phe Ala Val Trp Val Glu Lys Gly Cys Met Met Lys
                      325                      330                      335

```

<210> 1462

<211> 157

<212> PRT

<213> Unknown (H38g379 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1462

```

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
  1                      5                      10                      15
Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
                      20                      25                      30
Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
                      35                      40                      45
Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
  50                      55                      60
Phe Leu Pro Lys Leu Gln Pro Phe Ser S r Cys His Val Ser Glu Leu

```


65					70					75				80	
Cys	Thr	Cys	Leu	Asp	Thr	Phe	Thr	Lys	Ser	Tyr	Ile	Thr	Xaa	Ile	Arg
				85					90					95	
Gly	Leu	Lys	Gly	Phe	Asn	His	Leu	Cys	Phe	Leu	Leu	His	Tyr	Cys	His
			100					105					110		
Cys	Ala	Arg	Ala	Gln	Val	Ser	Xaa	Asn	Ala	Pro	Trp	Ser	Leu	Ala	Gln
		115					120					125			
Arg	Cys	Gln	Pro	Asn	Met	Leu	Ile	Arg	Xaa	Leu	Phe	Cys	Leu	Lys	Leu
		130					135				140				
Val	Val	His	Asp	Arg	Leu	Xaa	His	Val	Leu	Ser	Leu	Leu			
145					150					155					

<210> 1463

<211> 325

<212> PRT

<213> Unknown (H38g380 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1463

Met	Lys	Ile	Asn	Gln	Thr	Ile	Leu	Lys	Glu	Phe	Ile	Leu	Val	Gly	Phe
1				5				10						15	
Ser	Val	Tyr	Pro	His	Val	Gln	Thr	Phe	Leu	Phe	Val	Val	Phe	Phe	Cys
			20					25					30		
Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Gly	Asn	Leu	Thr	Ile	Met	Gly	Leu	Thr
		35					40					45			
Xaa	Val	Asp	Arg	Ser	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu	Ser	Ala
	50					55					60				
Leu	Ser	Phe	Ser	Glu	Thr	Cys	Tyr	Thr	Leu	Thr	Ile	Val	Pro	Lys	Met
65					70					75					80
Leu	Glu	Asp	Leu	Leu	Ala	Lys	Asp	Arg	Ser	Ile	Ser	Val	Thr	Gly	Cys
				85				90						95	
Ser	Leu	Gln	Met	Cys	Phe	Phe	Leu	Gly	Leu	Gly	Gly	Thr	Asn	Cys	Ile
			100					105					110		
Ile	Leu	Thr	Leu	Met	Gly	Tyr	Asp	Arg	Phe	Leu	Ala	Ile	Cys	Asn	Pro
		115					120					125			
Leu	Arg	Tyr	Pro	Leu	Leu	Met	Thr	Asn	Ile	Val	Cys	Gly	Gln	Leu	Val
		130					135					140			
Ala	Ser	Ala	Cys	Thr	Ala	Gly	Phe	Phe	Ile	Ser	Leu	Thr	Glu	Thr	Ala
145					150					155					160
Leu	Ile	Phe	Arg	Asp	Ser	Phe	Cys	Arg	Pro	Asn	Leu	Val	Lys	His	Phe
			165					170						175	
Phe	Cys	His	Met	Leu	Ala	Val	Ile	Arg	Leu	Ser	Cys	Ile	Asp	Ser	Asn
			180					185					190		
His	Thr	Glu	Phe	Ile	Ile	Thr	Leu	Ile	Ser	Val	Ser	Gly	Leu	Leu	Gly
		195					200					205			
Thr	Leu	Leu	Leu	Ile	Ile	Leu	Thr	Asp	Val	Phe	Ile	Ile	Ser	Thr	Val
		210					215					220			
Leu	Arg	Ile	Pro	Ser	Ala	Glu	Gly	Lys	Gln	Lys	Ala	Phe	Thr	Thr	Cys
225					230					235					240
Ala	Ser	His	Leu	Thr	Val	Val	Ile	Ile	His	Phe	Gly	Phe	Ala	Ser	Ile
				245					250					255	
Val	Tyr	Leu	Lys	Pro	Glu	Ala	Ser	Gly	Asp	Asp	Thr	Leu	Ile	Ala	Val
		260						265					270		
Pro	Tyr	Thr	Val	Ile	Thr	Pro	Phe	Leu	Ser	Pro	Ile	Ile	Phe	Ser	Leu
		275					280						285		

Arg Asn Lys Asp Met Lys Asn Ala Phe Arg Arg Met Met Gly Asn Thr
 290 295 300
 Val Ala Leu Lys Lys Ile Ile Leu Gly Cys Cys Cys Leu Phe Glu Glu
 305 310 315 320
 Gly Leu Asn Val Pro
 325

<210> 1464
 <211> 313
 <212> PRT
 <213> Unknown (H38g381 protein)

<220>
 <223> Synthetic construct

<400> 1464
 Met Gly Gln Thr Asn Val Thr Ser Trp Arg Asp Phe Val Phe Leu Gly
 1 5 10 15
 Phe Ser Ser Ser Gly Glu Leu Gln Leu Leu Leu Phe Ala Leu Phe Leu
 20 25 30
 Ser Leu Tyr Leu Val Thr Leu Thr Ser Asn Val Phe Ile Ile Ile Ala
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Phe Leu Ser Phe Ser Glu Thr Cys Tyr Thr Leu Gly Ile Ile Pro Arg
 65 70 75 80
 Met Leu Ser Gly Leu Ala Gly Gly Asp Gln Ala Ile Ser Tyr Val Gly
 85 90 95
 Cys Ala Ala Gln Met Phe Phe Ser Ala Ser Trp Ala Cys Thr Asn Cys
 100 105 110
 Phe Leu Leu Ala Ala Met Gly Phe Asp Arg Tyr Val Ala Ile Cys Ala
 115 120 125
 Pro Leu His Tyr Ala Ser His Met Asn Pro Thr Leu Cys Ala Gln Leu
 130 135 140
 Val Ile Thr Ser Phe Leu Thr Gly Tyr Leu Phe Gly Leu Gly Met Thr
 145 150 155 160
 Leu Val Ile Phe His Leu Ser Phe Cys Ser Ser His Glu Ile Gln His
 165 170 175
 Phe Phe Cys Asp Thr Pro Pro Val Leu Ser Leu Ala Cys Gly Asp Thr
 180 185 190
 Gly Pro Ser Glu Leu Arg Ile Phe Ile Leu Ser Leu Leu Val Leu Leu
 195 200 205
 Val Ser Phe Phe Phe Ile Thr Ile Ser Tyr Ala Tyr Ile Leu Ala Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Gln Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser
 245 250 255
 Phe Val Tyr Leu Arg Pro Lys Ala Ser Tyr Ser Leu Glu Arg Asp Gln
 260 265 270
 Leu Ile Ala Met Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Ile
 275 280 285
 Val Tyr Ser Leu Arg Thr Arg Ala Ile Gln Thr Ala Leu Arg Asn Ala
 290 295 300
 Phe Arg Gly Arg Leu Leu Gly Lys Gly
 305 310

<210> 1465
 <211> 289
 <212> PRT
 <213> Unknown (H38g382 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(289)

<223> Xaa = Any Amino Acid

<400> 1465

```

Leu Leu Phe Phe Ile Leu Leu Leu Leu Ile Tyr Leu Phe Thr Ile Ile
 1           5           10           15
Gly Ser Leu Met Val Phe Phe Ala Ile Lys Leu Asp Phe Cys Leu His
          20           25           30
Ser Ser Leu Tyr Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Trp
          35           40           45
Tyr Thr Thr Ile Thr Ile Pro Lys Met Phe Phe Asn Leu Ala Ser Glu
          50           55           60
Gln Lys Thr Thr Ser Leu Asp Gly Cys Leu Leu Gln Met Tyr Phe Phe
65          70          75          80
Tyr Ser Leu Gly Ile Thr Glu Val Cys Leu Leu Thr Thr Arg Ala Met
          85          90          95
Asp Arg Tyr Leu Ala Ile Cys Asn His Leu Cys Tyr Pro Thr Val Thr
          100          105          110
Thr Pro Xaa Leu Tyr Thr Gln Val Ile Leu Gly Cys Cys Ile Cys Gly
          115          120          125
Phe Phe Thr Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe
          130          135          140
Cys Gly Pro Asn Gln Ile His Asn Ile Phe Cys Asp Leu Asp Pro Ile
145          150          155          160
Leu Asn Leu Ala Cys Val Asp Thr Gly Pro Val Val Leu Ile Lys Val
          165          170          175
Val Asp Ile Val His Ala Val Glu Ile Ile Thr Ala Ile Met Leu Val
          180          185          190
Thr Leu Ala Tyr Val Gln Ile Ile Ala Val Ile Leu Arg Asn Cys Ser
          195          200          205
Ala Asp Gly Cys Gln Lys Ala Phe Ser Thr Tyr Ala Phe His Leu Ala
          210          215          220
Ile Phe Leu Ile Phe Phe Gly Ser Val Ala Leu Met Tyr Leu Leu Phe
225          230          235          240
Ser Ala Lys Tyr Ser Phe Phe Trp Asp Thr Thr Ile Ser Leu Met Phe
          245          250          255
Ala Val Leu Ser Pro Thr Pro Ile Ile Cys Ser Leu Arg Asn Lys Glu
          260          265          270
Ile Lys Glu Ala Ile Lys Lys His Met Cys Gln Ser Met Ile Cys Thr
          275          280          285
His

```

<210> 1466

<211> 318

<212> PRT

<213> Unknown (H38g383 protein)

<220>

<223> Synthetic construct

<400> 1466

```

Met Glu Ser Pro Asn Arg Thr Thr Ile Gln Glu Phe Ile Phe Ser Ala
 1           5           10           15
Phe Pro Tyr Ser Trp Val Lys Ser Val Val Cys Phe Val Pro Leu Leu
          20           25           30

```

Phe Ile Tyr Ala Phe Ile Val Val Gly Asn Leu Val Ile Ile Thr Val
 35 40 45
 Val Gln Leu Asn Thr His Leu His Thr Pro Met Tyr Thr Phe Ile Ser
 50 55 60
 Ala Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ser Ser Leu Leu Ser Glu Arg Ser Ile Ser Phe Asn Gly Cys
 85 90 95
 Leu Leu Gln Met Tyr Phe Phe His Ser Thr Gly Ile Cys Glu Val Cys
 100 105 110
 Leu Leu Thr Val Met Ala Phe Asp His Tyr Leu Ala Ile Cys Ser Pro
 115 120 125
 Leu His Tyr Pro Ser Ile Met Thr Pro Lys Leu Cys Thr Gln Leu Thr
 130 135 140
 Leu Ser Cys Trp Val Cys Gly Phe Ile Thr Pro Leu Pro Glu Ile Ala
 145 150 155 160
 Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn His Leu Glu His Ile
 165 170 175
 Phe Cys Asp Phe Leu Pro Val Leu Arg Leu Ala Cys Thr Asp Thr Arg
 180 185 190
 Ala Ile Val Met Ile Gln Val Val Asp Val Ile His Ala Val Glu Ile
 195 200 205
 Ile Thr Ala Val Met Leu Ile Phe Met Ser Tyr Asp Gly Ile Val Ala
 210 215 220
 Val Ile Leu Arg Ile His Ser Ala Gly Gly Arg Arg Thr Ala Phe Ser
 225 230 235 240
 Thr Cys Val Ser His Phe Ile Val Phe Ser Leu Phe Phe Gly Ser Val
 245 250 255
 Thr Leu Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Leu Phe Trp Asp
 260 265 270
 Ile Ala Ile Ala Leu Ala Phe Ala Val Leu Ser Pro Phe Phe Asn Pro
 275 280 285
 Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Glu Ala Ile Lys Lys
 290 295 300
 His Ile Gly Gln Ala Lys Ile Phe Phe Ser Val Arg Pro Gly
 305 310 315

<210> 1467

<211> 129

<212> PRT

<213> Unknown (H38g384 protein)

<220>

<223> Synthetic construct

<400> 1467

Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn Glu Val Ile Ile
 1 5 10 15
 Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe Leu Cys Ile Leu
 20 25 30
 Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys Val Pro Ser Thr
 35 40 45
 Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val
 50 55 60
 Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr Phe Asn Pro Leu
 65 70 75 80
 Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr Val Leu Tyr Thr
 85 90 95
 Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg
 100 105 110
 Tyr Leu Lys Gly Ala Leu Lys Lys Val Val Gly Arg Val Val Phe Ser

115 120 125

Val

<210> 1468
 <211> 162
 <212> PRT
 <213> Unknown (H38g385 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(162)
 <223> Xaa = Any Amino Acid

<400> 1468
 Leu Leu Ile Ile Pro Ala Ile Ala Thr Asp Thr Arg Leu Ser Val Leu
 1 5 10 15
 Val Arg Phe Phe Leu Ala Asn Leu Ala Phe Val Val Thr Cys Phe Thr
 20 25 30
 Ser Thr Thr Ile Pro Lys Met Leu Ala Cys Lys Glu Ile Pro Cys Val
 35 40 45
 Met Ser Gly Cys Lys Gly Ile Pro Tyr Ala Gly Cys Leu Thr Gln Met
 50 55 60
 Leu Phe Phe Ile Trp Leu Gly Ile His Ser Phe Leu Leu Thr Ala Met
 65 70 75 80
 Ala Asn Glu His Cys Val Ala Ile Cys His Ser Leu Asn Ser Ile Arg
 85 90 95
 Ser Val Thr Pro Xaa Leu Cys Gly Leu Leu Val Val Ala Ser Trp Thr
 100 105 110
 Phe Ala Phe Arg Asn Ala Leu Thr His Pro Val Leu Leu Thr Arg Leu
 115 120 125
 Ser Leu Cys Thr Tyr Glu Trp Val Ser His Val Phe Cys Asn Leu Ser
 130 135 140
 Gln Leu Leu Lys Leu Ala Cys Ser Asp Ala Thr Leu Asn Asn Val Thr
 145 150 155 160
 Val Gln

<210> 1469
 <211> 327
 <212> PRT
 <213> Unknown (H38g386 protein)

<220>
 <223> Synthetic construct

<400> 1469
 Met Leu Thr Pro Asn Asn Ala Cys Ser Val Pro Thr Ser Phe Arg Leu
 1 5 10 15
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Ile Trp Leu Ser Ile Pro
 20 25 30
 Phe Gly Ser Met Tyr Leu Val Ala Val Leu Gly Asn Ile Thr Ile Leu
 35 40 45
 Ala Val Val Arg Met Glu Tyr Ser Leu His Gln Pro Met Tyr Phe Phe
 50 55 60
 Leu Cys Met Leu Ala Val Ile Asp Leu Val Leu Ser Thr Ser Thr Met
 65 70 75 80
 Pro Lys Leu Leu Ala Ile Phe Trp Phe Gly Ala His Asn Ile Gly Val
 85 90 95

Asn Ala Cys Leu Ala Gln Met Phe Phe Ile His Cys Phe Ala Thr Val
 100 105 110
 Glu S r Gly Ile Phe Leu Ala Met Ala Phe Asp His Tyr Val Ala Ile
 115 120 125
 Cys Asp Pro Leu His His Thr Leu Leu Leu Thr His Ala Val Val Gly
 130 135 140
 Arg Leu Gly Leu Ala Ala Leu Leu Arg Gly Val Ile Tyr Ile Gly Pro
 145 150 155 160
 Leu Pro Leu Val Ile Cys Leu Arg Leu Pro Leu Tyr His Thr Gln Ile
 165 170 175
 Ile Ala His Ser Tyr Cys Glu His Met Ala Val Val Thr Leu Ala Cys
 180 185 190
 Gly Asp Asp Thr Arg Val Asn Asn Leu Tyr Gly Met Gly Ile Gly Phe
 195 200 205
 Leu Val Leu Ile Leu Asp Ser Leu Ala Ile Thr Ala Ser Tyr Val Met
 210 215 220
 Ile Phe Arg Ala Val Met Gly Leu Ala Thr Ser Glu Ala Arg Leu Lys
 225 230 235 240
 Thr Leu Gly Thr Cys Gly Ser His Ile Cys Ala Ile Leu Val Phe Tyr
 245 250 255
 Ile Pro Ile Ala Val Ser Ser Leu Thr His Arg Phe Gly His Arg Val
 260 265 270
 Pro Pro His Ile His Ile His Ile His Ile His Ile His Ile
 275 280 285
 Leu Leu Ala Asn Ile Tyr Leu Leu Ile Pro Pro Ile Leu Asn Pro Ile
 290 295 300
 Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu Ala Leu Leu His Ile
 305 310 315 320
 Lys Ala Arg Thr Gln Thr Arg
 325

<210> 1470

<211> 323

<212> PRT

<213> Unknown (H38g387 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1470

Val Ala Cys Tyr Leu Pro Glu Leu Ser Val Gly Cys Pro Gly Gly Lys
 1 5 10 15
 Glu Asn Glu Thr Gly Val Gly Glu Phe Leu Leu Leu Ser Ile Thr Ser
 20 25 30
 Asp Ser Glu Lys Gln Gln Ala Leu Phe Trp Leu Phe Leu Cys Met His
 35 40 45
 Leu Val Thr Glu Ala Gly Asn Thr Pro Ile Ile Leu Gly Ile Gly Ser
 50 55 60
 Asn Pro Arg Leu His Thr Pro Thr Tyr Phe Phe Thr His Leu Ser Phe
 65 70 75 80
 Val Asn Ile Cys Phe Ile Thr Asn Leu Ile Pro Lys Leu Leu Val Asn
 85 90 95
 His Val Ala Gly Thr Gly Met Ile Thr Ile Ser Ser Pro Gln Cys Leu
 100 105 110
 Thr Gln Met Tyr Phe Leu Ile Ser Phe Ala Asn Val Asp Thr Phe Leu
 115 120 125
 Leu Ala Ile Met Ala Leu Asp His Tyr Val Ala Ile Cys Ser Ala Leu

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      130              135              140
Arg Tyr Cys Ser Ile Ile Thr Pro Glu Leu Cys Gln Gly Leu Ala Val
145              150              155              160
Leu Ala Xaa Ala Gly Ser Ser Leu Ile Ser Leu Val His Thr Val Ile
      165              170              175
Met Ser Arg Leu Ala Phe Cys Ser Ser Ala Gln Ile Ser His Phe Tyr
      180              185              190
Cys Asp Ala Tyr Leu Leu Met Lys Ile Ala Cys Ser His Thr Val Asn
      195              200              205
Gln His Val Phe Leu Gly Ala Val Val Leu Phe Leu Ala Pro Cys Ala
      210              215              220
Leu Ile Leu Val Ser Tyr Ile Arg Ile Ala Ala Ile Leu Arg Ile
225              230              235              240
Pro Ser Pro Thr Arg Arg Lys Ala Cys Ser Ile Cys Ser Ser His
      245              250              255
Leu Ser Leu Val Thr Leu Phe Tyr Gly Thr Val Leu Gly Ile Cys Ile
      260              265              270
Xaa Pro Pro Asp Ser Phe Ser Ala Gln Asp Thr Ile Ala Thr Ile Met
      275              280              285
Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe Ile Tyr Ser Leu Met
      290              295              300
Asn Lys Glu Val Gln Glu Ala Val Arg Arg Leu Phe Ser Arg Gly Ser
305              310              315              320
His Ser Ser

```

<210> 1471

<211> 202

<212> PRT

<213> Unknown (H38g388 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(202)

<223> Xaa = Any Amino Acid

<400> 1471

```

Leu His Phe Cys Gly Ile Asp Val Thr Ser Tyr Gln Ala Xaa Gln Ile
1      5      10      15
Leu Ala Xaa Gln Pro Tyr Asp Thr Thr Xaa Cys Gly Gln Arg Ile Val
      20      25      30
Gly Ile Met Ala Val Ala Trp Gly Ile Gly Phe Leu His Ser Leu Ser
      35      40      45
Gln Leu Ala Phe Ala Val His Leu Pro Phe Cys Gly Pro Asn Glu Phe
      50      55      60
Asp Ser Phe Tyr Cys Asp Leu Pro Arg Val Ile Lys Leu Ala Cys Thr
65      70      75      80
Asp Thr Tyr Arg Leu Asp Ile Met Val Ile Ala Asn Ser Gly Val Leu
      85      90      95
Thr Val Cys Ser Phe Val Leu Leu Ile Ile Ser Tyr Thr Ile Ile Leu
      100      105      110
Met Thr Ile Gln His Arg Pro Leu Asp Lys Ser Ser Lys Ala Leu Ser
      115      120      125
Thr Leu Thr Ala His Ile Thr Val Val Leu Leu Phe Phe Gly Pro Cys
      130      135      140
Val Phe Ile Tyr Ala Trp Pro Phe Pro Ile Lys Ser Leu Asp Lys Phe
145      150      155      160
Leu Ala Val Phe Tyr Ser Val Ile Thr Pro Leu Leu Asn Pro Ile Ile
      165      170      175

```

Tyr Thr Leu Arg Asn Lys Asp Met Lys Thr Ala Ile Arg Gln Leu Arg
 180 185 190
 Lys Trp Asp Ala His Ser Ser Val Lys Phe
 195 200

<210> 1472

<211> 311

<212> PRT

<213> Unknown (H38g389 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1472

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu
 1 5 10 15
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro
 20 25 30
 Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu
 35 40 45
 Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe
 50 55 60
 Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile
 65 70 75 80
 Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu
 85 90 95
 Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val
 100 105 110
 Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly
 130 135 140
 Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro
 145 150 155 160
 Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val
 165 170 175
 Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys
 180 185 190
 Gly Asp Ser Lys Val Asn Asn Val Tyr Gly Met Ser Ile Gly Phe Leu
 195 200 205
 Val Leu Ile Met Glu Ser Val Asp Ser Asp Ala Ser Xaa Val Arg Ser
 210 215 220
 Ile Arg Ala Val Met Gly Leu Ala Asn His Glu Asp Arg Ile Lys Thr
 225 230 235 240
 Met Gly Thr Gly Glu Tyr His Ile Cys Ala Ile Met Ile Phe Arg Ile
 245 250 255
 Pro Val Met Tyr Ile Pro Xaa Asp His Arg Asp Gly Gln Cys Val His
 260 265 270
 His Pro Val His Asn Met Met Ala Arg Ile Tyr Ile Ile Ser His Pro
 275 280 285
 Ser Ile Lys Pro Ser Val Xaa Asp Asp Arg Thr Lys Gln Ser Arg Glu
 290 295 300
 Ser Tyr Ile Gln Arg Ala Arg
 305 310

<210> 1473

<211> 315

<212> PRT

<213> Unknown (H38g390 protein)

<220>

<223> Synthetic construct

<400> 1473

```

Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1          5          10          15
Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val
          20          25          30
Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Ile Phe
          35          40          45
Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
          65          70          75          80
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
          85          90          95
Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
          100          105          110
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
          115          120          125
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
          130          135          140
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
          145          150          155          160
Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
          165          170          175
His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp
          180          185          190
Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
          195          200          205
Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala His Ile Leu Gly
          210          215          220
Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
          225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
          245          250          255
Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
          260          265          270
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys
          290          295          300
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
          305          310          315

```

<210> 1474

<211> 326

<212> PRT

<213> Unknown (H38g391 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1474

```

Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1           5           10           15
Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
          20           25           30
Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
          35           40           45
Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro
          65           70           75           80
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
          85           90           95
Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
          100          105          110
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Ser
          115          120          125
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
          130          135          140
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
          145          150          155          160
Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
          165          170          175
His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
          180          185          190
Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
          195          200          205
Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
          210          215          220
Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
          225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
          245          250          255
Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
          260          265          270
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
          290          295          300
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His Xaa Thr Pro Glu Ser
          305          310          315          320
Gly Ala Cys Cys Ala Pro
          325

```

<210> 1475

<211> 314

<212> PRT

<213> Unknown (H38g392 protein)

<220>

<223> Synthetic construct

<400> 1475

```

Met Gly Asp Val Asn Gln Ser Val Ala Ser Asp Phe Ile Leu Val Gly
 1           5           10           15
Leu Phe Ser His Ser Gly Ser Arg Gln Leu Leu Phe Ser Leu Val Ala
          20           25           30
Val Met Phe Val Ile Gly Leu Leu Gly Asn Thr Val Leu Leu Phe Leu
          35           40           45
Ile Arg Val Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser
          50           55           60
Gln Leu Ser Leu Phe Asp Ile Gly Cys Pro Met Val Thr Ile Pro Lys

```

```

65          70          75          80
Met Ala Ser Asp Phe Leu Arg Gly Glu Gly Ala Thr Ser Tyr Gly Gly
      85          90          95
Gly Ala Ala Gln Ile Phe Phe Leu Thr Leu Met Gly Val Ala Glu Gly
      100          105          110
Val Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Gln
      115          120          125
Pro Leu Gln Tyr Pro Val Leu Met Arg Arg Gln Val Cys Leu Leu Met
      130          135          140
Met Gly Ser Ser Trp Val Val Gly Val Leu Asn Ala Ser Ile Gln Thr
      145          150          155
Ser Ile Thr Leu His Phe Pro Tyr Cys Ala Ser Arg Ile Val Asp His
      165          170          175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
      180          185          190
Cys Ala Tyr Glu Met Ala Leu Ser Thr Ser Gly Val Leu Ile Leu Met
      195          200          205
Leu Pro Leu Ser Leu Ile Ala Thr Ser Tyr Gly His Val Leu Gln Ala
      210          215          220
Val Leu Ser Met Arg Ser Glu Glu Ala Arg His Lys Ala Val Thr Thr
      225          230          235
Cys Ser Ser His Ile Thr Val Val Gly Leu Phe Tyr Gly Ala Ala Val
      245          250          255
Phe Met Tyr Met Val Pro Cys Ala Tyr His Ser Pro Gln Gln Asp Asn
      260          265          270
Val Val Ser Leu Phe Tyr Ser Leu Val Thr Pro Thr Leu Asn Pro Leu
      275          280          285
Ile Tyr Ser Leu Arg Asn Pro Glu Val Trp Met Ala Leu Val Lys Val
      290          295          300
Leu Ser Arg Ala Gly Leu Arg Gln Met Cys
305          310

```

<210> 1476

<211> 117

<212> PRT

<213> Unknown (H38g393 protein)

<220>

<223> Synthetic construct

<400> 1476

```

Asn Ile Lys Gly Ile Ala Val Pro Met Phe Ile Glu Val Leu Asp Leu
1          5          10          15
Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln Ala Val Leu Gln
      20          25          30
Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser
      35          40          45
His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser
      50          55          60
Val Met His Arg Val Ala Arg Cys Ala Ala Pro His Val His Ile Leu
      65          70          75          80
Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile
      85          90          95
Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val Leu Gly Val Phe
      100          105          110
Pro Arg Lys Asp Val
      115

```

<210> 1477

<211> 316

<212> PRT

<213> Unknown (H38g394 protein)

<220>

<223> Synthetic construct

<400> 1477

```

Met Pro Ser Gln Asn Tyr Ser Ile Ile Ser Glu Phe Asn Leu Phe Gly
1          5          10          15
Phe Ser Ala Phe Pro Gln His Leu Leu Pro Ile Leu Phe Leu Leu Tyr
20          25          30
Leu Leu Met Phe Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala
35          40          45
Thr Ile Trp Ile Glu His Arg Leu His Thr Pro Met Tyr Leu Phe Leu
50          55          60
Cys Thr Leu Ser Val Ser Glu Ile Leu Phe Thr Val Ala Ile Thr Pro
65          70          75          80
Arg Met Leu Ala Asp Leu Leu Ser Thr His His Ser Ile Thr Phe Val
85          90          95
Ala Cys Ala Asn Gln Met Phe Phe Ser Phe Met Phe Gly Phe Thr His
100         105         110
Ser Phe Leu Leu Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
115         120         125
His Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Asp Cys Ala His
130         135         140
Leu Val Ala Trp Thr Trp Ala Gly Gly Ser Val Met Gly Met Met Val
145         150         155         160
Thr Thr Ile Val Phe His Leu Thr Phe Cys Gly Ser Asn Val Ile His
165         170         175
His Phe Phe Cys His Val Leu Ser Leu Leu Lys Leu Ala Cys Glu Asn
180         185         190
Lys Thr Ser Ser Val Ile Met Gly Val Met Leu Val Cys Val Thr Ala
195         200         205
Leu Ile Gly Cys Leu Phe Leu Ile Ile Leu Ser Tyr Val Phe Ile Val
210         215         220
Ala Ala Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Thr Phe
225         230         235         240
Ser Thr Cys Val Ser His Leu Thr Val Val Val Thr His Tyr Ser Phe
245         250         255
Ala Ser Phe Ile Tyr Leu Lys Pro Lys Gly Leu His Ser Met Tyr Ser
260         265         270
Asp Ala Leu Met Ala Thr Thr Tyr Thr Val Phe Thr Pro Phe Leu Ser
275         280         285
Pro Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Asn Ala Ile Asn
290         295         300
Lys Asn Phe Tyr Arg Lys Phe Cys Pro Pro Ser Ser
305         310         315

```

<210> 1478

<211> 330

<212> PRT

<213> Unknown (H38g395 protein)

<220>

<223> Synthetic construct

<400> 1478

```

Met Cys Ser Phe Phe Leu Cys Gln Thr Gly Lys Gln Ala Lys Ile Ser
1          5          10          15
Met Gly Glu Glu Asn Gln Thr Phe Val Ser Lys Phe Ile Phe Leu Gly
20          25          30
Leu Ser Gln Asp Leu Gln Thr Gln Ile Leu Leu Phe Ile Leu Phe Leu

```

```

      35      40      45
Ile Ile Tyr Leu Leu Thr Val Leu Gly Asn Gln Leu Ile Ile Ile Leu
  50      55      60
Ile Phe Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Arg
65      70      75      80
Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Thr Ser Ile Val Pro Gln
      85      90      95
Val Leu Val His Phe Leu Val Lys Arg Lys Thr Ile Ser Phe Tyr Gly
      100      105      110
Cys Met Thr Gln Ile Ile Val Phe Leu Leu Val Gly Cys Thr Glu Cys
      115      120      125
Ala Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys
      130      135      140
Pro Leu Tyr Tyr Ser Thr Ile Met Thr Gln Arg Val Cys Leu Trp Leu
145      150      155      160
Ser Phe Arg Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr
      165      170      175
Ser Phe Thr Phe His Leu Pro Tyr Trp Gly Gln Asn Ile Ile Asn His
      180      185      190
Tyr Phe Cys Glu Pro Pro Ala Leu Lys Leu Ala Ser Ile Asp Thr
      195      200      205
Tyr Ser Thr Glu Met Ala Ile Phe Ser Met Gly Val Val Ile Leu Leu
      210      215      220
Ala Pro Val Ser Leu Ile Leu Gly Ser Tyr Trp Asn Ile Ile Ser Thr
225      230      235      240
Val Ile Gln Met Gln Ser Gly Glu Gly Arg Leu Lys Ala Phe Ser Thr
      245      250      255
Cys Gly Ser His Leu Ile Val Val Val Leu Phe Tyr Gly Ser Gly Ile
      260      265      270
Phe Thr Tyr Met Arg Pro Asn Ser Lys Thr Thr Lys Glu Leu Asp Lys
      275      280      285
Met Ile Ser Val Phe Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Ile
      290      295      300
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Arg Lys Leu
305      310      315      320
Val Gly Arg Lys Cys Phe Ser His Arg Gln
      325      330

```

<210> 1479

<211> 227

<212> PRT

<213> Unknown (H38g396 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(227)

<223> Xaa = Any Amino Acid

<400> 1479

```

Gly Lys Glu Arg Glu Thr Arg Val Trp Arg Pro Arg Ala Gln Asp Arg
  1      5      10      15
Gly Val Ser Thr Arg His Ala Ala Arg Val Thr Ser Tyr Gln Glu Cys
      20      25      30
Gly Val Arg Gly Gly Gly Val Leu Cys Gly Ala Val Arg Pro Ser Pro
      35      40      45
Leu Asp Ala Gln Leu His Asn Val Ile Ala Tyr Arg Arg Thr Cys Phe
      50      55      60
Lys Asp Val Glu Ile Pro Asn Phe Val Trp Asp Pro Ser Gln Leu Pro
65      70      75      80

```

Arg Leu Ala Cys Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe
 85 90 95
 Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser
 100 105 110
 Tyr Asp Lys Ile Val Phe Ser Ile Leu Arg Val Ser Ser Gly Gly
 115 120 125
 Lys His Lys Ala Phe Ser Thr Arg Gly Ser His Leu Ser Val Val Cys
 130 135 140
 Xaa Phe Tyr Gly Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser
 145 150 155 160
 Ser Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ala
 165 170 175
 Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile
 180 185 190
 Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Ser Ser Gln Tyr
 195 200 205
 Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser
 210 215 220
 Lys Val Lys
 225

<210> 1480

<211> 332

<212> PRT

<213> Unknown (H38g397 protein)

<220>

<223> Synthetic construct

<400> 1480

Met Lys Ile Phe Asn Thr Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe
 1 5 10 15
 Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Val
 20 25 30
 Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser
 35 40 45
 Ile Asn Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr
 50 55 60
 Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser
 65 70 75 80
 Thr Val Pro Asn Val Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile
 85 90 95
 Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
 100 105 110
 Ser Thr Glu Cys Phe Phe Leu Gly Ala Met Ala Phe Asp Leu Tyr Leu
 115 120 125
 Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu
 130 135 140
 Cys Asn Ile Leu Val Gly Ser Cys Trp Val Leu Gly Phe Leu Trp Phe
 145 150 155 160
 Leu Ile Pro Ile Ser Val Ile Ser Gln Met Thr Cys Gly Ser Arg Ile
 165 170 175
 Ile Asp His Phe Pro Cys Asp Pro Gly Pro Leu Leu Ala Leu Thr Cys
 180 185 190
 Ala Arg Ala Pro Leu Leu Glu Leu Thr Ser Ser Thr Leu Ser Ser Leu
 195 200 205
 Leu Leu Phe Ile Pro Phe Leu Phe Ile Val Gly Cys Tyr Ala Leu Val
 210 215 220
 Leu Arg Ala Val Leu Arg Val Pro Ser Ala Ser Gly Arg Arg Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly

```

                245                250                255
Ser Met Met Ile Thr Tyr Val Ser Pro Thr Ser Gly His Glu Phe Gly
                260                265                270
Met Gln Lys Thr Val Thr Leu Phe Tyr Ser Val Val Thr Pro Leu Ile
                275                280                285
Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys His Ala Met
                290                295                300
Arg Asn Tyr Thr Val Met Phe Tyr Leu Ser Arg Ile His Arg Ala Thr
305                310                315                320
Arg Asp Val Lys Asp Val Phe Tyr Leu Phe Asn Phe
                325                330

```

<210> 1481

<211> 269

<212> PRT

<213> Unknown (H38g398 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(269)

<223> Xaa = Any Amino Acid

<400> 1481

```

Phe Ser Ser Ile Tyr Ala Trp Tyr Ile Ser Asp Leu Tyr Leu Asn Tyr
1          5          10          15
Leu Ser Asn His Leu Ser Ile Phe Lys Leu Val Asp Trp Ile Ile Asn
20          25          30
Cys Tyr Leu Tyr Tyr Phe Tyr Ser Leu Leu Thr Leu Phe Xaa Gln Phe
35          40          45
Ile Tyr Thr Cys Glu Met Asn Gln Phe Lys Xaa Xaa Gln Asn Arg Asn
50          55          60
Asn Leu Thr Thr Phe Xaa Gly Tyr Phe Tyr Ser Gly Ile Cys Gly Arg
65          70          75          80
Arg Asn Cys Thr Met Xaa Leu Ile Thr Ile Phe Ile Leu Lys Tyr Cys
85          90          95
Xaa His Gly Phe Ile Thr Ile His Ser Val Met Asp Ser Gly Gln His
100         105         110
Leu Ala Ile Cys His Pro Leu His Tyr Leu Ile Leu Met Thr Asp Glu
115         120         125
Asn Arg Asp Arg Met Phe Met Gly Pro Leu Thr Ala Phe Pro Tyr Thr
130         135         140
Asp Ala Thr Ser Gln Asn Met His Tyr Val Asn Phe Leu Ile Ile Ile
145         150         155         160
Leu Ser Ile Leu Tyr Ile Pro Gly Pro Tyr Thr Leu Ile Leu Arg Ala
165         170         175
Met Leu Gln Leu Leu Ser Ala Ala Ser His Gln Asn Ala Phe Ser Ile
180         185         190
Arg Gly Ser His Leu Ile Val Val Ser Leu Phe Cys Glu Thr Ile Met
195         200         205
Met Met Cys Val Asn Leu Ile Ser Asp His Leu Val Xaa Met Lys Met
210         215         220
Thr Asn His Asn Ile Ile Met Ile Ser Ser Ile Lys Thr Leu Val Leu
225         230         235         240
Asn Phe Val Asn Tyr Thr Leu Leu Asn Met Asn Leu Lys Leu Tyr Leu
245         250         255
Gln Phe Phe Phe Tyr Gly Met Ser Ile Ser Gln Ser Ser
260         265

```

<210> 1482

<211> 311
 <212> PRT
 <213> Unknown (H38g399 protein)

<220>
 <223> Synthetic construct

<400> 1482

```

Met Lys Ile Phe Asn Ser Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe
 1           5           10           15
Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Phe
           20           25           30
Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser
           35           40           45
Ile Ile Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr
           50           55           60
Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser
65           70           75           80
Thr Val Pro Ser Met Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile
           85           90           95
Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
           100          105          110
Ser Thr Glu Cys Phe Phe Leu Ala Val Met Ala Phe Asp Arg Tyr Leu
           115          120          125
Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu
           130          135          140
Cys Thr Asn Leu Val Val Asn Cys Trp Val Leu Gly Phe Ile Trp Phe
145           150          155          160
Leu Ile Pro Ile Val Asn Ile Ser Gln Met Ser Phe Cys Gly Ser Arg
           165          170          175
Ile Ile Asp His Phe Leu Cys Asp Pro Ala Pro Leu Leu Thr Leu Thr
           180          185          190
Cys Lys Lys Gly Pro Val Ile Glu Leu Val Phe Ser Val Leu Ser Pro
           195          200          205
Leu Pro Val Phe Met Leu Phe Leu Phe Ile Val Gly Ser Tyr Ala Leu
           210          215          220
Val Val Arg Ala Val Leu Arg Val Pro Ser Ala Ala Gly Arg Arg Lys
225           230          235          240
Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr
           245          250          255
Gly Ser Val Leu Val Met Tyr Gly Ser Pro Pro Ser Lys Asn Glu Ala
           260          265          270
Gly Lys Gln Lys Thr Val Thr Leu Phe Tyr Ser Val Val Thr Pro Leu
           275          280          285
Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Asp Met Arg Lys Ala
           290          295          300
Leu Lys Lys Phe Trp Gly Thr
305           310

```

<210> 1483
 <211> 326
 <212> PRT
 <213> Unknown (H38g400 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(326)
 <223> Xaa = Any Amino Acid

<400> 1483

```

Thr Ala Leu Glu Phe Thr Asn Asn Ser Glu Thr Ser Thr Met Thr Glu
 1          5          10          15
Phe Val Leu Leu Gly Phe Pro Gly Cys Gln Glu Met Gln Ser Phe Leu
      20          25          30
Phe Ser Leu Phe Phe Val Ile Tyr Val Phe Thr Ile Ile Gly Asn Gly
      35          40          45
Thr Ile Val Cys Ala Val Arg Leu Asp Lys Arg Leu His Thr Pro Met
      50          55          60
Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu Glu Ile Arg Xaa Val Thr
      65          70          75          80
Ser Thr Val Pro Asn Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr
      85          90          95
Ile Ser Phe Val Gly Cys Phe Leu Gln Phe Tyr Phe Phe Thr Ser Leu
      100          105          110
Gly Thr Ile Glu Ala Tyr Phe Leu Cys Ile Met Ala Tyr Asp Arg Tyr
      115          120          125
Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Thr Ile Met Thr Pro Gln
      130          135          140
Leu Cys Tyr Ile Leu Met Ser Phe Cys Trp Val Phe Gly Phe Leu Ser
      145          150          155          160
Tyr Ser Val Ser Thr Val Gln Leu Ser Gln Leu Pro Phe Cys Gly Pro
      165          170          175
Asn Ile Ile Asn His Phe Leu Cys Asp Met Asp Pro Leu Met Ala Leu
      180          185          190
Ser Cys Ala Ser Ala Pro Ile Thr Glu Ile Ile Phe Tyr Ile Leu Ser
      195          200          205
Ser Leu Ile Ile Ile Leu Thr Leu Leu Tyr Ile Cys Gly Ser Tyr Met
      210          215          220
Leu Leu Leu Ile Ala Val Leu Lys Val Pro Ser Ala Ala Gly Gln Gln
      225          230          235          240
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe
      245          250          255
Phe Gly Ala Leu Ala Met Tyr Val Ser Pro Thr Thr Asp Asn Pro
      260          265          270
Ala Ala Ile Xaa Lys Ile Ile Thr Leu Phe Tyr Ser Val Val Thr Pro
      275          280          285
Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Ala
      290          295          300
Ala Leu Lys Lys Val Leu Arg Ile Glu Xaa Glu Xaa Ser His Leu His
      305          310          315          320
Glu Thr Lys Gln Thr Ile
      325

```

<210> 1484

<211> 315

<212> PRT

<213> Unknown (H38g401 protein)

<220>

<223> Synthetic construct

<400> 1484

```

Met Glu Ser Gly Asn Gln Ser Thr Val Thr Glu Phe Ile Phe Thr Gly
 1          5          10          15
Phe Pro Gln Leu Gln Asp Gly Ser Leu Leu Tyr Phe Phe Pro Leu Leu
      20          25          30
Phe Ile Tyr Thr Phe Ile Ile Ile Asp Asn Leu Leu Ile Phe Ser Ala
      35          40          45
Val Arg Leu Asp Thr His Leu His Asn Pro Met Tyr Asn Phe Ile Ser
      50          55          60

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```

Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys
65          70          75          80
Met Leu Ser Asn Leu Ile Ser Glu Lys Lys Ala Ile Ser Met Thr Gly
          85          90          95
Cys Ile Leu Gln Met Tyr Phe Phe His Ser Leu Glu Asn Ser Glu Gly
          100          105          110
Ile Leu Leu Thr Thr Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Arg Tyr Gln Met Ile Met Thr Pro Arg Leu Cys Ala Gln Leu
          130          135          140
Ser Ala Gly Ser Cys Leu Phe Gly Phe Leu Ile Leu Leu Pro Glu Ile
145          150          155          160
Val Met Ile Ser Thr Leu Pro Phe Cys Gly Pro Asn Gln Ile His Gln
          165          170          175
Ile Phe Cys Asp Leu Val Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
          180          185          190
Ser Met Ile Leu Ile Glu Asp Val Ile His Ala Val Thr Ile Ile Ile
          195          200          205
Thr Phe Leu Ile Ile Ala Leu Ser Tyr Val Arg Ile Val Thr Val Ile
210          215          220
Leu Arg Ile Pro Ser Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys
225          230          235          240
Ala Gly His Leu Met Val Phe Leu Ile Phe Phe Gly Ser Val Ser Leu
          245          250          255
Met Tyr Leu Arg Phe Ser Asp Thr Tyr Pro Pro Val Leu Asp Thr Ala
          260          265          270
Ile Ala Leu Met Phe Thr Val Leu Ala Pro Phe Phe Asn Pro Ile Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Met Asn Asn Ala Ile Lys Lys Leu Phe
          290          295          300
Cys Leu Gln Lys Val Leu Asn Lys Pro Gly Gly
305          310          315

```

<210> 1485

<211> 307

<212> PRT

<213> Unknown (H38g402 protein)

<220>

<223> Synthetic construct

<400> 1485

```

Met His Phe Val Thr Glu Phe Val Leu Leu Gly Phe His Gly Gln Arg
1          5          10          15
Glu Met Gln Ser Cys Phe Phe Ser Phe Ile Leu Val Leu Tyr Leu Leu
          20          25          30
Thr Leu Leu Gly Asn Gly Ala Ile Val Cys Ala Val Lys Leu Asp Arg
          35          40          45
Arg Leu His Thr Pro Met Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu
          50          55          60
Glu Ile Trp Tyr Ile Ser Ser Thr Val Pro Asn Met Leu Val Asn Ile
65          70          75          80
Leu Ser Glu Ile Lys Thr Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe
          85          90          95
Tyr Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Phe Phe Leu Ser Val
          100          105          110
Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr Pro
          115          120          125
Ser Ile Met Thr Gly Lys Phe Cys Ile Ile Leu Val Cys Val Cys Trp
          130          135          140
Val Gly Gly Phe Leu Cys Tyr Pro Val Pro Ile Val Leu Ile Ser Gln

```

```

145          150          155          160
L u Pro Phe Cys Gly Pro Asn Ile Ile Asp His Leu Val Cys Asp Pro
          165          170          175
Gly Pro Leu Phe Ala Leu Ala Cys Ile Ser Ala Pro Ser Thr Glu Leu
          180          185          190
Ile Cys Tyr Thr Phe Asn Ser Met Ile Ile Phe Gly Pro Phe Leu Ser
          195          200          205
Ile Leu Gly Ser Tyr Thr Leu Val Ile Arg Ala Val Leu Cys Ile Pro
          210          215          220
Ser Gly Ala Gly Arg Thr Lys Ala Phe Ser Thr Cys Gly Ser His Leu
225          230          235          240
Met Val Val Ser Leu Phe Tyr Gly Thr Leu Met Val Met Tyr Val Ser
          245          250          255
Pro Thr Ser Gly Asn Pro Ala Gly Met Gln Lys Ile Ile Thr Leu Val
          260          265          270
Tyr Thr Ala Met Thr Pro Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg
          275          280          285
Asn Lys Asp Met Lys Asp Ala Leu Lys Arg Val Leu Gly Leu Thr Val
          290          295          300
Ser Gln Asn
305

```

<210> 1486

<211> 256

<212> PRT

<213> Unknown (H38g403 protein)

<220>

<223> Synthetic construct

<400> 1486

```

Met Tyr Asn Phe Ile Ser Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr
1          5          10          15
Thr Ala Thr Ile Pro Lys Met Leu Ser Ile Leu Ile Ser Arg Gln Arg
          20          25          30
Thr Ile Ser Met Val Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser
          35          40          45
Leu Gly Asn Ser Glu Gly Ile Leu Leu Thr Thr Met Ala Ile Asp Arg
          50          55          60
Tyr Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Thr Pro
65          70          75          80
Gly Leu Cys Val Gln Leu Ser Val Gly Ser Cys Ile Phe Gly Phe Leu
          85          90          95
Val Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly
          100          105          110
Pro Asn Gln Ile His Gln Ile Phe Cys Asp Phe Glu Pro Val Leu Arg
          115          120          125
Leu Ala Cys Thr Asp Thr Ser Met Ile Leu Ile Glu Asp Val Ile His
          130          135          140
Ala Val Ala Ile Val Phe Ser Val Leu Ile Ile Ala Leu Ser Tyr Ile
145          150          155          160
Arg Ile Ile Thr Val Ile Leu Arg Ile Pro Ser Val Glu Gly Arg Gln
          165          170          175
Lys Ala Phe Ser Thr Cys Ala Ala His Leu Ser Val Phe Leu Met Phe
          180          185          190
Tyr Gly Ser Val Ser Leu Met Tyr Leu Arg Phe Ser Ala Thr Phe Pro
          195          200          205
Pro Ile Leu Asp Thr Ala Val Ala Leu Met Phe Ala Val Leu Ala Pro
          210          215          220
Phe Phe Asn Pro Ile Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Ile
225          230          235          240

```

Ala Ile Lys Lys Leu Phe Cys Pro Gln Lys Met Val Asn Leu Ser Val
 245 250 255

<210> 1487

<211> 320

<212> PRT

<213> Unknown (H38g404 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1487

Ser Leu Gly Ser Met Asn Asn Ser Gln Ile Ser Thr Val Thr Gln Phe
 1 5 10 15
 Val Leu Leu Gly Phe Pro Gly Pro Trp Lys Ile Gln Ile Ile Phe Phe
 20 25 30
 Ser Met Ile Leu Leu Val Tyr Ile Phe Thr Leu Thr Gly Asn Met Ala
 35 40 45
 Ile Ile Cys Ala Val Arg Trp Asp His Arg Leu His Thr Pro Met Tyr
 50 55 60
 Val Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Cys
 65 70 75 80
 Thr Val Pro Asn Met Leu Val Asn Phe Phe Ser Lys Thr Lys Thr Ile
 85 90 95
 Ser Phe Ser Gly Cys Phe Thr Gln Phe His Phe Phe Phe Ser Leu Gly
 100 105 110
 Thr Thr Glu Cys Phe Phe Leu Cys Val Met Ala Tyr Asp Arg Tyr Leu
 115 120 125
 Ala Ile Cys His Pro Leu His Tyr Pro Ser Ile Met Thr Gly Gln Leu
 130 135 140
 Cys Gly Ile Leu Val Ser Leu Cys Trp Leu Ile Gly Phe Leu Gly His
 145 150 155 160
 Ser Ile Ser Ile Phe Phe Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn
 165 170 175
 Ile Ile Asp His Phe Leu Cys Asp Val Asp Pro Leu Met Ala Leu Ser
 180 185 190
 Ser Ala Pro Thr His Ile Ile Gly His Val Phe His Ser Val Ser Ser
 195 200 205
 Leu Phe Ile Asn Leu Thr Met Val Tyr Ile Leu Gly Ser Tyr Thr Leu
 210 215 220
 Val Leu Arg Thr Val Leu Xaa Val Pro Ser Ser Ala Gly Trp Gln Lys
 225 230 235 240
 Ala Ile Ser Thr Cys Gly Ser His Leu Val Val Val Ser Leu Phe Tyr
 245 250 255
 Gly Ala Ile Met Leu Met Tyr Val Ser Pro Thr Pro Gly Asn Ser Val
 260 265 270
 Ala Met His Lys Leu Ile Thr Leu Ile Tyr Ser Val Val Thr Pro Val
 275 280 285
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Tyr Ala
 290 295 300
 Leu His His Val Phe Cys Gly Met Arg Ile Ile Gln Arg Ser Xaa Ile
 305 310 315 320

<210> 1488

<211> 319

<212> PRT

<213> Unknown (H38g405 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1488

```

Met Asp Pro Glu Asn Gln Thr Met Val Thr Glu Phe Tyr Phe Ser Asp
1          5          10          15
Phe Pro Gln Ser Lys Asn Gly Ser Leu Phe Phe Ile Pro Met Leu
20          25          30
Phe Ile Tyr Ile Phe Ile Leu Val Gly Asn Phe Met Ile Phe Phe Ala
35          40          45
Val Gln Pro Asp Pro His Leu His Asn Pro Met Tyr Ser Phe Ile Ser
50          55          60
Val Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Val Thr Ile Pro Lys
65          70          75          80
Met Leu Ser Asn Leu Leu Ser Glu Gln Lys Thr Ile Ser Phe Ile Gly
85          90          95
Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly Val Thr Glu Ala
100         105         110
Leu Val Leu Thr Val Met Ala Ile Asp Arg Cys Val Ala Ile Cys Asn
115         120         125
Pro Leu Arg Tyr Ala Ile Thr Met Ser Pro Xaa Leu Cys Ile Gln Leu
130         135         140
Ser Thr Gly Ser Cys Ile Phe Gly Phe Leu Met Leu Leu Pro Glu Ile
145         150         155         160
Val Cys Ile Ser Thr Leu Pro Phe Cys Gly Ala Asn Gln Ile His Gln
165         170         175
Leu Phe Cys Asp Phe Glu Pro Val Leu Gln Leu Ala Cys Thr Asp Thr
180         185         190
Tyr Ile Ile Leu Val Glu Asp Val Ile Arg Ala Ile Ser Ile Leu Thr
195         200         205
Ser Val Ser Val Ile Thr Leu Phe Tyr Leu Arg Ile Ile Thr Val Ile
210         215         220
Leu Arg Ile Pro Ser Gly Glu Ser Arg Gln Lys Ala Phe Phe Thr Cys
225         230         235         240
Ala Ala His Ile Ala Ile Phe Leu Leu Phe Phe Gly Ser Val Ser Leu
245         250         255
Met Tyr Leu Arg Phe Ser Val Thr Phe Pro Pro Leu Leu Asp Lys Ala
260         265         270
Ile Ala Leu Met Phe Ala Val Leu Ala Leu Leu Phe Asn Pro Val Ile
275         280         285
Tyr Ser Leu Arg Asn Lys Asp Met Lys Asn Ala Thr Lys Lys Ile Leu
290         295         300
Cys Ser Gln Lys Met Phe Asn Ala Ser Gly Ser Xaa Trp Ser Ser
305         310         315

```

<210> 1489

<211> 317

<212> PRT

<213> Unknown (H38g406 protein)

<220>

<223> Synthetic construct

<400> 1489

```

Met Thr Gln Leu Thr Ala Ser Gly Asn Gln Thr Met Val Thr Glu Phe
1          5          10          15

```

```

Leu Phe Ser Met Phe Pro His Ala His Arg Gly Gly Leu Leu Phe Phe
      20      25      30
Ile Pro Leu Leu Leu Ile Tyr Gly Phe Ile Leu Thr Gly Asn Leu Ile
      35      40      45
Met Phe Ile Val Ile Gln Val Gly Met Ala Leu His Thr Pro Leu Tyr
      50      55      60
Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Cys Tyr Thr Thr Thr
65      70      75      80
Thr Ile Pro Lys Met Leu Ser Cys Leu Ile Ser Glu Gln Lys Ser Ile
      85      90      95
Ser Val Ala Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly
      100     105     110
Ile Thr Glu Ser Cys Val Leu Thr Ala Met Ala Ile Asp Arg Tyr Ile
      115     120     125
Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Ile Pro Lys Leu
      130     135     140
Cys Ile Gln Leu Thr Val Gly Ser Cys Phe Cys Gly Phe Leu Leu Val
145     150     155     160
Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn
      165     170     175
Gln Ile His Gln Ile Phe Cys Asp Phe Thr Pro Val Leu Ser Leu Ala
      180     185     190
Cys Thr Asp Thr Phe Leu Val Val Ile Val Asp Ala Ile His Ala Ala
      195     200     205
Glu Ile Val Ala Ser Phe Leu Val Ile Ala Leu Ser Tyr Ile Arg Ile
      210     215     220
Ile Ile Val Ile Leu Gly Met His Ser Ala Glu Gly His His Lys Ala
225     230     235     240
Phe Ser Thr Cys Ala Ala His Leu Ala Val Phe Leu Leu Phe Phe Gly
      245     250     255
Ser Val Ala Val Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Val Phe
      260     265     270
Trp Asp Thr Ala Ile Ala Val Thr Phe Val Ile Leu Ala Pro Phe Phe
      275     280     285
Asn Pro Ile Ile Tyr Ser Leu Lys Asn Lys Asp Met Lys Glu Ala Ile
      290     295     300
Gly Arg Leu Phe His Tyr Gln Lys Arg Ala Gly Trp Ala
305      310      315

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<210> 1490

<211> 277

<212> PRT

<213> Unknown (H38g407 protein)

<220>

<223> Synthetic construct

<400> 1490

```

Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu Asp
 1      5      10      15
Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser Leu
      20      25      30
Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Ala Ser Asp
      35      40      45
Phe Leu Ser Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile Gln
      50      55      60
Ser Phe Phe Phe Ser Ala Leu Gly Gly Ala Glu Ala Leu Leu Leu Ala
65      70      75      80
Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro Leu His Tyr
      85      90      95
Pro Ile Arg Met Ser Lys Arg Met Cys Val Leu Met Ile Thr Gly Ser

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      100              105              110
Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val Tyr Val Leu
      115              120              125
His Ile Pro Tyr Cys Gln Ser Arg Ala Ile Asn His Phe Phe Cys Asp
      130              135              140
Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp Val Tyr Glu
      145              150              155              160
Gly Thr Val Phe Leu Ser Thr Thr Ile Phe Leu Val Phe Pro Phe Ile
      165              170              175
Ala Ile Ser Cys Ser Tyr Gly Arg Val Leu Leu Ala Val Tyr His Met
      180              185              190
Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu Thr Cys Ser Thr His
      195              200              205
Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr Thr Tyr Leu
      210              215              220
Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Val Leu Ala Val
      225              230              235              240
Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu
      245              250              255
Arg Asn Lys Glu Val Met Gly Ala Leu Thr Arg Val Ser Gln Arg Ile
      260              265              270
Cys Ser Val Lys Met
      275

```

<210> 1491

<211> 241

<212> PRT

<213> Unknown (H38g408 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(241)

<223> Xaa = Any Amino Acid

<400> 1491

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
 1          5          10          15
Leu Ser Ser Ser Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe Ser
      20          25          30
Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
      35          40          45
Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
      50          55          60
Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
      65          70          75          80
Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
      85          90          95
Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
      100          105          110
Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
      115          120          125
Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
      130          135          140
Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
      145          150          155          160
Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
      165          170          175
Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
      180          185          190

```

Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu
 195 200 205
 Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser
 210 215 220
 Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val
 225 230 235 240
 Gly

<210> 1492

<211> 312

<212> PRT

<213> Unknown (H38g409 protein)

<220>

<223> Synthetic construct

<400> 1492

Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly
 1 5 10 15
 Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu Leu
 20 25 30
 Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val
 35 40 45
 Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser
 50 55 60
 Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys
 100 105 110
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile
 130 135 140
 Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile
 145 150 155 160
 Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
 165 170 175
 Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
 195 200 205
 Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
 210 215 220
 Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
 245 250 255
 Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
 260 265 270
 Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Val Arg Arg Gln
 290 295 300
 Leu Lys Arg Ile Gly Ile Leu Ala
 305 310

<210> 1493

<211> 212

<212> PRT

<213> Unknown (H38g410 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1493

```

Glu Phe Leu Phe Tyr Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu
 1           5           10           15
Leu Gly Leu Phe Pro Gln Ser Arg Ile Gly Leu Phe Val Phe Thr Leu
      20           25           30
Ile Phe Leu Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile
      35           40           45
Leu Leu Ile Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu
      50           55           60
Leu Ser Gln Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val
      65           70           75           80
Pro Lys Met Val Tyr Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe
      85           90           95
Thr Gly Cys Gly Ile Gln Ser Phe Phe Phe Leu Thr Leu Ala Val Ala
      100          105          110
Glu Gly Leu Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile
      115          120          125
Cys Phe Pro Leu His Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys Val
      130          135          140
Met Met Ile Thr Gly Ser Trp Met Ile Ser Ser Ile Asn Ser Cys Ala
      145          150          155          160
His Thr Val Tyr Ala Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala Ile
      165          170          175
Asn His Phe Phe Cys Glu Gly Ser Ser Glu Arg Tyr Leu Gly Cys Met
      180          185          190
Gln Ala Trp Arg Trp Ala Ala Val Glu Thr Ala Xaa Leu Val Lys Pro
      195          200          205
Trp Ala Gly Pro
      210

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<210> 1494

<211> 263

<212> PRT

<213> Unknown (H38g411 protein)

<220>

<223> Synthetic construct

<400> 1494

```

Met Leu Gly Asn Tyr Ser Ser Ala Thr Glu Phe Phe Leu Leu Gly Phe
 1           5           10           15
Pro Gly Ser Gln Glu Val Cys Arg Ile Leu Phe Ala Thr Phe Phe Leu
      20           25           30
Leu Tyr Ala Val Thr Val Met Gly Asn Val Val Ile Ile Thr Val
      35           40           45
Cys Val Asp Lys Cys Leu Gln Ser Pro Ile Tyr Phe Phe Leu Gly His
      50           55           60
Leu Cys Val Leu Glu Ile Leu Ile Thr Ser Thr Ala Val Pro Phe Met
      65           70           75           80
Leu Trp Gly Leu Leu Leu Pro Ser Thr Gln Ile Met Ser Leu Thr Ala
      85           90           95

```

Cys Ala Ala Gln Leu Tyr Leu Tyr Leu Ser Leu Gly Thr Leu Glu Leu
 100 105 110
 Ala Leu Met Gly Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn
 115 120 125
 Pro Leu Arg Tyr Asn Ile Ile Met Asn Ser Ser Thr Phe Ile Trp Val
 130 135 140
 Ile Ile Val Ser Trp Val Leu Gly Phe Leu Ser Glu Ile Trp Pro Val
 145 150 155 160
 Tyr Ala Thr Phe Gln Leu Thr Phe Cys Lys Ser Ser Val Leu Asp His
 165 170 175
 Phe Tyr Cys Asp Arg Gly Gln Leu Leu Lys Val Ser Cys Glu Asp Thr
 180 185 190
 Leu Phe Arg Glu Phe Ile Leu Phe Leu Met Ala Val Phe Ile Ile Ile
 195 200 205
 Gly Ser Leu Ile Pro Thr Ile Val Ser Tyr Thr Tyr Ile Ile Ser Thr
 210 215 220
 Asn Leu Lys Ile Pro Ser Ala Ser Gly Trp Arg Lys Ser Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Phe Thr Tyr Val Val Ile Gly Tyr Gly Ser Cys Leu
 245 250 255
 Phe Leu Tyr Val Lys Pro Lys
 260

<210> 1495

<211> 317

<212> PRT

<213> Unknown (H38g412 protein)

<220>

<223> Synthetic construct

<400> 1495

Met Asp Gln Tyr Asn His Ser Ser Leu Ala Glu Phe Val Phe Leu Gly
 1 5 10 15
 Phe Ala Ser Val Gly Tyr Val Arg Gly Trp Leu Phe Val Leu Leu Leu
 20 25 30
 Leu Ala Tyr Leu Phe Thr Ile Cys Gly Asn Met Leu Ile Phe Ser Val
 35 40 45
 Ile Arg Leu Asp Ala Ala Leu His Thr Pro Met Tyr His Phe Val Ser
 50 55 60
 Val Leu Ser Phe Leu Glu Leu Trp Tyr Thr Ala Thr Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ser Asn Ile Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly
 85 90 95
 Cys Leu Leu Gln Thr Tyr Phe Phe His Ser Leu Gly Ala Ser Glu Cys
 100 105 110
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Ile Ile Met Thr Thr Thr Leu Cys Ala Lys Met
 130 135 140
 Ala Ala Ala Cys Trp Thr Cys Gly Phe Leu Cys Pro Ile Ser Glu Val
 145 150 155 160
 Ile Leu Ala Ser Gln Leu Pro Phe Cys Ala Tyr Asn Glu Ile Gln His
 165 170 175
 Ile Phe Cys Asp Phe Pro Pro Leu Leu Ser Leu Ala Cys Lys Asp Thr
 180 185 190
 Ser Ala Asn Ile Leu Val Asp Phe Ala Ile Asn Ala Phe Ile Ile Leu
 195 200 205
 Ile Thr Phe Phe Phe Ile Met Ile Ser Tyr Ala Arg Ile Ile Gly Ala
 210 215 220
 Val Leu Lys Ile Lys Thr Ala Ser Gly Arg Lys Lys Ala Phe Ser Thr

225 230 235 240
 Cys Ala Ser His Leu Ala Val Val L u Ile Phe Phe Gly Ser Ile Ile
 245 250 255
 Phe Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Thr Leu Asp Arg
 260 265 270
 Thr Leu Ala Ile Val Tyr Ser Val Leu Thr Pro Met Val Asn Pro Ile
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Ile Ile Lys Ala Ile Lys Arg Thr
 290 295 300
 Ile Phe Gln Lys Gly Asp Lys Ala Ser Leu Ala His Leu
 305 310 315

<210> 1496

<211> 315

<212> PRT

<213> Unknown (H38g413 protein)

<220>

<223> Synthetic construct

<400> 1496

Met Gln Gly Leu Asn His Thr Ser Val Ser Glu Phe Ile Leu Val Gly
 1 5 10 15
 Phe Ser Ala Phe Pro His Leu Gln Leu Met Leu Phe Leu Leu Phe Leu
 20 25 30
 Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala Thr
 35 40 45
 Val Trp Ser Glu Arg Ser Leu His Met Pro Met Tyr Leu Phe Leu Cys
 50 55 60
 Ala Leu Ser Ile Thr Glu Ile Leu Tyr Thr Val Ala Ile Ile Pro Arg
 65 70 75 80
 Met Leu Ala Asp Leu Leu Ser Thr Gln Arg Ser Ile Ala Phe Leu Ala
 85 90 95
 Cys Ala Ser Gln Met Phe Phe Ser Phe Ser Phe Gly Phe Thr His Ser
 100 105 110
 Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Asn Val Leu Met Ser Leu Arg Gly Cys Thr Cys Arg
 130 135 140
 Val Gly Cys Ser Trp Ala Gly Gly Leu Val Met Gly Met Val Val Thr
 145 150 155 160
 Ser Ala Ile Phe His Leu Ala Phe Cys Gly His Lys Glu Ile His His
 165 170 175
 Phe Phe Cys His Val Pro Pro Leu Leu Lys Leu Ala Cys Gly Asp Asp
 180 185 190
 Val Leu Val Val Ala Lys Gly Val Gly Leu Val Cys Ile Thr Ala Leu
 195 200 205
 Leu Gly Cys Phe Leu Leu Ile Leu Leu Ser Tyr Ala Phe Ile Val Ala
 210 215 220
 Ala Ile Leu Lys Ile Pro Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Val Val Val His Tyr Gly Phe Ala
 245 250 255
 Ser Val Ile Tyr Leu Lys Pro Lys Gly Pro Gln Ser Pro Glu Gly Asp
 260 265 270
 Thr Leu Met Gly Ile Thr Tyr Thr Val Leu Thr Pro Phe Leu Ser Pro
 275 280 285
 Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Val Ala Met Lys Lys
 290 295 300
 Thr Cys Phe Thr Lys Leu Phe Pro Gln Asn Cys
 305 310 315

<210> 1497
 <211> 319
 <212> PRT
 <213> Unknown (H38g414 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(319)
 <223> Xaa = Any Amino Acid

<400> 1497
 His Thr Glu Pro Arg His Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
 20 25 30
 Pro Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Val Ile Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Pro Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
 65 70 75 80
 Lys Met Thr Val Asp Met Gln Ser His Ile Arg Val Ile Ser Tyr Ala
 85 90 95
 Ser Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 100 105 110
 Asp Met Leu Leu Thr Val Met Ala Xaa Asp Cys Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Ala Val Ile Val Asn Pro His Leu Cys Val Phe
 130 135 140
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Ser Xaa Ile Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser His
 165 170 175
 Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180 185 190
 Val Ile Asn Ser Ile Phe Met Tyr Phe Asn Ser Thr Met Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser
 210 215 220
 Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg Asn Gly Val
 260 265 270
 Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu
 290 295 300
 Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser
 305 310 315

<210> 1498
 <211> 157
 <212> PRT
 <213> Unknown (H38g415 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1498

Val	Ser	Pro	Leu	Trp	Glu	Cys	Val	Ser	Xaa	Gln	Arg	Ser	Pro	His	Phe
1				5					10					15	
Leu	Cys	Ser	Gly	Asp	Ser	Val	Phe	Cys	Leu	Val	His	Ser	Val	Gly	Cys
			20					25					30		
Cys	Thr	Leu	Leu	Leu	Ser	Gln	Ser	Leu	Arg	Leu	Leu	Ser	Val	Phe	Leu
		35				40						45			
Leu	Ser	Ser	Cys	Ala	Ala	Ser	Trp	Lys	Lys	Val	His	Ser	Met	Asn	Leu
		50				55					60				
Tyr	Thr	Pro	Phe	Cys	Leu	Ser	Lys	Trp	Xaa	Asn	His	Val	Asn	Asn	Ala
65					70					75				80	
Phe	Asn	Leu	Pro	Ser	Trp	Lys	Lys	Ser	Lys	Ser	Val	Val	Thr	Met	Phe
				85					90					95	
Xaa	Gly	Pro	Ala	Met	Ile	Thr	Tyr	Leu	Arg	Ser	Asp	Ser	Xaa	Tyr	Asn
			100					105					110		
Pro	Thr	Val	Gly	Lys	Gln	Leu	Val	Leu	Phe	Tyr	Ser	Ile	Val	Ser	Ala
		115				120						125			
Phe	Ile	Lys	Pro	Ile	Ile	Ser	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Gly
		130				135					140				
Ala	Ser	Trp	Lys	Val	Leu	Arg	Val	Lys	Gly	Thr	Ala	Gln			
145					150					155					

<210> 1499

<211> 287

<212> PRT

<213> Unknown (H38g416 protein)

<220>

<223> Synthetic construct

<400> 1499

Met	Glu	Asn	Tyr	Asn	Gln	Thr	Ser	Thr	Asp	Phe	Ile	Leu	Leu	Gly	Leu
1				5					10					15	
Phe	Pro	Pro	Ser	Arg	Ile	Asp	Leu	Phe	Phe	Phe	Ile	Leu	Phe	Val	Leu
			20					25					30		
Ile	Phe	Leu	Met	Ala	Leu	Ile	Gly	Asn	Leu	Ser	Met	Ile	Leu	Leu	Ile
		35				40						45			
Phe	Leu	Asp	Thr	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Leu	Leu	Ser	Gln
		50				55				60					
Leu	Ser	Leu	Ile	Asp	Leu	Asn	Tyr	Ile	Ser	Thr	Ile	Val	Pro	Lys	Met
65					70					75				80	
Ala	Ser	Asp	Phe	Leu	Tyr	Gly	Asn	Lys	Ser	Ile	Ser	Phe	Ile	Gly	Cys
			85					90						95	
Gly	Ile	Gln	Ser	Phe	Phe	Phe	Met	Thr	Phe	Ala	Gly	Ala	Glu	Ala	Leu
		100						105					110		
Leu	Leu	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe	Pro
		115				120						125			
Leu	His	Tyr	Pro	Ile	Arg	Met	Ser	Lys	Arg	Met	Tyr	Val	Leu	Met	Ile
		130				135					140				
Thr	Gly	Ser	Trp	Met	Ile	Gly	Ser	Ile	Asn	Ser	Cys	Ala	His	Thr	Val
145					150					155				160	
Tyr	Ala	Phe	Arg	Ile	Pro	Tyr	Cys	Lys	Ser	Arg	Ala	Ile	Asn	His	Phe
			165					170					175		
Phe	Cys	Asp	Val	Pro	Ala	Met	Leu	Thr	Leu	Ala	Cys	Thr	Asp	Thr	Trp
			180					185					190		

Val Tyr Glu Tyr Thr Val Phe Leu Ser Ser Thr Ile Phe Leu Val Phe
 195 200 205
 Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Trp Val Leu Leu Ala Val
 210 215 220
 Tyr Arg Met His Ser Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys
 225 230 235 240
 Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Leu Arg Tyr
 245 250 255
 Thr Tyr Leu Cys Pro Arg Ser Leu Phe Ile Ser Thr Glu Asp Lys Val
 260 265 270
 Gly Gly Gly Gly Tyr Thr Ile Leu Thr Ser Met Leu Asn Pro Ile
 275 280 285

<210> 1500

<211> 310

<212> PRT

<213> Unknown (H38g417 protein)

<220>

<223> Synthetic construct

<400> 1500

Met Asp Lys Glu Asn Ser Ser Met Val Thr Glu Phe Ile Phe Met Gly
 1 5 10 15
 Ile Thr Gln Asp Pro Gln Met Glu Ile Ile Phe Phe Val Val Phe Leu
 20 25 30
 Ile Val Tyr Leu Val Asn Val Val Gly Asn Ile Gly Met Ile Ile Leu
 35 40 45
 Ile Thr Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50 55 60
 Asn Leu Ser Phe Val Asp Leu Gly Tyr Ser Ser Ala Ile Ala Pro Arg
 65 70 75 80
 Met Leu Ala Asp Phe Leu Thr Asn His Lys Val Ile Ser Phe Ser Ser
 85 90 95
 Cys Ala Thr Gln Phe Ala Phe Phe Val Gly Phe Val Asp Ala Glu Cys
 100 105 110
 Tyr Val Leu Ala Ala Met Ala Tyr Gly Arg Phe Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ser Thr Phe Met Ser Lys Gln Val Cys Leu Ala Leu
 130 135 140
 Met Leu Gly Ser Tyr Leu Ala Gly Leu Val Ser Leu Val Ala His Thr
 145 150 155 160
 Thr Leu Thr Phe Ser Leu Ser Tyr Cys Gly Ser Asn Ile Ile Asn His
 165 170 175
 Phe Phe Cys Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
 180 185 190
 Tyr Ile Ser Glu Ile Leu Leu Phe Ser Leu Cys Gly Phe Ile Glu Phe
 195 200 205
 Ser Thr Ile Leu Ile Ile Phe Ile Ser Tyr Thr Phe Ile Leu Val Ala
 210 215 220
 Ile Ile Arg Met Arg Ser Ala Glu Gly Arg Leu Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Gly Ile Thr Leu Phe Tyr Gly Thr Val Met
 245 250 255
 Phe Met Tyr Leu Arg Pro Thr Ser Ser Tyr Ser Leu Asp Gln Asp Lys
 260 265 270
 Trp Ala Ser Val Phe Tyr Thr Val Ile Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Phe Lys Lys Leu
 290 295 300
 Ile Gly Lys Lys Ser Gln

305

310

<210> 1501

<211> 335

<212> PRT

<213> Unknown (H38g418 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1501

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Ser Thr Asp Pro Gln Asn Leu Ile Asp Val Ser Ile Phe Leu Leu Leu
 1           5           10           15
Gly Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe
          20           25           30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
          35           40           45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65          70          75          80
Lys Met Ile Val Asp Ile Arg Ser His Ser Arg Val Ile Ser Tyr Ala
          85          90          95
Gly Cys Leu Thr Gln Thr Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100         105         110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile
          115         120         125
Cys His Pro Leu Tyr His Ser Ala Val Met Asn Pro Cys Phe Cys Gly
          130         135         140
Phe Leu Val Leu Leu Thr Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln
145         150         155         160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
          165         170         175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Pro Leu Pro His Leu Ala Cys
          180         185         190
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
          195         200         205
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
          210         215         220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225         230         235         240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
          245         250         255
Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
          260         265         270
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
          275         280         285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu
          290         295         300
Arg Trp Leu His Gly Ser Ser Val Xaa Ser Gln His Leu Leu Ile Cys
305         310         315         320
Cys Ile Pro Phe Val Trp Val Lys Lys Gly Ser Arg Val Lys
          325         330         335

```

<210> 1502

<211> 303

<212> PRT

<213> Unknown (H38g419 protein)

<220>

<223> Synthetic construct

<400> 1502

```

Met Asp His Val Ser His Asn Trp Thr Gln Ser Phe Ile Leu Ala Gly
 1           5           10           15
Phe Thr Thr Thr Gly Thr Leu Gln Pro Leu Ala Phe Leu Gly Thr Leu
      20           25           30
Cys Ile Tyr Leu Leu Thr Leu Ala Gly Asn Ile Leu Ile Ile Val Leu
      35           40           45
Val Gln Leu Asp Ser Gly Leu Phe Thr Pro Met Tyr Leu Phe Ile Ser
      50           55           60
Val Leu Ser Phe Val Glu Val Trp Tyr Val Ser Thr Thr Val Pro Met
      65           70           75           80
Leu Leu His Thr Leu Leu Gln Gly Cys Ser Pro Val Ser Ser Ala Val
      85           90           95
Cys Phe Ile Gln Thr Met Phe Phe His Ser Leu Gly Met Thr Glu Cys
      100          105          110
Tyr Leu Leu Gly Val Met Ala Leu Asp Ser Tyr Leu Ile Ile Cys His
      115          120          125
Pro Leu His Tyr His Ala Leu Met Ser Arg Gln Val Gln Leu Arg Leu
      130          135          140
Ala Gly Ala Ser Trp Val Ala Gly Phe Ser Ala Ala Leu Val Pro Ala
      145          150          155          160
Thr Leu Thr Ala Thr Leu Pro Phe Cys Leu Lys Glu Val Ala His Tyr
      165          170          175
Phe Cys Asp Leu Ala Pro Leu Met Arg Leu Ala Cys Val Asp Thr Ser
      180          185          190
Trp His Ala Arg Ala His Gly Thr Val Ile Gly Val Ala Thr Gly Cys
      195          200          205
Asn Phe Val Leu Ile Leu Gly Leu Tyr Gly Gly Ile Leu Asn Ala Val
      210          215          220
Leu Lys Leu Pro Ser Ala Ala Ser Ser Ala Lys Ala Phe Ser Thr Cys
      225          230          235          240
Ser Ser His Val Thr Val Val Ala Leu Phe Tyr Ala Ser Ala Phe Thr
      245          250          255
Val Tyr Val Gly Ser Pro Gly Ser Arg Pro Glu Ser Thr Asp Lys Leu
      260          265          270
Val Ala Leu Val Tyr Ala Leu Ile Thr Pro Phe Leu Asn Pro Ile Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Arg Arg Val
      290          295          300

```

<210> 1503

<211> 336

<212> PRT

<213> Unknown (H38g420 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 1503

```

Pro Thr Lys Arg Glu Asn His Thr Val Ile Arg Glu Phe Val Phe Gln
 1           5           10           15
Gly Phe Ser Ser Phe His Glu His Lys Leu Thr Leu Phe Val Val Phe

```



```
<210> 1504
<211> 315
<212> PRT
<213> Unknown (H38g421 protein)
```

<220>
<223> Synthetic construct

<400> 1504															
Met	Ser	Ile	Thr	Lys	Ala	Trp	Asn	Ser	Ser	Ser	Val	Thr	Met	Phe	Ile
1				5					10					15	
Leu	Leu	Gly	Phe	Thr	Asp	His	Pro	Glu	Leu	Gln	Ala	Leu	Leu	Phe	Val
			20					25					30		
Thr	Phe	Leu	Gly	Ile	Tyr	Leu	Thr	Thr	Leu	Ala	Trp	Asn	Leu	Ala	Leu
		35					40					45			
Ile	Phe	Leu	Ile	Arg	Gly	Asp	Thr	His	Leu	His	Thr	Pro	Met	Tyr	Phe
	50					55					60				
Phe	Leu	Ser	Asn	Leu	Ser	Phe	Ile	Asp	Ile	Cys	Tyr	Ser	Ser	Ala	Val
65					70					75				80	
Ala	Pro	Asn	Met	Leu	Thr	Asp	Phe	Phe	Trp	Glu	Gln	Lys	Thr	Ile	Ser
				85					90					95	

Phe Val Gly Cys Ala Ala Gln Phe Phe Phe Phe Val Gly Met Gly Leu
 100 105 110
 Ser Glu Cys Leu Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala
 115 120 125
 Ile Ser Ser Pro Leu Leu Tyr Pro Thr Ile Met Thr Gln Gly Leu Cys
 130 135 140
 Thr Arg Met Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Leu
 145 150 155 160
 Ile Gln Ala Ser Ser Ile Phe Arg Leu His Phe Cys Gly Pro Asn Ile
 165 170 175
 Ile Asn His Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys
 180 185 190
 Ser Asp Thr Phe Leu Ser Gln Val Val Asn Phe Leu Val Val Val Thr
 195 200 205
 Val Gly Gly Thr Ser Phe Leu Gln Leu Leu Ile Ser Tyr Gly Tyr Ile
 210 215 220
 Val Ser Ala Val Leu Lys Ile Pro Ser Ala Glu Gly Arg Trp Lys Ala
 225 230 235 240
 Cys Asn Thr Cys Ala Ser His Leu Met Val Val Thr Leu Leu Phe Gly
 245 250 255
 Thr Ala Leu Phe Val Tyr Leu Arg Pro Ser Ser Ser Tyr Leu Leu Gly
 260 265 270
 Arg Asp Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu
 275 280 285
 Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu
 290 295 300
 Trp Lys Val Leu Glu Arg Lys Lys Val Phe Ser
 305 310 315

<210> 1505

<211> 317

<212> PRT

<213> Unknown (H38g422 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1505

Met Pro Xaa Lys Met Glu Ser Ile Asn Thr Asn Phe Thr Val Thr Glu
 1 5 10 15
 Phe Val Phe Leu Gly Leu Ser Ser Glu Pro Lys Ile Gln Leu Ile Leu
 20 25 30
 Phe Ile Met Phe Leu Phe Tyr Leu Ser Thr Val Ala Gly Asn Val Ile
 35 40 45
 Ile Ile Thr Ile Ile Xaa Met Glu Pro Leu Leu Gln Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Thr Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Thr
 65 70 75 80
 Asn Val Pro Gln Met Leu Ser Asn Met Ala Gly Lys Lys Asn Thr Ile
 85 90 95
 Ser Phe Ser Ser Cys Ala Thr Gln Met Tyr Phe Ser Leu Ser Phe Gly
 100 105 110
 Ser Asp Cys Val Leu Leu Gly Val Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn Thr Cys
 130 135 140
 Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Ser Ser Met

```

145          150          155          160
Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro Asn Ile
          165          170          175
Leu Asn His Phe Phe Cys Glu Val Leu Ser Val Leu Arg Leu Ala Cys
          180          185          190
Thr Asn Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser Ile Ile
          195          200          205
Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Arg Ile
          210          215          220
Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr Gln Ala
225          230          235          240
Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly
          245          250          255
Thr Ala Ile Phe Met Asp Met Arg Pro Gln Ser Arg Ser Ser Trp Ala
          260          265          270
Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Asp Val Lys Gly Ala Arg
          290          295          300
Arg Arg Ala Ile Ala Lys Gln Arg Met Xaa Gln Leu Leu
305          310          315

```

<210> 1506

<211> 340

<212> PRT

<213> Unknown (H38g423 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(340)

<223> Xaa = Any Amino Acid

<400> 1506

```

Met Pro Lys Leu Asn Ser Thr Phe Val Thr Glu Phe Leu Phe Glu Gly
1          5          10          15
Phe Ser Ser Phe Arg Arg Gln His Lys Leu Val Phe Phe Val Val Phe
          20          25          30
Leu Thr Leu Tyr Leu Leu Thr Leu Ser Gly Asn Val Ile Ile Met Thr
          35          40          45
Ile Ile Arg Leu Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Cys Met Leu Ser Ile Ser Glu Thr Cys Tyr Thr Val Ala Ile Ile Pro
65          70          75          80
His Met Leu Ser Gly Leu Leu Asn Pro His Gln Pro Ile Ala Thr Gln
          85          90          95
Ser Cys Ala Thr Gln Leu Phe Phe Tyr Leu Thr Phe Gly Ile Asn Asn
          100          105          110
Cys Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
          115          120          125
Asn Pro Leu Arg Tyr Ser Val Ile Met Gly Lys Arg Ala Cys Ile Gln
          130          135          140
Leu Ala Ser Gly Ser Leu Gly Ile Gly Leu Gly Met Ala Ile Val Gln
145          150          155          160
Val Thr Ser Val Phe Gly Leu Pro Phe Cys Asp Ala Phe Val Ile Ser
          165          170          175
His Phe Phe Cys Asp Val Arg His Leu Leu Lys Leu Ala Cys Thr Asp
          180          185          190
Thr Thr Val Asn Glu Ile Ile Asn Phe Val Val Ser Val Cys Val Leu
195          200          205

```

```

Val Leu Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser
210                215                220
Thr Ile Leu Lys Ile Ala Ser Ala Glu Gly Gln Lys Lys Ala Phe Ala
225                230                235                240
Thr Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala
                245                250                255
Ser Ile Ile Tyr Leu Lys Pro Lys Ser Gln Ser Ser Leu Gly Gln Asp
                260                265                270
Arg Leu Ile Ser Val Thr Tyr Thr Ile Thr Pro Leu Leu Asn Pro Val
                275                280                285
Val Tyr Ser Leu Lys Asn Lys Glu Val Lys Asp Ala Leu His Arg Ala
                290                295                300
Val Gly Gln Lys Thr Leu Ser Pro Xaa Xaa Arg Glu Val Val Lys Ala
305                310                315                320
Phe Pro Phe Val Tyr Lys Tyr Val Leu Ile Phe Asn Ala Leu Ser Ile
                325                330                335
Met Pro Leu Cys
                340

```

```

<210> 1507
<211> 313
<212> PRT
<213> Unknown (H38g424 protein)

```

```

<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(313)
<223> Xaa = Any Amino Acid

```

```

<400> 1507
Met Asp Ile Gly Leu Ser Ile Ala Asn Ser Ser Gly Phe Gln Leu Ser
1          5          10          15
Glu Phe Ile Leu Ile Gly Phe Pro Gly Ile His Glu Trp Gln His Trp
20        25        30
Leu Ser Leu Pro Leu Ala Leu Gly Ala Asn Leu Leu Ile Ile Ile Thr
35        40        45
Ile Gln His Glu Thr Met Leu His Glu Pro Met Tyr His Leu Leu Gly
50        55        60
Ile Leu Ala Val Val Asp Ile Gly Leu Ala Thr Thr Ile Met Pro Lys
65        70        75        80
Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Ala Ile Ser Leu Pro Glu
85        90        95
Cys Phe Ala Gln Ile Tyr Ala Ile His Ser Phe Met Cys Met Glu Ser
100       105       110
Gly Ile Phe Leu Cys Met Ala Val Asp Arg Tyr Met Ala Ile Cys Tyr
115       120       125
Pro Leu Gln Tyr Thr Ser Ile Val Thr Glu Ala Phe Val Ile Lys Ala
130       135       140
Thr Leu Ser Val Val Leu Arg Asn Gly Leu Leu Thr Ile Pro Val Pro
145       150       155       160
Val Leu Ala Ala Gln Arg His Tyr Cys Ser Arg Asn Glu Ile Asp Gln
165       170       175
Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ala Cys Asp Asp Thr
180       185       190
Thr Ile Asn Arg Phe Tyr Gln Leu Ala Leu Val Trp Val Val Val Gly
195       200       205
Ser Asp Met Gly Leu Val Phe Ala Ser Tyr Ser Leu Ile Ile His Ser
210       215       220
Val Leu Lys Leu Asn Ser Ala Lys Ala Thr Ser Lys Ala Leu Asn Thr

```

225		230		235		240									
Cys	Ser	Ser	His	Leu	Ile	Leu	Ile	Leu	Phe	Phe	Tyr	Thr	Ala	Ile	Ile
			245						250					255	
Val	Val	Ser	Val	Thr	Asn	Leu	Ala	Gly	Arg	Arg	Ala	Pro	Arg	Ile	Pro
			260						265					270	
Val	Leu	Leu	Asn	Val	Leu	His	Ile	Val	Ile	Pro	Ser	Ala	Leu	Asn	Pro
			275						280					285	
Ile	Val	Tyr	Ala	Leu	Arg	Thr	Xaa	Glu	Leu	Arg	Ala	Gly	Phe	Gln	Lys
		290					295				300				
Leu	Leu	Gly	Leu	Gly	Glu	Tyr	Val	Ser							
305					310										

<210> 1508

<211> 315

<212> PRT

<213> Unknown (H38g425 protein)

<220>

<223> Synthetic construct

<400> 1508

Met	Phe	Ser	Pro	Asn	His	Thr	Ile	Val	Thr	Glu	Phe	Ile	Leu	Leu	Gly
1			5						10					15	
Leu	Thr	Asp	Asp	Pro	Val	Leu	Glu	Lys	Ile	Leu	Phe	Gly	Val	Phe	Leu
			20					25					30		
Ala	Ile	Tyr	Leu	Ile	Thr	Leu	Ala	Gly	Asn	Leu	Cys	Met	Ile	Leu	Leu
			35					40					45		
Ile	Arg	Thr	Asn	Ser	His	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly
			50				55				60				
His	Leu	Ser	Phe	Val	Asp	Ile	Cys	Tyr	Ser	Ser	Asn	Val	Thr	Pro	Asn
					70					75					80
Met	Leu	His	Asn	Phe	Leu	Ser	Glu	Gln	Lys	Thr	Ile	Ser	Tyr	Ala	Gly
				85					90					95	
Cys	Phe	Thr	Gln	Cys	Leu	Leu	Phe	Ile	Ala	Leu	Val	Ile	Thr	Glu	Phe
			100					105					110		
Tyr	Ile	Leu	Ala	Ser	Met	Ala	Leu	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Ser
			115				120					125			
Pro	Leu	His	Tyr	Ser	Ser	Arg	Met	Ser	Lys	Asn	Ile	Cys	Val	Cys	Leu
			130			135					140				
Val	Thr	Ile	Pro	Tyr	Met	Tyr	Gly	Phe	Leu	Ser	Gly	Phe	Ser	Gln	Ser
					150					155				160	
Leu	Leu	Thr	Phe	His	Leu	Ser	Phe	Cys	Gly	Ser	Leu	Glu	Ile	Asn	His
				165					170					175	
Phe	Tyr	Cys	Ala	Asp	Pro	Pro	Leu	Ile	Met	Leu	Ala	Cys	Ser	Asp	Thr
			180					185					190		
Arg	Val	Lys	Lys	Met	Ala	Met	Phe	Val	Val	Ala	Gly	Phe	Asn	Leu	Ser
			195				200					205			
Ser	Ser	Leu	Phe	Ile	Ile	Leu	Leu	Ser	Tyr	Leu	Phe	Ile	Phe	Ala	Ala
			210			215					220				
Ile	Phe	Arg	Ile	Arg	Ser	Ala	Glu	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr
					230				235						240
Cys	Ala	Ser	His	Leu	Thr	Ile	Val	Thr	Leu	Phe	Tyr	Gly	Thr	Leu	Phe
				245					250					255	
Cys	Met	Tyr	Val	Arg	Pro	Pro	Ser	Glu	Lys	Ser	Val	Glu	Glu	Ser	Lys
			260					265					270		
Ile	Thr	Ala	Val	Phe	Tyr	Thr	Phe	Leu	Ser	Pro	Met	Leu	Asn	Pro	Leu
			275					280					285		
Ile	Tyr	Ser	Leu	Arg	Asn	Thr	Asp	Val	Ile	Leu	Ala	Met	Gln	Gln	Met
		290				295					300				
Ile	Arg	Gly	Lys	Ser	Phe	His	Lys	Ile	Ala	Val					
305					310					315					

<210> 1509
 <211> 257
 <212> PRT
 <213> Unknown (H38g426 protein)

<220>
 <223> Synthetic construct

<400> 1509
 Met Phe Leu Leu Leu Ala Ile Leu Ala Ala Thr Asp Leu Gly Leu Ala
 1 5 10 15
 Thr Ser Ile Ala Pro Gly Leu Leu Ala Val Leu Trp Leu Gly Pro Arg
 20 25 30
 Ser Val Pro Tyr Ala Val Cys Leu Val Gln Met Phe Phe Val His Ala
 35 40 45
 Leu Thr Ala Met Glu Ser Gly Val Leu Leu Ala Met Ala Cys Asp Arg
 50 55 60
 Ala Ala Ala Ile Gly Arg Pro Leu His Tyr Pro Val Leu Val Thr Lys
 65 70 75 80
 Ala Cys Val Gly Tyr Ala Ala Leu Ala Leu Lys Ala Val Ala
 85 90 95
 Ile Val Val Pro Phe Pro Leu Leu Val Ala Lys Phe Glu His Phe Gln
 100 105 110
 Ala Lys Thr Ile Gly His Thr Tyr Cys Ala His Met Ala Val Val Glu
 115 120 125
 Leu Val Val Gly Asn Thr Gln Ala Thr Asn Leu Tyr Gly Leu Ala Leu
 130 135 140
 Ser Leu Ala Ile Ser Gly Met Asp Ile Leu Gly Ile Thr Gly Ser Tyr
 145 150 155 160
 Gly Leu Ile Ala His Ala Val Leu Gln Leu Pro Thr Arg Glu Ala His
 165 170 175
 Ala Lys Ala Phe Gly Thr Cys Ser Ser His Ile Cys Val Ile Leu Ala
 180 185 190
 Phe Tyr Ile Pro Gly Leu Phe Ser Tyr Leu Ala His Arg Phe Gly His
 195 200 205
 His Thr Val Pro Lys Pro Val His Ile Leu Leu Ser Asn Ile Tyr Leu
 210 215 220
 Leu Leu Pro Pro Ala Leu Asn Pro Leu Ile Tyr Gly Ala Arg Thr Lys
 225 230 235 240
 Gln Ile Arg Asp Arg Leu Leu Glu Thr Phe Thr Phe Arg Lys Ser Pro
 245 250 255
 Leu

<210> 1510
 <211> 358
 <212> PRT
 <213> Unknown (H38g427 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(358)
 <223> Xaa = Any Amino Acid

<400> 1510
 Val Ser Met Ser Phe Leu Ile Arg Ser Asp Ser Thr Leu His Thr Pro
 1 5 10 15
 Met Cys Leu Phe Leu Ser His Leu Ser Phe Val Asp Leu Tyr Tyr Ala

```

      20      25      30
Thr Asn Ala Thr Pro Pro Met Leu Val Asn Phe Val Phe Ser Lys Arg
      35      40      45
Lys Thr Val Ser Phe Ile Gly Cys Phe Ile Gln Phe His Leu Phe Ile
      50      55      60
Ala Leu Val Ile Thr Asp Tyr His Met Leu Thr Val Met Val Tyr Asp
65      70      75      80
His Tyr Met Ala Ile Cys Lys Pro Leu Leu Tyr Gly Ser Lys Met Ser
      85      90      95
Arg Cys Val Cys Leu Cys Leu Thr Ala Ala Pro Tyr Ile Tyr Gly Ser
      100      105      110
Ala Asn Gly Leu Val Gln Val Ile Leu Met Leu Cys Leu Phe Phe Cys
      115      120      125
Glu Pro Asn Glu Ile Asn His Phe Phe Phe Phe Gly Glu Asn Ala Leu
      130      135      140
Tyr Ala His Leu Ile Pro Leu Xaa Ile Phe Glu Trp Thr Val Gly Glu
145      150      155      160
Glu Gly Arg Asn Asn Ile Asn Gly Glu Asn Thr Thr Gln Lys Val Tyr
      165      170      175
Thr Met Gly Glu Arg Asn Leu Leu Ile Gln Val Ser Ile Phe Leu Leu
      180      185      190
Trp His Ile Arg Ser Xaa Leu Phe Ser Gln Tyr Glu Ala Ser Pro Arg
      195      200      205
Ala Asp Ser Asp Val Lys Leu Glu Ile Asn His Phe Tyr Tyr Ala Glu
      210      215      220
Pro Pro Leu Leu Val Leu Ala Cys Leu Asp Thr Tyr Val Lys Glu Thr
225      230      235      240
Ala Met Phe Met Val Ala Gly Ser Asn Leu Ile Cys Pro Leu Thr Ile
      245      250      255
Ile Phe Ile Ser Tyr Thr Phe Ile Phe Thr Asp Ile Leu His Ile Cys
      260      265      270
Thr Ala Glu Gly Arg Tyr Asn Ala Phe Ser Thr Cys Gly Ser Leu Val
      275      280      285
Thr Ala Val Thr Val Phe Gln Gly Thr Leu Phe His Met Cys Leu Arg
      290      295      300
Pro Pro Ser Glu Ala Ser Val Glu Gln Gly Lys Ile Val Ala Ala Phe
305      310      315      320
Tyr Ile Phe Val Ser Pro Thr Leu Asn Pro Leu Ile Tyr Arg Leu Arg
      325      330      335
Asn Lys Asn Val Lys Arg Thr Ile Arg Glu Val Ile Gln Lys Lys Leu
      340      345      350
Phe Ala Lys Xaa Gly Arg
      355

```

<210> 1511

<211> 313

<212> PRT

<213> Unknown (H38g428 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1511

```

Met Phe Gly Ala Asn Leu Thr Thr Phe His Pro Thr Leu Phe Ile Leu
1      5      10      15
Leu Gly Ile Pro Gly Leu Glu Gln Tyr His Ile Trp Leu Ser Ile Pro
      20      25      30

```

Phe Tyr Leu Met Tyr Ile Thr Ala Val Leu Gly Asn Gly Ala Leu Ile
 35 40 45
 Leu Val Val Leu Ser Glu His Thr Leu His Val Phe Leu Ser Met Leu
 50 55 60
 Ala Gly Thr Asp Ile Leu Leu Ser Thr Thr Thr Val Pro Lys Ala Leu
 65 70 75 80
 Ala Ile Phe Trp Val His Ala Gly Glu Ile Ala Phe Asp Ala Cys Ile
 85 90 95
 Thr Gln Met Phe Ile His Val Ala Phe Val Ala Glu Ser Gly Ile
 100 105 110
 Leu Leu Ala Met Ala Phe Asp Ser Tyr Val Ala Ile Cys Thr Pro Leu
 115 120 125
 Arg Tyr Thr Thr Ile Leu Thr Ser Met Val Asn Gly Lys Met Thr Leu
 130 135 140
 Thr Ile Trp Gly Gln Ser Ile Gly Thr Ile Phe Pro Val Ile Phe Leu
 145 150 155 160
 Leu Lys Arg Leu Pro Tyr Cys Gln Thr Asn Ile Ile Pro His Ser Tyr
 165 170 175
 Cys Glu His Ile Gly Val Ala Gln Leu Ala Cys Ala Asp Ile Thr Val
 180 185 190
 Asn Ile Trp Tyr Gly Phe Ser Val Pro Met Ala Ser Val Leu Val Asp
 195 200 205
 Val Ala Phe Ile Gly Phe Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe
 210 215 220
 Arg Leu Pro Ser Gln Glu Ser Gln His Lys Ala Leu Asn Thr Cys Gly
 225 230 235 240
 Ser His Ile Gly Val Val Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr
 245 250 255
 Phe Leu Thr His Arg Phe Gly Lys Asn Ile Pro His His Val His Ile
 260 265 270
 Leu Leu Ala Asn Leu Tyr Leu Leu Val Pro Pro Met Leu Asn Pro Ile
 275 280 285
 Ile Tyr Gly Glu Lys Thr Lys Gln Ile Arg Asp Ser Met Ala His Met
 290 295 300
 Leu Ser Val Val Gly Lys Ser Xaa Asp
 305 310

<210> 1512

<211> 314

<212> PRT

<213> Unknown (H38g429 protein)

<220>

<223> Synthetic construct

<400> 1512

Met Lys Met Lys Ile Asp Pro Lys Cys Asn Gly Thr Glu Val Thr Glu
 1 5 10 15
 Phe Ile Leu Leu Gly Leu Thr Ser Gln Pro Glu Leu Gln Pro Met Leu
 20 25 30
 Phe Val Val Phe Leu Leu Ile Tyr Leu Ile Thr Leu Thr Gly Lys Phe
 35 40 45
 Gly Met Ile Phe Leu Ile Arg Phe Thr Pro Gln Leu Gln Thr His Met
 50 55 60
 Tyr Phe Phe Leu Thr His Leu Ala Cys Val Asp Ile Phe Tyr Ser Thr
 65 70 75 80
 Asn Val Ser Pro Gln Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr
 85 90 95
 Ile Ser Tyr Ala Gly Cys Leu Ala Gln Cys Phe Val Phe Val Thr Leu
 100 105 110
 Leu Leu Thr Glu Tyr Tyr Met Leu Gly Ala Met Ala Tyr Asp Cys Tyr

115	120	125
Met Ala Ile Cys Asn Pro Leu His Tyr Ser Ser Lys Met Ser Arg Ala		
130	135	140
Val Cys Ile Cys Leu Val Thr Phe Pro Tyr Phe Trp Gly Ser Met Val		
145	150	155
Gly Thr Met Gln Val Ile Leu Thr Ser Arg Leu Ser Phe Phe Gly Pro		
165	170	175
Asn Thr Ile Asn His Phe Tyr Cys Thr Asp Pro Pro Leu Leu Met Leu		
180	185	190
Thr Ser Ser Asp Thr Tyr Ile Lys Gln Thr Ala Leu Phe Val Ser Ala		
195	200	205
Gly Ile Asn Leu Thr Val Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile		
210	215	220
Phe Ile Phe Ile Thr Ile Met Arg Ile Arg Ser Ser Glu Gly Gln Leu		
225	230	235
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Ala Val Thr Met Phe		
245	250	255
Tyr Gly Ser Leu Phe Cys Met Tyr Leu Arg Pro Thr Asn Glu Leu Ser		
260	265	270
Val Glu Gln Gly Lys Met Gly Val Val Phe Cys Ile Phe Val Ser Pro		
275	280	285
Met Leu Asn Pro Phe Ile Tyr Arg Leu Arg Asn Lys Asp Val Lys Gln		
290	295	300
Ala Leu Lys Arg Val Phe Met Arg Asn Leu		
305	310	

<210> 1513

<211> 320

<212> PRT

<213> Unknown (H38g430 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1513

Met Ser Leu Leu Phe Xaa Asp Xaa Asp Met Arg Asn Phe Thr Pro Leu	
1	15
Ser Gly Phe Ile Ile Leu Gly Phe Thr Asp His Pro Glu Leu Gln Cys	
20	30
Leu Leu Phe Val Leu Phe Leu Leu Ile Tyr Met Phe Thr Val Val Gly	
35	45
Asn Leu Gly Met Ile Leu Leu Ile Lys Ile Asp Ser His Leu His Thr	
50	60
Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Leu Val Asp Phe Cys Tyr	
65	80
Ser Ser Val Ile Ala Pro Asn Met Leu Ile Asn Phe Trp Val Glu Asn	
85	95
Pro Val Ile Ser Phe Asn Glu Cys Ala Thr Gln Phe Phe Phe Phe Gly	
100	110
Ser Phe Ala Gly Ile Glu Gly Phe Leu Leu Ala Val Met Ala Tyr Asp	
115	125
Cys Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Thr Val Leu Met Ser	
130	140
Pro His Leu Ser Ala Leu Leu Val Leu Ala Thr Tyr Leu Leu Gly Phe	
145	155
Val Asn Ala Ala Ile His Thr Gly Phe Thr Phe Gln Leu Ser Phe Cys	
165	175

His Ser Asn Ile Ile Asn Tyr Phe Phe Cys Asp Ile Pro Pro Leu Leu
 180 185 190
 Lys Leu Cys Ser Asp Thr His Ile Asn Glu Val Val Ile Phe Ala Phe
 195 200 205
 Ala Ser Phe Asn Glu Leu Ser Cys Leu Leu Leu Ile Leu Val Ser Cys
 210 215 220
 Leu Tyr Ile Leu Ala Ala Ile Leu Lys Ile His Ser Ala Glu Gly Arg
 225 230 235 240
 His Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Ile
 245 250 255
 Phe Phe Gly Thr Ile Leu Phe Met Tyr Leu Leu Arg Pro Ser Ser Ser
 260 265 270
 Tyr Ser Met Asp Gln Asp Lys Val Val Ser Val Phe Tyr Thr Val Val
 275 280 285
 Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val
 290 295 300
 Lys Ala Ser Leu Ser Lys Met Phe Lys Thr Val Ser Tyr Ile Ser Thr
 305 310 315 320

<210> 1514

<211> 299

<212> PRT

<213> Unknown (H38g431 protein)

<220>

<223> Synthetic construct

<400> 1514

Met Gly Leu Pro Gly Ile His Glu Trp Gln His Trp Leu Ser Leu Pro
 1 5 10 15
 Leu Thr Leu Leu Tyr Leu Leu Ala Leu Gly Ala Asn Leu Leu Ile Ile
 20 25 30
 Ile Thr Ile Gln His Glu Thr Val Leu His Glu Pro Met Tyr His Leu
 35 40 45
 Leu Gly Ile Leu Ala Val Val Asp Ile Gly Leu Ala Thr Thr Ile Met
 50 55 60
 Pro Lys Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Ala Ile Ser Leu
 65 70 75 80
 Pro Met Cys Phe Ala Gln Ile Tyr Ala Ile His Cys Phe Phe Cys Ile
 85 90 95
 Glu Ser Gly Ile Phe Leu Cys Met Ala Val Asp Arg Tyr Ile Ala Ile
 100 105 110
 Cys Arg Pro Leu Gln Tyr Pro Ser Ile Val Thr Lys Ala Phe Val Phe
 115 120 125
 Lys Ala Thr Gly Phe Ile Met Leu Arg Asn Gly Leu Leu Thr Ile Pro
 130 135 140
 Val Pro Ile Leu Ala Ala Gln Arg His Tyr Cys Ser Arg Asn Glu Ile
 145 150 155 160
 Glu His Cys Leu Cys Ser Asn Leu Gly Val Ile Ser Leu Ala Cys Asp
 165 170 175
 Asp Ile Thr Val Asn Lys Phe Tyr Gln Leu Met Leu Ala Trp Val Leu
 180 185 190
 Val Gly Ser Asp Met Ala Leu Val Phe Ser Ser Tyr Ala Val Ile Leu
 195 200 205
 His Ser Val Leu Arg Leu Asn Ser Ala Glu Ala Met Ser Lys Ala Leu
 210 215 220
 Ser Thr Cys Ser Ser His Leu Ile Leu Ile Leu Phe His Thr Gly Ile
 225 230 235 240
 Ile Val Leu Ser Val Thr His Leu Ala Glu Lys Lys Ile Pro Leu Ile
 245 250 255
 Pro Val Phe Leu Asn Val Leu His Asn Val Ile Pro Pro Ala Leu Asn

	260		265		270										
Pro	Leu	Ala	Cys	Ala	Leu	Arg	Met	His	Lys	Leu	Arg	Leu	Gly	Phe	Gln
	275				280							285			
Arg	Leu	Leu	Gly	Leu	Gly	Gln	Asp	Val	Ser	Lys					
	290				295										

<210> 1515

<211> 317

<212> PRT

<213> Unknown (H38g432 protein)

<220>

<223> Synthetic construct

<400> 1515

Met	Met	Arg	Leu	Met	Lys	Glu	Val	Arg	Gly	Arg	Asn	Gln	Thr	Glu	Val
1				5					10					15	
Thr	Glu	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Asp	Asn	Pro	Asp	Leu	Gln	Gly
			20					25					30		
Val	Leu	Phe	Ala	Leu	Phe	Leu	Leu	Ile	Tyr	Met	Ala	Asn	Met	Val	Gly
		35				40						45			
Asn	Leu	Gly	Met	Ile	Val	Leu	Ile	Lys	Ile	Asp	Leu	Cys	Leu	His	Thr
	50					55					60				
Pro	Met	Tyr	Phe	Phe	Leu	Ser	Ser	Leu	Ser	Phe	Val	Asp	Ala	Ser	Tyr
65					70					75				80	
Ser	Ser	Ser	Val	Thr	Pro	Lys	Met	Leu	Val	Asn	Leu	Met	Ala	Glu	Asn
				85					90					95	
Lys	Ala	Ile	Ser	Phe	His	Gly	Cys	Ala	Ala	Gln	Phe	Tyr	Phe	Phe	Gly
			100					105					110		
Ser	Phe	Leu	Gly	Thr	Glu	Cys	Phe	Leu	Leu	Ala	Met	Met	Ala	Tyr	Asp
	115					120						125			
Arg	Tyr	Ala	Ala	Ile	Trp	Asn	Pro	Leu	Leu	Tyr	Pro	Val	Leu	Val	Ser
	130					135					140				
Gly	Arg	Ile	Cys	Phe	Leu	Leu	Ile	Ala	Thr	Ser	Phe	Leu	Ala	Gly	Cys
145					150					155				160	
Gly	Asn	Ala	Ala	Ile	His	Thr	Gly	Met	Thr	Phe	Arg	Leu	Ser	Phe	Cys
			165					170						175	
Gly	Ser	Asn	Arg	Ile	Asn	His	Phe	Tyr	Cys	Asp	Thr	Pro	Pro	Leu	Leu
		180						185					190		
Lys	Leu	Ser	Cys	Ser	Asp	Thr	His	Phe	Asn	Gly	Ile	Val	Ile	Met	Ala
	195					200						205			
Phe	Ser	Ser	Phe	Ile	Val	Ile	Ser	Cys	Val	Met	Ile	Val	Leu	Ile	Ser
	210					215						220			
Tyr	Leu	Cys	Ile	Phe	Ile	Ala	Val	Leu	Lys	Met	Pro	Ser	Leu	Glu	Gly
225					230					235				240	
Arg	His	Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser	Tyr	Leu	Met	Ala	Val	Thr
			245					250						255	
Ile	Phe	Phe	Gly	Thr	Ile	Leu	Phe	Met	Tyr	Leu	Arg	Pro	Thr	Ser	Ser
		260						265					270		
Tyr	Ser	Met	Glu	Gln	Asp	Lys	Val	Val	Ser	Val	Phe	Tyr	Thr	Val	Ile
	275					280						285			
Ile	Pro	Val	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Lys	Asn	Lys	Asp	Val
	290					295					300				
Lys	Lys	Ala	Leu	Lys	Lys	Ile	Leu	Trp	Lys	His	Ile	Leu			
305					310						315				

<210> 1516

<211> 317

<212> PRT

<213> Unknown (H38g433 protein)

<220>

<223> Synthetic construct

<400> 1516

```

Met Ser His Thr Asn Val Thr Ile Phe His Pro Ala Val Phe Val Leu
 1           5           10           15
Pro Gly Ile Pro Gly Leu Glu Ala Tyr His Ile Trp Leu Ser Ile Pro
      20           25           30
Leu Cys Leu Ile Tyr Ile Thr Ala Val Leu Gly Asn Ser Ile Leu Ile
      35           40           45
Val Val Ile Val Met Glu Arg Asn Leu His Val Pro Met Tyr Phe Phe
      50           55           60
Leu Ser Met Leu Ala Val Met Asp Ile Leu Leu Ser Thr Thr Thr Val
      65           70           75           80
Pro Lys Ala Leu Ala Ile Phe Trp Leu Gln Ala His Asn Ile Ala Phe
      85           90           95
Asp Ala Cys Val Thr Gln Gly Phe Phe Val His Met Met Phe Val Gly
      100          105          110
Glu Ser Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile
      115          120          125
Cys Ala Pro Leu Arg Tyr Thr Thr Val Leu Thr Trp Pro Val Val Gly
      130          135          140
Arg Ile Ala Leu Ala Val Ile Thr Arg Ser Phe Cys Ile Ile Phe Pro
      145          150          155          160
Val Ile Phe Leu Leu Lys Arg Leu Pro Phe Cys Leu Thr Asn Ile Val
      165          170          175
Pro His Ser Tyr Cys Glu His Ile Gly Val Ala Arg Leu Ala Cys Ala
      180          185          190
Asp Ile Thr Val Asn Ile Trp Tyr Gly Phe Ser Val Pro Ile Val Met
      195          200          205
Val Ile Leu Asp Val Ile Leu Ile Ala Val Ser Tyr Ser Leu Ile Leu
      210          215          220
Arg Ala Val Phe Arg Leu Pro Ser Gln Asp Ala Arg His Lys Ala Leu
      225          230          235          240
Ser Thr Cys Gly Ser His Leu Cys Val Ile Leu Met Phe Tyr Val Pro
      245          250          255
Ser Phe Phe Thr Leu Leu Thr His His Phe Gly Arg Asn Ile Pro Gln
      260          265          270
His Val His Ile Leu Leu Ala Asn Leu Tyr Val Ala Val Pro Pro Met
      275          280          285
Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gly
      290          295          300
Val Ala His Arg Phe Phe Asp Ile Lys Thr Trp Cys Cys
      305          310          315

```

<210> 1517

<211> 305

<212> PRT

<213> Unknown (H38g434 protein)

<220>

<223> Synthetic construct

<400> 1517

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1           5           10           15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
      20           25           30
Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile
      35           40           45
Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Val Ala Gly Asn

```

50 55 60
 Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
 65 70 75 80
 Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
 85 90 95
 Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Tyr
 100 105 110
 Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro
 115 120 125
 Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val
 130 135 140
 Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys
 145 150 155 160
 Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe
 165 170 175
 Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly
 180 185 190
 Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys
 195 200 205
 Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val
 210 215 220
 Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr
 245 250 255
 Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile
 260 265 270
 Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu
 290 295 300
 Pro
 305

<210> 1518

<211> 314

<212> PRT

<213> Unknown (H38g435 protein)

<220>

<223> Synthetic construct

<400> 1518

Met Leu Pro Ser Asn Ile Thr Ser Thr His Pro Ala Val Phe Leu Leu
 1 5 10 15
 Val Gly Ile Pro Gly Leu Glu His Leu His Ala Trp Ile Ser Ile Pro
 20 25 30
 Phe Cys Phe Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu
 35 40 45
 Phe Ile Ile Arg Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe
 50 55 60
 Leu Ala Met Leu Ala Thr Ile Asp Leu Val Leu Ser Ser Thr Thr Leu
 65 70 75 80
 Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Gln Glu Ile Asn Phe
 85 90 95
 Phe Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met
 100 105 110
 Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr
 130 135 140

Lys Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Arg Arg Phe His Tyr Cys Arg Gly Pro Val Ile
 165 170 175
 Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly
 180 185 190
 Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ser
 195 200 205
 Val Val Leu Asp Leu Leu Phe Val Ile Leu Ser Tyr Val Phe Ile Leu
 210 215 220
 Gln Ala Val Leu Gln Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe
 225 230 235 240
 Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ser Thr Tyr Thr Pro
 245 250 255
 Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro
 260 265 270
 Arg Val His Ile Leu Leu Ala Ile Phe Tyr Leu Leu Phe Pro Pro Met
 275 280 285
 Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Tyr
 290 295 300
 Val Leu Ser Leu Phe Gln Arg Lys Asn Met
 305 310

<210> 1519

<211> 312

<212> PRT

<213> Unknown (H38g436 protein)

<220>

<223> Synthetic construct

<400> 1519

Met Leu Lys Lys Asn His Thr Ala Val Thr Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Arg Ala Glu Leu Gln Ser Leu Leu Phe Val Val Phe Leu
 20 25 30
 Val Ile Tyr Leu Ile Thr Val Ile Gly Asn Val Ser Met Ile Leu Leu
 35 40 45
 Ile Arg Ser Asp Ser Thr Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 His Leu Ser Phe Val Asp Leu Cys Tyr Thr Thr Asn Val Thr Pro Gln
 65 70 75 80
 Met Leu Val Asn Phe Leu Ser Lys Arg Lys Thr Ile Ser Phe Ile Gly
 85 90 95
 Cys Phe Ile Gln Phe His Phe Phe Ile Ala Leu Val Ile Thr Asp Tyr
 100 105 110
 Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Met Ala Ile Cys Lys
 115 120 125
 Pro Leu Leu Tyr Gly Ser Lys Met Thr Arg Cys Val Cys Leu Cys Leu
 130 135 140
 Ala Ala Ala Pro Tyr Ile Tyr Gly Phe Ala Asn Gly Leu Ser Gln Thr
 145 150 155 160
 Thr Leu Met Leu Arg Leu Ser Phe Cys Gly Pro Asn Asp Ile Asn His
 165 170 175
 Phe Tyr Cys Ala Asp Pro Pro Leu Leu Val Leu Ala Cys Ser Asp Thr
 180 185 190
 Tyr Val Lys Glu Thr Ala Met Leu Val Val Ala Gly Ser Asn Leu Ile
 195 200 205
 Cys Ser Leu Thr Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Thr Ala
 210 215 220
 Ile Leu Arg Ile His Thr Ala Glu Gly Arg Arg Lys Ala Phe Ser Thr

225					230					235				240	
Cys	Gly	Ser	His	Val	Thr	Ala	Val	Thr	Val	Phe	Tyr	Gly	Thr	Leu	Phe
				245					250					255	
Cys	Met	Tyr	Leu	Arg	Pro	Pro	Ser	Glu	Thr	Ser	Ile	Gln	Gln	Gly	Lys
			260					265					270		
Ile	Val	Ala	Val	Phe	Tyr	Ile	Phe	Val	Ser	Pro	Met	Leu	Asn	Pro	Leu
		275					280					285			
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Arg	Ser	Ile	Arg	Lys	Val
	290					295					300				
Ile	Gln	Lys	Lys	Leu	Phe	Ala	Lys								
305					310										

<210> 1520

<211> 314

<212> PRT

<213> Unknown (H38g437 protein)

<220>

<223> Synthetic construct

<400> 1520

Met	Ser	Ala	Ser	Asn	Ile	Thr	Leu	Thr	His	Pro	Thr	Ala	Phe	Leu	Leu
1				5					10					15	
Val	Gly	Ile	Pro	Gly	Leu	Glu	His	Leu	His	Ile	Trp	Ile	Ser	Ile	Pro
			20					25				30			
Phe	Cys	Leu	Ala	Tyr	Thr	Leu	Ala	Leu	Leu	Gly	Asn	Cys	Thr	Leu	Leu
	35					40					45				
Leu	Ile	Ile	Gln	Ala	Asp	Ala	Ala	Leu	His	Glu	Pro	Met	Tyr	Leu	Phe
	50				55					60					
Leu	Ala	Met	Leu	Ala	Ala	Ile	Asp	Leu	Val	Leu	Ser	Ser	Ser	Ala	Leu
65				70					75					80	
Pro	Lys	Met	Leu	Ala	Ile	Phe	Trp	Phe	Arg	Asp	Arg	Glu	Ile	Asn	Phe
			85					90						95	
Phe	Ala	Cys	Leu	Ala	Gln	Met	Phe	Phe	Leu	His	Ser	Phe	Ser	Ile	Met
	100						105					110			
Glu	Ser	Ala	Val	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile
	115					120						125			
Cys	Lys	Pro	Leu	His	Tyr	Thr	Lys	Val	Leu	Thr	Gly	Ser	Leu	Ile	Thr
	130					135					140				
Lys	Ile	Gly	Met	Ala	Ala	Val	Ala	Arg	Ala	Val	Thr	Leu	Met	Thr	Pro
145				150					155					160	
Leu	Pro	Phe	Leu	Leu	Arg	Cys	Phe	His	Tyr	Cys	Arg	Gly	Pro	Val	Ile
			165					170					175		
Ala	His	Cys	Tyr	Cys	Glu	His	Met	Ala	Val	Val	Arg	Leu	Ala	Cys	Gly
	180						185					190			
Asp	Thr	Ser	Phe	Asn	Asn	Ile	Tyr	Gly	Ile	Ala	Val	Ala	Met	Phe	Ile
	195					200					205				
Val	Val	Leu	Asp	Leu	Leu	Leu	Val	Ile	Leu	Ser	Tyr	Ile	Phe	Ile	Leu
	210					215					220				
Gln	Ala	Val	Leu	Leu	Leu	Ala	Ser	Gln	Glu	Ala	Arg	Tyr	Lys	Ala	Phe
225				230					235					240	
Gly	Thr	Cys	Val	Ser	His	Ile	Gly	Ala	Ile	Leu	Ala	Phe	Tyr	Thr	Thr
			245					250					255		
Val	Val	Ile	Ser	Ser	Val	Met	His	Arg	Val	Ala	Arg	His	Ala	Ala	Pro
	260						265					270			
His	Val	His	Ile	Leu	Leu	Ala	Asn	Phe	Tyr	Leu	Leu	Phe	Pro	Pro	Met
	275					280						285			
Val	Asn	Pro	Ile	Ile	Tyr	Gly	Val	Lys	Thr	Lys	Gln	Ile	Arg	Glu	Ser
	290					295					300				
Ile	Leu	Gly	Val	Phe	Pro	Arg	Lys	Asp	Met						
305					310										

<210> 1521
 <211> 313
 <212> PRT
 <213> Unknown (H38g438 protein)

<220>
 <223> Synthetic construct

<400> 1521
 Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu
 1 5 10 15
 Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
 20 25 30
 Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu
 35 40 45
 Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Ile Tyr Leu Phe Leu
 50 55 60
 Ala Met Leu Ala Ala Ile Asp Leu Val Leu Ser Ser Ser Ala Leu Pro
 65 70 75 80
 Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Arg Glu Ile Asn Phe Phe
 85 90 95
 Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met Glu
 100 105 110
 Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr Lys
 130 135 140
 Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro Leu
 145 150 155 160
 Pro Phe Leu Leu Arg Cys Phe His Tyr Cys Arg Gly Pro Val Ile Ala
 165 170 175
 Arg Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly Asn
 180 185 190
 Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile Gly
 195 200 205
 Val Leu Asp Leu Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln
 210 215 220
 Ala Val Leu Gln Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly
 225 230 235 240
 Thr Cys Val Ser His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser
 245 250 255
 Val Ile Ser Ser Val Met His Arg Val Ala Arg Cys Ala Ala Pro His
 260 265 270
 Val His Ile Leu Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val
 275 280 285
 Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val
 290 295 300
 Leu Gly Val Phe Pro Arg Lys Asp Val
 305 310

<210> 1522
 <211> 318
 <212> PRT
 <213> Unknown (H38g439 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1522

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Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
 1          5          10          15
Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
 20          25          30
Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
 35          40          45
Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe
 50          55          60
Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val
 65          70          75          80
Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu
 85          90          95
Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu
 100          105          110
Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
 115          120          125
Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr
 130          135          140
Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro
 145          150          155          160
Asp Val Phe Leu Val Lys Arg Leu Pro Phe Cys His Ser Asn Leu Leu
 165          170          175
Pro His Thr Tyr Cys Glu His Met Ala Val Ala Lys Phe Ala Cys Ala
 180          185          190
Asp Ile His Val Asn Val Trp Tyr Gly Leu Ser Val Leu Leu Tyr Thr
 195          200          205
Val Val Leu Asp Ala Leu Leu Ile Leu Val Ser Xaa Ser Phe Ile Leu
 210          215          220
Tyr Thr Gly Phe His Leu Pro Ser Pro Gly Ala Arg Gln Lys Ala Leu
 225          230          235          240
Gly Thr Cys Gly Ser His Leu Arg Val Ile Ser Met Phe Tyr Leu Pro
 245          250          255
Gly Ile Phe Thr Ile Ile Thr Gln Arg Phe Gly His His Val Pro Leu
 260          265          270
His Thr His Ile Leu Leu Gly Asn Val Trp Val Leu Ala Pro Pro Met
 275          280          285
Leu Asn Pro Ile Ile Tyr Gly Ile Asn Thr Arg Gln Ile Gln Glu Cys
 290          295          300
Val Leu Ser Leu Leu Ser Ser Gln Arg Lys Xaa Cys Xaa Ile
 305          310          315

```

<210> 1523

<211> 313

<212> PRT

<213> Unknown (H38g440 protein)

<220>

<223> Synthetic construct

<400> 1523

```

Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly
 1          5          10          15
Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
 20          25          30
Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
 35          40          45
Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50          55          60

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Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
65          70          75          80
Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
      85          90          95
Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
      100        105        110
Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
      115        120        125
Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
      130        135        140
Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
145          150          155          160
Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
      165        170        175
Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
      180        185        190
Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
      195        200        205
Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
      210        215        220
Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
225          230          235          240
Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
      245        250        255
Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
      260        265        270
Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
      275        280        285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu
      290        295        300
Val Ala Arg Val Phe Leu Ile Lys Lys
305          310

```

<210> 1524

<211> 333

<212> PRT

<213> Unknown (H38g441 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1524

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Met Glu Lys Ser Asn Val Ser Ser Val Tyr Gly Phe Ile Leu Val Gly
1          5          10          15
Phe Ser Asp Arg Pro Lys Leu Glu Met Val Leu Phe Thr Val Asn Phe
      20          25          30
Ile Leu Tyr Ser Val Ala Val Leu Gly Asn Ser Thr Ile Ile Leu Val
      35          40          45
Cys Ile Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50          55          60
Asn Leu Ser Phe Leu Asp Leu Cys Phe Ser Thr Ser Cys Ile Pro Gln
65          70          75          80
Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Cys Ala Gly
      85          90          95
Cys Val Val Gln Leu Phe Ser Phe Leu Ser Val Arg Gly Ile Glu Cys
      100        105        110
Ile Leu Leu Ala Val Met Ala Tyr Asp Ser Tyr Ala Ala Val Cys Lys

```

```

      115      120      125
Pro Leu Arg Tyr Leu Val Ile Met His Leu Gln Leu Cys Leu Gly Leu
  130      135      140
Met Ala Ala Ala Trp Gly Ser Gly Leu Val Asn Ala Val Val Met Ser
  145      150      155      160
Pro Leu Thr Met Thr Leu Ser Arg Ser Gly Arg Arg Arg Val Asn His
      165      170      175
Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Met Ala Cys Leu Asp Val
      180      185      190
Arg Ala Val Glu Met Leu Ala Phe Ala Phe Ala Val Leu Ile Val Leu
  195      200      205
Leu Pro Leu Thr Leu Ile Leu Val Ser Tyr Gly Tyr Ile Ala Ala Ala
  210      215      220
Val Leu Ser Ile Lys Ser Ala Ala Arg Gln Trp Lys Ala Phe His Thr
  225      230      235      240
Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Ser Ile Ile
      245      250      255
Tyr Met Tyr Met Gln Pro Gly Asn Ser Ser Ser Gln Asp Gln Gly Lys
      260      265      270
Phe Leu Thr Leu Phe Tyr Asn Leu Val Thr Pro Met Leu Asn Leu Leu
      275      280      285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Lys Val
  290      295      300
Leu Gly Arg Gln Xaa Xaa Thr Gly Glu Ile Xaa Xaa Val Val Lys Ser
  305      310      315      320
Xaa Ala Lys Tyr Leu Phe Gln Tyr Thr Phe Ile Leu Cys
      325      330

```

<210> 1525

<211> 317

<212> PRT

<213> Unknown (H38g442 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1525

```

Gln Val Val His Thr Gly Phe Ser Pro Xaa Leu Tyr Val Phe Thr Leu
  1      5      10      15
Leu Gly Asn Gly Ser Ile Leu Gly Leu Ile Trp Leu Asp Ser Arg Leu
      20      25      30
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Ile Ile Asp Ile
      35      40      45
Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Thr Asn Leu Gly Leu
      50      55      60
Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr Met Gln Thr Phe
  65      70      75      80
Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile Leu Val Met Met
      85      90      95
Ser Tyr Asp Arg Tyr Met Ala Val Cys His Pro Leu Gln Tyr Ser Val
      100      105      110
Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val Thr Ser Trp Ala
      115      120      125
Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu Ile Leu Arg Leu
      130      135      140
Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe Cys Glu Ile Leu
  145      150      155      160

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Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val
 165 170 175
 Ile Phe Ala Ser Ser Val Phe Ile Leu Val Gly Ala Leu Cys Leu Val
 180 185 190
 Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu Arg Asn Gln Ser
 195 200 205
 Gly Glu Gly Arg Arg Lys Gly Phe Ser Thr Cys Tyr Ser His Leu Cys
 210 215 220
 Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met Ala Pro
 225 230 235 240
 Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Ser Leu Phe Tyr
 245 250 255
 Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn
 260 265 270
 Ala Glu Val Lys Gly Ala Leu Arg Ser Ala Leu Arg Lys Glu Arg Leu
 275 280 285
 Thr Xaa Asp Ile Ser Lys Gly Thr Met Gly Arg Glu Pro Cys Ser Leu
 290 295 300
 Gln Asn Ile Glu Val Gly Phe Phe Phe Cys Leu Leu Leu
 305 310 315

<210> 1526

<211> 239

<212> PRT

<213> Unknown (H38g443 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(239)

<223> Xaa = Any Amino Acid

<400> 1526

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val
 1 5 10 15
 Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr
 20 25 30
 Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr
 35 40 45
 Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Met Thr
 50 55 60
 Trp Ser Asp Asn Ser Phe Ile Phe Val Ile Met Tyr Thr Leu Ile Leu
 65 70 75 80
 Lys Phe Pro Ser Met Lys Lys Lys Asn Leu Gln Asp Asn Ser Leu His
 85 90 95
 Val Leu Leu Ala Met Leu Lys Thr Val Phe Leu Asp Ala Thr Ile Glu
 100 105 110
 Glu Met Ser Val Phe Val Leu Asn Asn Val Asn Val Leu Ile Cys Leu
 115 120 125
 Ile Ser Asn Phe Thr Cys Tyr Gly Tyr Ile Ala Gly Ala Leu Arg Met
 130 135 140
 Asn Thr Ser Asn Xaa Ile Arg Ser Lys Leu Arg Asn Gln Tyr His His
 145 150 155 160
 His His His Arg Cys His Phe Ile Ile Asp Ser Ile Phe Tyr Gly Ile
 165 170 175
 Ile Val Xaa Met Leu Leu Gln Asp Gly Asn Asn Ser Ser Gln Asp Gln
 180 185 190
 Glu Arg Phe Phe Ile Leu Phe Tyr Thr Ile Leu Thr Pro Ser Leu Lys
 195 200 205
 Leu Leu Val Tyr Leu Leu Arg Asn Lys Asp Ile Lys Asp Ile Ser Arg

<400> 1528
Leu Ser Xaa Pro Thr Arg Ala Ala Gln Lys Gln Phe Ile Leu Leu Gly
1 5 10 15

Phe Ser Gly Arg Pro Arg Leu Glu His Val Leu Phe Val Phe Val Leu
 20 25 30
 Ile Phe Tyr Leu Val Thr Leu Val Gly Asn Ile Ile Ile Ile Leu Ile
 35 40 45
 Ser His Leu Asp Pro Cys Leu His Met Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ser Ile Pro Gln
 65 70 75 80
 Leu Leu Phe Asn Leu Gly Ser Pro Gly Lys Thr Ile Ser His Thr Gly
 85 90 95
 Cys Ala Ile Gln Leu Phe Met Phe Leu Gly Leu Gly Gly Thr Glu Cys
 100 105 110
 Ile Leu Leu Ala Ala Val Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Ser Val Ile Met His Pro Gln Leu Cys Trp Lys Leu
 130 135 140
 Val Ser Val Ala Arg Gly Cys Trp Thr Pro Gln Phe Ser Ser Tyr Val
 145 150 155 160
 Ser Trp Thr Met Lys Leu Pro Arg Cys Gly Arg Cys Lys Leu Lys His
 165 170 175
 Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Ile Thr Cys Val Asp Thr
 180 185 190
 Val Ala Met Glu Ser Thr Val Phe Thr Leu Ser Val Val Ile Val Leu
 195 200 205
 Met Pro Leu Cys Leu Ile Leu Ile Ser Tyr Ser Tyr Ile Ala Leu Ala
 210 215 220
 Val Leu Arg Ile Lys Ser Ala Ala Gly Arg Arg Lys Ala Phe Asn Met
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile
 245 250 255
 Tyr Met Tyr Met Gln Pro Xaa Asn Asn Ser Ser Gln Asp Gln Gly Lys
 260 265 270
 Phe Leu Thr Leu Phe Tyr Asn Leu Met Thr Pro Met Leu Asn Pro Val
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Arg Leu
 290 295 300
 Val Ser Arg Lys His Ser Asp Ser Asp Cys Ser Xaa Asp Cys Phe Phe
 305 310 315 320

<210> 1529

<211> 126

<212> PRT

<213> Unknown (H38g446 protein)

<220>

<223> Synthetic construct

<400> 1529

Met Glu Asn Tyr Asn Gln Thr Ser Thr Ala Phe Ile Leu Leu Gly Leu
 1 5 10 15
 Ser Pro Pro Pro Lys Ile Gly His Phe Ile Phe Ile Leu Ile Asn Phe
 20 25 30
 Val Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile
 35 40 45
 Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
 50 55 60
 Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met
 65 70 75 80
 Val Tyr Asp Phe Ser Cys His Gly Asn Lys Ser Ile Ser Phe Thr Gly
 85 90 95
 Cys Gly Ile Gln Ser Phe Phe Phe Leu Thr Leu Ala Gly Ala Glu Ala

		100						105				110	
Leu	Leu	Leu	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile
		115					120					125	

<210> 1530

<211> 326

<212> PRT

<213> Unknown (H38g447 protein)

<220>

<223> Synthetic construct

<400> 1530

Met	Glu	Arg	Ala	Asn	Asp	Ser	Thr	Phe	Ser	Gly	Phe	Ile	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Asn	Arg	Pro	Gln	Leu	Glu	Thr	Ala	Leu	Phe	Val	Val	Ile	Leu
		20						25					30		
Ile	Ile	Tyr	Phe	Leu	Ser	Phe	Leu	Gly	Asn	Gly	Thr	Ile	Ile	Leu	Leu
		35					40					45			
Ser	Ile	Val	Asp	Pro	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
		50				55					60				
Asn	Leu	Ser	Phe	Met	Asp	Leu	Cys	Leu	Thr	Thr	Cys	Thr	Val	Pro	Gln
65				70					75					80	
Thr	Leu	Val	Asn	Phe	Lys	Gly	Lys	Asp	Lys	Thr	Ile	Thr	Tyr	Gly	Gly
			85						90					95	
Cys	Val	Thr	Gln	Leu	Phe	Ile	Ala	Leu	Gly	Leu	Gly	Gly	Ser	Glu	Cys
			100					105					110		
Val	Leu	Leu	Ser	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Ala	Ala	Val	Cys	Arg
		115					120					125			
Pro	Leu	His	Tyr	Met	Val	Ser	Met	His	Pro	Gln	Leu	Cys	Leu	Gln	Leu
		130				135					140				
Val	Val	Thr	Thr	Trp	Leu	Thr	Gly	Phe	Gly	Asn	Ser	Val	Ile	Gln	Thr
145				150					155					160	
Ala	Leu	Thr	Met	Thr	Leu	Pro	Leu	Cys	Asp	Lys	Asn	Gln	Val	Asp	His
			165						170					175	
Phe	Phe	Cys	Glu	Val	Pro	Val	Met	Leu	Lys	Leu	Ser	Cys	Thr	Asn	Thr
		180					185						190		
Ser	Ile	Asn	Glu	Ala	Glu	Ile	Phe	Ala	Val	Ser	Val	Phe	Phe	Leu	Val
		195				200					205				
Val	Pro	Leu	Ser	Leu	Ile	Leu	Ala	Ser	Tyr	Gly	His	Ile	Thr	His	Ala
		210			215						220				
Val	Leu	Lys	Ile	Lys	Ser	Ala	Gln	Gly	Arg	Gln	Lys	Ala	Phe	Gly	Thr
225				230					235					240	
Cys	Gly	Ser	His	Leu	Leu	Val	Val	Ile	Ile	Phe	Phe	Gly	Thr	Leu	Ile
			245					250						255	
Ser	Met	Tyr	Leu	Gln	Pro	Pro	Ser	Ser	Tyr	Ser	Gln	Asp	Val	Asn	Lys
		260					265						270		
Ser	Ile	Ala	Leu	Phe	Tyr	Thr	Leu	Val	Thr	Pro	Leu	Leu	Asn	Pro	Leu
		275				280						285			
Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Lys	Gly	Ala	Thr	Lys	Lys	Thr
		290			295						300				
Ser	Gly	Glu	Asp	His	Arg	Cys	Met	Arg	Lys	Leu	Thr	Gln	Gly	Leu	Gln
305				310					315					320	
Phe	Gln	Thr	Phe	Val	His										
				325											

<210> 1531

<211> 312

<212> PRT

<213> Unknown (H38g448 protein)

<220>

<223> Synthetic construct

<400> 1531

```

Met Glu Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu Leu Gly Leu
 1          5          10          15
Phe Pro Pro Ser Ile Ile Asp Leu Phe Phe Phe Ile Leu Ile Val Phe
 20          25          30
Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile
 35          40          45
Phe Leu Asp Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
 50          55          60
Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met
 65          70          75          80
Ala Ser Asp Phe Leu His Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys
 85          90          95
Gly Ile Gln Ser Phe Phe Phe Leu Ala Leu Gly Gly Ala Glu Ala Leu
100          105          110
Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro
115          120          125
Leu His Tyr Leu Ile Arg Met Ser Lys Arg Val Cys Val Leu Met Ile
130          135          140
Thr Gly Ser Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val
145          150          155          160
Tyr Val Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asn His Phe
165          170          175
Phe Cys Asp Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp
180          185          190
Val Tyr Glu Gly Thr Val Phe Leu Ser Ala Thr Ile Phe Leu Val Phe
195          200          205
Pro Phe Ile Gly Ile Ser Cys Ser Tyr Gly Gln Val Leu Phe Ala Val
210          215          220
Tyr His Met Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu Thr Cys
225          230          235          240
Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr
245          250          255
Thr Tyr Leu Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Val
260          265          270
Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile
275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Met Gly Ala Leu Thr Arg Val Ser
290          295          300
Gln Arg Ile Cys Ser Val Lys Met
305          310

```

<210> 1532

<211> 312

<212> PRT

<213> Unknown (H38g449 protein)

<220>

<223> Synthetic construct

<400> 1532

```

Met Pro Asn Ser Thr Thr Val Met Glu Phe Leu Leu Met Arg Phe Ser
 1          5          10          15
Asp Val Trp Thr Leu Gln Ile Leu His Ser Ala Ser Phe Phe Met Leu
 20          25          30
Tyr Leu Val Thr Leu Met Gly Asn Ile Leu Ile Val Thr Val Thr Thr
 35          40          45
Cys Asp Ser Ser Leu His Met Pro Met Tyr Phe Phe Leu Arg Asn Leu

```


50	55	60
Ser Ile Leu Asp Ala Cys Tyr Ile Ser Val Thr Val Pro Thr Ser Cys		
65	70	75
Val Asn Ser Leu Leu Asp Ser Thr Thr Ile Ser Lys Ala Gly Cys Val		80
	85	90
Ala Gln Val Phe Leu Val Val Phe Phe Val Tyr Val Glu Leu Leu Phe		95
	100	105
Leu Thr Ile Met Ala His Asp Arg Tyr Val Ala Val Cys Gln Pro Leu		110
	115	120
His Tyr Pro Val Ile Val Asn Ser Arg Ile Cys Ile Gln Met Thr Leu		125
	130	135
Ala Ser Leu Leu Ser Gly Leu Val Tyr Ala Gly Met His Thr Gly Ser		140
145	150	155
Thr Phe Gln Leu Pro Phe Cys Arg Ser Asn Val Ile His Gln Phe Phe		160
	165	170
Cys Asp Ile Pro Ser Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Ser		175
	180	185
Asn Glu Val Met Ile Val Val Ser Ala Leu Gly Val Gly Gly Gly Cys		190
	195	200
Phe Ile Phe Ile Ile Arg Ser Tyr Ile His Ile Phe Ser Thr Val Leu		205
	210	215
Gly Phe Pro Arg Gly Ala Asp Arg Thr Lys Ala Phe Ser Thr Cys Ile		220
225	230	235
Pro His Ile Leu Val Ser Val Phe Leu Ser Ser Cys Ser Ser Val		240
	245	250
Tyr Leu Arg Pro Pro Ala Ile Pro Ala Ala Thr Gln Asp Leu Ile Leu		255
	260	265
Ser Gly Phe Tyr Ser Ile Met Pro Pro Leu Phe Asn Pro Ile Ile Tyr		270
	275	280
Ser Leu Arg Asn Lys Gln Ile Lys Val Ala Ile Lys Lys Ile Met Lys		285
	290	295
Arg Ile Phe Tyr Ser Glu Asn Val		300
305	310	

<210> 1533

<211> 311

<212> PRT

<213> Unknown (H38g450 protein)

<220>

<223> Synthetic construct

<400> 1533

Arg Asn Ala Pro Leu Glu Lys Tyr Asn Gln Thr Ser Thr Asp Phe Ile		
1	5	10
Leu Leu Gly Ile Phe Pro Pro Ser Arg Ile Gly Phe Leu Leu Phe Ile		15
	20	25
Leu Leu Val Leu Ile Leu Leu Leu Ala Leu Ile Gly Asn Gln Ser Val		30
	35	40
Ile Leu Leu Ile Phe Leu Asp Thr His Leu His Thr Pro Ile Tyr Phe		45
	50	55
Leu Leu Ser Arg Leu Tyr Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile		60
65	70	75
Val Pro Lys Met Phe Ser Asp Phe Leu Phe Gly Asn Lys Ser Ile Ser		80
	85	90
Phe Ile Gly Cys Gly Ile Gln Ser Phe Phe Phe Val Thr Leu Ala Gly		95
	100	105
Ala Glu Met Leu Pro Leu Thr Ser Met Ala Cys Asp His Tyr Val Ala		110
	115	120
Val Cys Phe Pro Leu His Tyr Pro Ile His Met Ser Lys Ile Val Cys		125
	130	135
		140

```

Leu Met Ile Ile Gly Ser Trp Ile Met Gly Ser Ile Asp Thr Cys Ala
145          150          155          160
His Ile Ser Tyr Met Pro His Ile Pro Val Cys Ser Ala Arg Ala Cys
          165          170          175
Asp Val Pro Ala Met Val Thr Leu Ala Phe Val Asp Thr Trp Val Tyr
          180          185          190
Glu Cys Thr Val Phe Leu Ser Thr Thr Leu Phe Leu Met Phe Thr Phe
          195          200          205
Ile Gly Ile Ala Cys Ser Tyr Gly Glu Val Leu Leu Thr Val Tyr His
          210          215          220
Ile Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys Ser Thr
225          230          235          240
His Leu Thr Val Val Ile Ile Tyr Tyr Ala Met Phe Ala Tyr Thr Tyr
          245          250          255
Leu Tyr Pro Arg Tyr Leu Gln Ser Pro Thr Glu Asp Lys Val Leu Ala
          260          265          270
Val Phe Tyr Thr Ile Leu Thr Ser Met Leu Asn Pro Ile Ile Tyr Ser
          275          280          285
Leu Arg Asn Arg Glu Val Met Gly Ala Leu Thr Arg Val Ser Gln Arg
          290          295          300
Ile Phe Pro Val Lys Met Lys
305          310

```

<210> 1534

<211> 192

<212> PRT

<213> Unknown (H38g451 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(192)

<223> Xaa = Any Amino Acid

<400> 1534

```

Arg His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu
1          5          10          15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu
          20          25          30
Ser Leu Ser Leu Ser Leu Ser Leu Tyr Leu Val Met Val Leu Arg Asn
          35          40          45
Leu Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro
          50          55          60
Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr
65          70          75          80
Ser Ala Thr Val Pro Lys Val Thr Val Asp Met Gln Ser His Ser Arg
          85          90          95
Val Ile Ser His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu
          100          105          110
Phe Ala Cys Ile Glu Cys Met Leu Leu Thr Val Met Ala Tyr Asp Gly
          115          120          125
Phe Val Ala Ile Cys Leu Pro Leu His Tyr Pro Val Ile Met Asn Pro
          130          135          140
His Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu
145          150          155          160
Asp Ser Gln Leu His Gly Trp Ile Val Xaa Gln Phe Thr Ile Met Lys
          165          170          175
Asn Val Glu Ile Ser His Phe Val Ser Asp Pro Ser Gln Leu Leu Asn
          180          185          190

```

<210> 1535
 <211> 317
 <212> PRT
 <213> Unknown (H38g452 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(317)
 <223> Xaa = Any Amino Acid

<400> 1535
 Met Asp Arg Arg Asn Gln Thr Cys Ile Tyr Glu Phe Leu Leu Met Gly
 1 5 10 15
 Phe Ser Glu His Gln Glu Gln Ala Leu Leu Phe Gly Leu Phe Leu
 20 25 30
 Val Met Tyr Leu Val Thr Val Leu Glu Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile Gly Ser Asp Leu His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Gly Phe Ile Ser Thr Ile Ile Pro Lys
 65 70 75 80
 Met Leu Asp His Ile Ser Ser Gly Ile Lys Leu Ile Ser Tyr Gly Glu
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Ser Gly Leu Phe Ala Asp Leu Asp Asn
 100 105 110
 Asn Phe Leu Leu Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile Ser
 115 120 125
 His Pro Leu His Tyr Ala Leu Thr Met Asn Ser Gln Arg Cys Val Leu
 130 135 140
 Leu Val Ala Val Ser Trp Val Ile Thr Ile Leu His Ala Leu Val His
 145 150 155 160
 Thr Leu Leu Val Thr Arg Leu Ser Phe Cys Gly Pro Asn Ile Ile Pro
 165 170 175
 His Phe Phe Cys Asp Leu Val Pro Leu Leu Lys Leu Ala Cys Ser Ser
 180 185 190
 Thr Cys Val Asn Asp Leu Val Leu Ile Leu Val Ala Gly Thr Leu Leu
 195 200 205
 Ile Ala Pro Phe Val Cys Ile Leu Met Ser Tyr Phe Tyr Ile Ala Leu
 210 215 220
 Ala Ile Leu Arg Ile Asp Ser Pro Arg Gly Lys Gln Arg Ala Phe Ser
 225 230 235 240
 Ser Cys Thr Ser His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Ala
 245 250 255
 Ile Gly Val Tyr Leu Cys Pro Pro Ser Ser His Ser Asp Gly Lys Asp
 260 265 270
 Arg Val Phe Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Gly Lys
 290 295 300
 Leu Leu Gly Ile Lys Thr Ser Xaa His Pro Tyr Ser Arg
 305 310 315

<210> 1536
 <211> 252
 <212> PRT
 <213> Unknown (H38g453 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(252)

<223> Xaa = Any Amino Acid

<400> 1536

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His Leu Xaa Trp Cys Val Phe Arg Tyr Leu Gly Ile Val Val Glu Ile
 1           5           10           15
His Ile Val Phe Xaa Thr Phe Arg Cys Arg Ser Leu Val Ala Gly Tyr
          20           25           30
Val Leu Xaa Thr Phe Val Ala Ile His Leu Arg Arg Asn Ala Ala Phe
          35           40           45
Ser Ile Glu Phe Leu Cys Tyr Lys Xaa Arg Met Gln Asp Ile Asn Xaa
 50           55           60
Thr Lys Xaa Gly Lys Ile Leu Tyr Ser Leu Arg Glu Phe Lys Arg Leu
65           70           75           80
Leu Ala Thr Ser Leu Tyr Ser Ala Xaa Val Asn Arg Phe Leu Leu Asn
          85           90           95
Lys Leu Leu Pro Gly Leu Val Ser Lys Gln Ile Glu Thr Tyr Phe Arg
          100          105          110
Lys Glu Ile Tyr Ile Leu Ile Ser Thr Ile Arg Phe Ser Tyr Val Glu
          115          120          125
Thr Leu Glu Gly Glu Xaa Gly Val Asn Val Ser Ser Ile Ile Phe Leu
          130          135          140
Leu Ile Pro Phe Ser Met Ile Ser Ala Ser Ser Val Gln Ile Leu Xaa
          145          150          155          160
Gly Val Leu Xaa Met Lys Leu Ser Gln Ala Trp Lys Arg Ser Phe Ser
          165          170          175
Thr Trp Ser Ile Leu Met Ile Ala Val Val Thr Tyr Trp Asp Ser Phe
          180          185          190
Ile Phe Thr Tyr Val Tyr Glu Thr Xaa Ile Ile His Ile Ser Gly Gln
          195          200          205
Val Lys Phe Leu Glu Ile Phe Tyr Ala Phe Leu Ala Leu Thr Leu Asn
          210          215          220
Pro Val Val Tyr Ser Val Gly Thr Asp Ser Val Leu Val Ala Met Lys
          225          230          235          240
Asn Met Leu Xaa Ser Asn Ile Leu His Lys Lys Lys
          245          250

```

<210> 1537

<211> 313

<212> PRT

<213> Unknown (H38g454 protein)

<220>

<223> Synthetic construct

<400> 1537

```

Met Asp Gln Ile Asn His Thr Asn Val Lys Glu Phe Phe Phe Leu Glu
 1           5           10           15
Leu Thr Arg Ser Arg Glu Leu Glu Phe Phe Leu Phe Val Val Phe Phe
          20           25           30
Ala Val Tyr Val Ala Thr Val Leu Gly Asn Ala Leu Ile Val Val Thr
          35           40           45
Ile Thr Cys Glu Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50           55           60
Asn Lys Ser Val Leu Asp Ile Val Phe Ser Ser Ile Thr Val Pro Lys
65           70           75           80
Phe Leu Val Asp Leu Leu Ser Asp Arg Lys Thr Ile Ser Tyr Asn Asp
          85           90           95
Cys Met Ala Gln Ile Phe Phe Phe His Phe Ala Gly Gly Ala Asp Ile

```

```

      100      105      110
Phe Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Ala Lys
      115      120      125
Pro Leu His Tyr Val Thr Met M t Arg Lys Glu Val Trp Val Ala Leu
      130      135      140
Val Val Ala Ser Trp Val Ser Gly Gly Leu His Ser Ile Ile Gln Val
      145      150      155      160
Ile Leu Met Leu Pro Phe Pro Phe Cys Gly Pro Asn Thr Leu Asp Ala
      165      170      175
Phe Tyr Cys Tyr Val Leu Gln Val Val Lys Leu Ala Cys Thr Asp Thr
      180      185      190
Phe Ala Leu Glu Leu Phe Met Ile Ser Asn Asn Gly Leu Val Thr Leu
      195      200      205
Leu Trp Phe Leu Leu Leu Leu Gly Ser Tyr Thr Val Ile Leu Val Met
      210      215      220
Leu Arg Ser His Ser Gly Glu Gly Arg Asn Lys Ala Leu Ser Thr Cys
      225      230      235      240
Thr Ser His Met Leu Val Val Thr Leu His Phe Val Pro Cys Val Tyr
      245      250      255
Ile Tyr Cys Arg Pro Phe Met Thr Leu Pro Met Asp Thr Thr Ile Ser
      260      265      270
Ile Asn Asn Thr Val Ile Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser
      275      280      285
Leu Arg Asn Gln Glu Met Lys Ser Ala Met Gln Arg Leu Gln Arg Arg
      290      295      300
Leu Gly Pro Ser Glu Ser Arg Lys Trp
      305      310

```

<210> 1538

<211> 309

<212> PRT

<213> Unknown (H38g455 protein)

<220>

<223> Synthetic construct

<400> 1538

```

Met Glu Arg Ile Asn His Thr Ser Ser Val Ser Glu Phe Ile Leu Leu
  1      5      10      15
Gly Leu Ser Ser Arg Pro Glu Asp Gln Lys Thr Leu Phe Val Leu Phe
      20      25      30
Leu Ile Val Tyr Leu Val Thr Ile Thr Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Ile Arg Phe Asn Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Phe Leu Ser Leu Thr Asp Ile Cys Phe Thr Thr Ser Val Val Pro
      65      70      75      80
Lys Met Leu Met Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Tyr Phe Leu Tyr Ala Leu Gly Asn Ser Asp
      100      105      110
Ser Cys Leu Leu Ala Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys
      115      120      125
Asp Pro Phe His Tyr Val Thr Thr Met Ser His His His Cys Val Leu
      130      135      140
Leu Val Ala Phe Ser Cys Ser Phe Pro His Leu His Ser Leu Leu His
      145      150      155      160
Thr Leu Leu Leu Asn Arg Leu Thr Phe Cys Asp Ser Asn Val Ile His
      165      170      175
His Phe Leu Cys Asp Leu Ser Pro Val Leu Lys Leu Ser Cys Ser Ser
      180      185      190

```

Ile Phe Val Asn Glu Ile Val Gln Met Thr Glu Ala Pro Ile Val Leu
 195 200 205
 Val Thr Arg Phe Leu Cys Ile Ala Phe Ser Tyr Ile Arg Ile Leu Thr
 210 215 220
 Thr Val Leu Lys Ile Pro Ser Thr Ser Gly Lys Arg Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Phe Tyr Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile
 245 250 255
 Phe Cys Val Tyr Leu Gln Pro Pro Ser Thr Tyr Ala Val Lys Asp His
 260 265 270
 Val Ala Thr Ile Val Tyr Thr Val Leu Ser Ser Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Leu Lys Gln Gly Leu Arg Lys Leu
 290 295 300
 Met Ser Lys Arg Ser
 305

<210> 1539

<211> 313

<212> PRT

<213> Unknown (H38g456 protein)

<220>

<223> Synthetic construct

<400> 1539

Met Ala Asn Val Thr Leu Val Thr Gly Phe Leu Leu Met Gly Phe Ser
 1 5 10 15
 Asn Ile Gln Lys Leu Arg Ile Leu Tyr Gly Val Leu Phe Leu Leu Ile
 20 25 30
 Tyr Leu Ala Ala Leu Met Ser Asn Leu Leu Ile Ile Thr Leu Ile Thr
 35 40 45
 Leu Asp Val Lys Leu Gln Thr Pro Met Tyr Phe Phe Leu Lys Asn Leu
 50 55 60
 Ser Phe Leu Asp Val Phe Leu Val Ser Val Pro Ile Pro Lys Phe Ile
 65 70 75 80
 Val Asn Asn Leu Thr His Asn Asn Ser Ile Ser Ile Leu Gly Cys Ala
 85 90 95
 Phe Gln Leu Leu Leu Met Thr Ser Phe Ser Ala Gly Glu Ile Phe Ile
 100 105 110
 Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu
 115 120 125
 Asn Tyr Glu Val Ile Met Asn Thr Gly Val Cys Val Leu Met Ala Ser
 130 135 140
 Val Ser Trp Ala Ile Gly Gly Leu Phe Gly Thr Ala Tyr Thr Ala Gly
 145 150 155 160
 Thr Phe Ser Met Pro Phe Cys Gly Ser Ser Val Ile Pro Gln Phe Phe
 165 170 175
 Cys Asp Val Pro Ser Leu Leu Arg Ile Ser Cys Ser Glu Thr Leu Met
 180 185 190
 Val Ile Tyr Ala Gly Ile Gly Val Gly Ala Cys Leu Ser Ile Ser Cys
 195 200 205
 Phe Ile Cys Ile Val Ile Ser Tyr Ile Tyr Ile Phe Ser Thr Val Leu
 210 215 220
 Lys Ile Pro Thr Thr Lys Gly Gln Ser Lys Ala Phe Ser Thr Cys Phe
 225 230 235 240
 Pro His Leu Thr Val Phe Thr Val Phe Ile Ile Thr Ala Tyr Phe Val
 245 250 255
 Tyr Leu Lys Pro Pro Ser Asn Ser Pro Ser Val Ile Asp Arg Leu Leu
 260 265 270
 Ser Val Ile Tyr Thr Val Met Pro Pro Val Phe Asn Pro Val Thr Tyr

275 280 285
 Ser Leu Arg Asn Asn Asp Met Lys Cys Ala Leu Ile Arg Leu Leu Gln
 290 295 300
 Lys Thr Tyr Gly Gln Glu Ala Tyr Phe
 305 310

<210> 1540
 <211> 324
 <212> PRT
 <213> Unknown (H38g457 protein)

<220>
 <223> Synthetic construct

<400> 1540
 Met Ala Val Gly Arg Asn Asn Thr Ile Val Thr Lys Phe Ile Leu Leu
 1 5 10 15
 Gly Leu Ser Asp His Pro Gln Met Lys Ile Phe Leu Phe Met Leu Phe
 20 25 30
 Leu Gly Leu Tyr Leu Leu Thr Leu Ala Trp Asn Leu Ser Leu Ile Ala
 35 40 45
 Leu Ile Lys Met Asp Ser His Leu His Met Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Leu Asp Ile Cys Tyr Val Ser Ser Thr Ala Pro
 65 70 75 80
 Lys Met Leu Ser Asp Ile Ile Thr Glu Gln Lys Thr Ile Ser Phe Val
 85 90 95
 Gly Cys Ala Thr Gln Tyr Phe Val Phe Cys Gly Met Gly Leu Thr Glu
 100 105 110
 Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Thr Val Leu Ile Ser His Thr Leu Cys Leu Lys
 130 135 140
 Met Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Phe Ile Glu
 145 150 155 160
 Thr Tyr Ser Val Tyr Gln His Asp Phe Cys Gly Pro Tyr Met Ile Asn
 165 170 175
 His Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys Ser Asp
 180 185 190
 Thr Phe Thr Ser Glu Val Val Thr Phe Ile Val Ser Val Val Val Gly
 195 200 205
 Ile Val Ser Val Leu Val Val Leu Ile Ser Tyr Gly Tyr Ile Val Ala
 210 215 220
 Ala Val Val Lys Ile Ser Ser Ala Thr Gly Arg Thr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ser Gly
 245 250 255
 Phe Phe Met Tyr Met Arg Pro Ser Ser Ser Tyr Ser Leu Asn Arg Asp
 260 265 270
 Lys Val Val Ser Ile Phe Tyr Ala Leu Val Ile Pro Val Val Asn Pro
 275 280 285
 Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Asn Ala Met Arg Lys
 290 295 300
 Ala Met Glu Arg Asp Pro Gly Ile Ser His Gly Gly Pro Phe Ile Phe
 305 310 315 320
 Met Thr Leu Gly

<210> 1541
 <211> 314
 <212> PRT

<213> Unknown (H38g458 protein)

<220>

<223> Synthetic construct

<400> 1541

```

Met Thr Asn Gln Thr Gln Met Met Glu Phe Leu Leu Val Arg Phe Thr
 1           5           10           15
Glu Asn Trp Val Leu Leu Arg Leu His Ala Leu Leu Phe Ser Leu Ile
      20           25           30
Tyr Leu Thr Ala Val Leu Met Asn Leu Val Ile Ile Leu Leu Met Ile
      35           40           45
Leu Asp His Arg Leu His Met Ala Met Tyr Phe Phe Leu Arg His Leu
      50           55           60
Ser Phe Leu Asp Leu Cys Leu Ile Ser Ala Thr Val Pro Lys Ser Ile
      65           70           75           80
Leu Asn Ser Val Ala Ser Thr Asp Ser Ile Ser Phe Leu Gly Cys Val
      85           90           95
Leu Gln Leu Phe Leu Val Val Leu Leu Ala Gly Ser Glu Ile Gly Ile
      100          105          110
Leu Thr Ala Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Cys Pro Leu
      115          120          125
His Cys Glu Ala Val Met Ser Arg Gly Leu Cys Val Gln Leu Met Ala
      130          135          140
Leu Ser Trp Leu Asn Arg Gly Ala Leu Gly Leu Leu Tyr Thr Ala Gly
      145          150          155          160
Thr Phe Ser Leu Asn Phe Tyr Gly Ser Asp Glu Leu His Gln Phe Phe
      165          170          175
Cys Asp Val Pro Ala Leu Leu Lys Leu Thr Cys Ser Lys Glu His Ala
      180          185          190
Ile Ile Ser Val Ser Val Ala Ile Gly Val Cys Tyr Ala Phe Ser Cys
      195          200          205
Leu Val Cys Ile Val Val Ser Tyr Val Tyr Ile Phe Ser Ala Val Leu
      210          215          220
Arg Ile Ser Gln Arg Gln Arg Gln Ser Lys Ala Phe Ser Asn Cys Val
      225          230          235          240
Pro His Leu Ile Val Val Thr Val Phe Leu Val Thr Gly Ala Val Ala
      245          250          255
Tyr Leu Lys Pro Gly Ser Asp Ala Pro Ser Ile Leu Asp Leu Leu Val
      260          265          270
Ser Val Phe Tyr Ser Val Ala Pro Pro Thr Leu Asn Pro Val Ile Tyr
      275          280          285
Cys Leu Lys Asn Lys Asp Ile Lys Ser Ala Leu Ser Lys Val Leu Trp
      290          295          300
Asn Val Arg Ser Ser Gly Val Met Lys Arg
      305          310

```

<210> 1542

<211> 307

<212> PRT

<213> Unknown (H38g459 protein)

<220>

<223> Synthetic construct

<400> 1542

```

Met Asn His Ser Val Val Thr Glu Phe Ile Ile Leu Gly Leu Thr Lys
 1           5           10           15
Lys Pro Glu Leu Gln Gly Ile Ile Phe Leu Phe Phe Leu Ile Val Tyr
      20           25           30
Leu Val Ala Phe Leu Gly Asn Met Leu Ile Ile Ile Ala Lys Ile Tyr

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      35      40      45
Asn Asn Thr Leu His Thr Pro Met Tyr Val Phe Leu Leu Thr Leu Ala
  50      55      60
Val Val Asp Ile Ile Cys Thr Thr Ser Ile Ile Pro Lys Met Leu Gly
  65      70      75      80
Thr Met Leu Thr Ser Glu Asn Thr Ile Ser Tyr Ala Gly Cys Met Ser
      85      90      95
Gln Leu Phe Leu Phe Thr Trp Ser Leu Gly Ala Glu Met Val Leu Phe
      100      105      110
Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      115      120      125
Tyr Ser Thr Val Met Asn His His Met Cys Val Ala Leu Leu Ser Met
      130      135      140
Val Met Ala Ile Ala Val Thr Asn Ser Trp Val His Thr Ala Leu Ile
      145      150      155      160
Met Arg Leu Thr Phe Cys Gly Pro Asn Thr Ile Asp His Phe Phe Cys
      165      170      175
Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Pro Val Arg Ile Asn
      180      185      190
Glu Val Met Val Tyr Val Ala Asp Ile Thr Leu Ala Ile Gly Asp Phe
      195      200      205
Ile Leu Thr Cys Ile Ser Tyr Gly Phe Ile Ile Val Ala Ile Leu Arg
      210      215      220
Ile Arg Thr Val Glu Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser
      225      230      235      240
His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val Ile Tyr Thr Tyr
      245      250      255
Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp Lys Val Val Ala
      260      265      270
Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro Met Val Tyr Ser
      275      280      285
Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys Val Phe Ala Phe
      290      295      300
Leu Lys His
305

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<210> 1543
 <211> 270
 <212> PRT
 <213> Unknown (H38g460 protein)

<220>
 <223> Synthetic construct

```

<400> 1543
Met Glu Val Ser Gly Asn His Thr Ser Val Ala Met Phe Val Leu Leu
  1      5      10      15
Gly Leu Ser Asp Glu Lys Glu Leu Gln Leu Ile Leu Phe Pro Val Phe
      20      25      30
Leu Val Ile Tyr Leu Val Thr Leu Ile Trp Asn Met Gly Leu Ile Ile
      35      40      45
Leu Ile Arg Ile Asp Ser His Leu Asn Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Phe Leu Ser Phe Thr Asp Ile Cys Tyr Ser Ser Thr Ile Ser Pro
      65      70      75      80
Arg Met Leu Ser Asp Phe Leu Lys Asp Lys Lys Thr Ile Ser Phe Leu
      85      90      95
Ala Cys Ala Thr Gln Tyr Phe Leu Gly Ala Trp Met Ser Leu Ala Glu
      100      105      110
Cys Cys Leu Leu Val Ile Met Ala Cys Asp Arg Tyr Val Ala Ile Gly
      115      120      125

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Ser Pro Leu Gln Tyr Ser Ala Ile Met Val Pro Ser Ile Cys Trp Lys
  130                      135                      140
Met Val Ala Gly Val Cys Gly Gly Gly Phe Leu Ser Ser Leu Val His
145                      150                      155                      160
Thr Val Pro Cys Phe Asn Leu Tyr Tyr Cys Gly Pro Asn Ile Ile Gln
                      165                      170                      175
His Phe Phe Cys Asn Thr Leu Gln Ile Ile Ser Leu Ser Cys Ser Asn
                      180                      185                      190
Pro Phe Ile Ser Gln Met Ile Leu Phe Leu Glu Ala Ile Phe Val Gly
                      195                      200                      205
Leu Gly Ser Leu Leu Val Ile Leu Leu Ser Tyr Gly Phe Ile Val Ala
                      210                      215                      220
Ser Ile Leu Lys Ile Ser Ser Thr Lys Cys Cys Ala Lys Ala Phe Asn
225                      230                      235                      240
Thr Cys Ala Ser His Leu Ala Ala Val Ala Leu Phe Tyr Gly Thr Ala
                      245                      250                      255
Leu Ser Val Tyr Met His Pro Ser Ser Ser His Ser Met Lys
                      260                      265                      270

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<210> 1544

<211> 329

<212> PRT

<213> Unknown (H38g461 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1544

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Tyr Ser Lys Glu Ile Ile Glu Xaa Cys Thr Ser Asn Asp Ile Ile Lys
  1                      5                      10                      15
Cys Gly Xaa His Asn Lys Ile Thr Phe Phe Leu Phe Ile Leu Leu Glu
                      20                      25                      30
Phe Thr Glu Asp Leu Gly Leu Gln Gln Val Leu Phe Phe Ile Phe Leu
                      35                      40                      45
Ile Ile Tyr Val Ile Ser Leu Ser Gly Asn Ile Ile Leu Asn Ser Leu
                      50                      55                      60
Ile Cys Ala Asp Ser Trp Pro Tyr Thr Pro Met Tyr Phe Phe Thr Gly
65                      70                      75                      80
Asn Arg Phe Leu Leu Asp Leu Trp Tyr Ser Ser Val His Ile Pro Asp
                      85                      90                      95
Ile Leu Leu Thr Cys Ile Ser Asp Asp Lys Thr Ile Ser Phe Pro Gly
                      100                      105                      110
Cys Leu Ala Gln Phe Phe Ser Ala Val Leu Ala Xaa Asn Glu Cys Tyr
                      115                      120                      125
Met Met Ala Ser Met Ala Tyr Asp Arg Tyr Met Ala Ile Ser Lys Pro
130                      135                      140
Leu Leu Tyr Ser Arg Ala Thr Phe Pro Glu Leu Cys Ala Ser Leu Val
145                      150                      155                      160
Glu Ala Ser His Leu Gly Gly Phe Val Asn Ser Thr Ile Ile Thr Ser
                      165                      170                      175
Glu Thr Pro Thr Leu Ser Phe Cys Gly Ser Asn Ile Ile Asp Asp Phe
                      180                      185                      190
Phe Cys Asp Leu Pro Pro Leu Val Lys Leu Val Cys Asp Val Lys Glu
195                      200                      205
Arg Tyr Gln Ala Val Leu His Phe Met Leu Ala Ser Asn Ile Thr Pro
210                      215                      220
Thr Ala Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Ala Ala Ile Ser

```

225 230 235 240
 Lys Ile Arg Ser Ile Lys Gly Arg Leu Gln Val Phe Ser Thr Cys Gly
 245 250 255
 Ser Pro Leu Thr Ala Leu Thr Leu Tyr Tyr Gly Ala Ile Phe Phe Ile
 260 265 270
 Tyr Ser Gln Pro Arg Thr Ser Tyr Ala Leu Lys Met Asp Lys Leu Gly
 275 280 285
 Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr
 290 295 300
 Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Leu Lys Lys Met Leu Asp
 305 310 315 320
 Arg Leu Gln Phe Leu Lys Glu Lys Tyr
 325

<210> 1545

<211> 349

<212> PRT

<213> Unknown (H38g462 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(349)

<223> Xaa = Any Amino Acid

<400> 1545

Met Glu Gln Ser Asn Tyr Ser Val Tyr Ala Asp Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Phe Ser Lys Pro Val Ser Pro Gly Phe Phe Ala Leu Ile Leu Leu
 20 25 30
 Val Phe Val Thr Ser Ile Ala Ser Asn Val Val Lys Ile Ile Leu Ile
 35 40 45
 His Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
 50 55 60
 Leu Ser Leu Arg Asp Ile Leu Tyr Ile Ser Thr Ile Val Pro Lys Met
 65 70 75 80
 Leu Val Asp Gln Val Met Ser Gln Arg Ala Ile Ser Phe Ala Gly Cys
 85 90 95
 Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Ala Gly Ala Glu Phe Phe
 100 105 110
 Leu Leu Gly Leu Met Ser Cys Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115 120 125
 Leu His Tyr Pro Asp Leu Met Ser Arg Lys Ile Cys Trp Leu Ile Val
 130 135 140
 Ala Ala Ala Trp Leu Gly Gly Ser Ile Asn Gly Phe Leu Leu Thr Pro
 145 150 155 160
 Val Thr Thr Gln Phe Pro Phe Cys Ala Ser Arg Glu Ile Asn His Phe
 165 170 175
 Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Thr Asp Thr Ser
 180 185 190
 Ala Tyr Glu Thr Ala Met Tyr Val Cys Cys Ile Met Met Leu Leu Ile
 195 200 205
 Pro Phe Ser Val Ile Ser Gly Ser Tyr Thr Arg Ile Leu Ile Thr Val
 210 215 220
 Tyr Arg Met Ser Glu Ala Glu Gly Arg Arg Lys Ala Val Ala Thr Cys
 225 230 235 240
 Ser Ser His Met Val Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr
 245 250 255
 Thr Tyr Val Leu Pro His Ser Tyr His Thr Pro Glu Gln Asp Lys Ala
 260 265 270

Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Gln Lys Val Val
 290 295 300
 Gly Arg Cys Val Ser Ser Gly Lys Val Thr Thr Phe Lys Gln Ile Ala
 305 310 315 320
 Tyr Ala Ala Arg Asp Leu Lys Xaa Arg Ile Gln Asp Phe Ile Ile Ala
 325 330 335
 Leu Glu Phe Lys Tyr Ser Leu Pro Gly Asn Lys Xaa Pro
 340 345

<210> 1546

<211> 319

<212> PRT

<213> Unknown (H38g463 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1546

Met Gly Val His Asn Leu Phe Thr Val Thr Gln Phe Ile Leu Ile Gly
 1 5 10 15
 Leu Ser Tyr Phe Ser Asn Glu His Tyr Leu Leu Phe Val Ala Leu Ala
 20 25 30
 Ile Ile Cys Gln Val Phe Leu Val Arg Ser Gly Asp Ile Leu Leu Ala
 35 40 45
 Ile Gly Thr Val Ile Lys Leu His Thr Thr Met Tyr Tyr Phe Leu Ala
 50 55 60
 Asn Val Ser Ile Leu Asp Ile Leu Cys Ser Ser Ala Thr Ile Pro Lys
 65 70 75 80
 Met Pro Lys Ile Leu Xaa Thr Glu Asp His Ser Ile Ser Phe Val Arg
 85 90 95
 Xaa Ala Leu Gln Pro Tyr Phe Leu Val Ala Trp Ala Gly Lys Lys Cys
 100 105 110
 Phe Leu Thr Val Thr Ala Tyr Asp Trp Cys Val Val Thr Cys Phe Ser
 115 120 125
 Leu Cys Tyr Ile Leu Ile Met Asn Lys Leu Val Ser Val Gln Leu Val
 130 135 140
 Tyr Gly Thr Xaa Ala Ala Gly Phe Leu Asn Phe Leu Leu Leu His Val
 145 150 155 160
 Val Ser Thr Leu Cys Leu Ser Phe Cys Lys Pro Asp Arg Val Asn Gln
 165 170 175
 Tyr Tyr Cys Asp Ile Ser Pro Met Gly Ala Leu Leu Cys Gln Ser Met
 180 185 190
 His Leu Ala Asn Met Leu Val Leu Val Glu Ser Val Ile Leu Gly Ile
 195 200 205
 Ser Ala Phe Leu Ala Ala Phe Asn Phe Tyr Ile Tyr Ile Ile Ser Thr
 210 215 220
 Ile Leu Lys Ile Gln Cys Val Glu Trp Ser Ala Lys Cys Phe Ser Thr
 225 230 235 240
 Cys Thr Ser His Leu Leu Thr Val Cys Leu Phe Tyr Gly Ile Leu Thr
 245 250 255
 Phe Thr Tyr Ile Tyr Ser Phe Ser Ser His Thr His Met Ser Lys Ala
 260 265 270
 Ser Pro Asp Leu Ala Thr Asp Arg Leu Ile Ser Met Leu Tyr Arg Val
 275 280 285
 Ile Thr Leu Met Phe Asn Phe Ile Thr Asp Asn Leu Arg Asn Thr Glu

290 295 300
 Val Lys Gly Ala Ser Glu Arg Phe Tyr Val Ile Glu His Val Tyr
 305 310 315

<210> 1547
 <211> 280
 <212> PRT
 <213> Unknown (H38g464 protein)

<220>
 <223> Synthetic construct

<400> 1547
 Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Leu Ile Met Leu Leu Ile
 1 5 10 15
 Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
 20 25 30
 Leu Ala Leu Thr Tyr Phe Ser Phe Ser Ser Val Thr Val Pro Lys Met
 35 40 45
 Leu Met Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu Cys
 50 55 60
 Ile Ser Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser Phe
 65 70 75 80
 Leu Ile Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
 85 90 95
 Leu His Tyr Thr Val Ile Met Arg Glu Glu Leu Cys Val Phe Leu Val
 100 105 110
 Ala Val Ser Trp Ile Leu Ser Cys Ala Ser Ser Leu Ser His Thr Leu
 115 120 125
 Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His Val
 130 135 140
 Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile Phe
 145 150 155 160
 Leu Asn Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr Leu
 165 170 175
 Pro Phe Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile
 180 185 190
 Leu Arg Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr Cys
 195 200 205
 Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe Gly
 210 215 220
 Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val Ile
 225 230 235 240
 Val Ala Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile
 245 250 255
 Tyr Ser Ile Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu Phe
 260 265 270
 Ser Arg Ala Thr Phe Phe Ser Trp
 275 280

<210> 1548
 <211> 303
 <212> PRT
 <213> Unknown (H38g465 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(303)
 <223> Xaa = Any Amino Acid

<400> 1548
 Met Asn Ser Ser Ser Asp Xaa Arg Gln Pro Val Met Asp Gly Val Asn
 1 5 10 15
 Asp Ser Ser Leu Gln Gly Phe Val Leu Met Gly Ile Ser Asp His Pro
 20 25 30
 Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu Phe Ser Tyr Leu Leu
 35 40 45
 Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu Ser Arg Leu Glu Ala
 50 55 60
 Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Ser Leu
 65 70 75 80
 Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln Met Leu Ile Asn Leu
 85 90 95
 Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly Cys Ile Thr Gln Leu
 100 105 110
 Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys Ile Leu Leu Val Val
 115 120 125
 Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg Pro Leu Arg Tyr Thr
 130 135 140
 Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu Ala Val Ile Ala Cys
 145 150 155 160
 Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser Thr Phe Thr Leu Gln
 165 170 175
 Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly Phe Leu Cys Glu Val
 180 185 190
 Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr Ser Leu Asn Gln Ala
 195 200 205
 Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala Val Pro Leu Ser Ile
 210 215 220
 Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala Val Leu Lys Ile Arg
 225 230 235 240
 Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Leu Ser His Leu
 245 250 255
 Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser Tyr Gly Tyr Leu Leu
 260 265 270
 Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys Phe Ile Ser Leu Phe
 275 280 285
 Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu Ile Tyr Thr Leu
 290 295 300

<210> 1549

<211> 309

<212> PRT

<213> Unknown (H38g466 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(309)

<223> Xaa = Any Amino Acid

<400> 1549

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1 5 10 15
 Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
 20 25 30
 Val Tyr Cys Leu Thr Val Val Gly Ser Ser Thr Leu Ile Val Leu Ile
 35 40 45
 Cys Asn Asp Ser His Leu His Thr Pro Met Tyr Phe Val Ile Gly Asn

```

      50              55              60
Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
65              70              75              80
Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
      85              90              95
Leu Cys Gln Phe Phe Ser Ala Arg Leu Ala Tyr Ser Glu Cys Tyr Leu
      100              105              110
Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu
      115              120              125
Leu Tyr Ala Gln Thr Met Pro Arg Arg Leu Cys Ile Cys Leu Val Leu
      130              135              140
Tyr Ser Tyr Thr Gly Gly Phe Val Asn Ala Ile Ile Leu Thr Ser Asn
145              150              155              160
Thr Phe Thr Leu Asp Phe Cys Gly Asp Asn Val Ile Asp Asp Phe Phe
      165              170              175
Cys Asp Val Pro Pro Leu Val Lys Leu Ala Cys Ser Arg Glu Ser Tyr
      180              185              190
Gln Ala Val Leu His Phe Leu Leu Ala Ser Asn Val Ile Ser Pro Thr
      195              200              205
Val Leu Ile Leu Ala Ser Tyr Leu Ser Ile Ile Thr Thr Ile Leu Arg
      210              215              220
Ile His Ser Thr Gln Gly Arg Ile Lys Val Phe Ser Thr Cys Ser Ser
225              230              235              240
His Leu Ile Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr Asn Tyr
      245              250              255
Ser Arg Pro Ser Ser Ser Tyr Ser Leu Lys Arg Asp Lys Met Val Ser
      260              265              270
Thr Phe Tyr Thr Met Leu Phe Pro Met Leu Asn Pro Met Ile Tyr Ser
      275              280              285
Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Phe Phe Lys Ser
      290              295              300
Ala Xaa Ser Lys Val
305

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<210> 1550

<211> 312

<212> PRT

<213> Unknown (H38g467 protein)

<220>

<223> Synthetic construct

<400> 1550

```

Met Asp Gly Val Asn Asp Ser Ser Leu Gln Gly Phe Val Leu Met Ser
1      5      10      15
Ile Ser Asp His Pro Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu
      20      25      30
Phe Ser Tyr Leu Leu Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu
      35      40      45
Ser Arg Leu Glu Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln
65      70      75      80
Met Leu Ile Asn Leu Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly
      85      90      95
Cys Ile Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
      100      105      110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
      115      120      125
Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu
      130      135      140

```

Ala Val Ile Ala Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
 145 150 155 160
 Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly
 165 170 175
 Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr
 180 185 190
 Ser Leu Asn Gln Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala
 195 200 205
 Val Pro Leu Ser Ile Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala
 210 215 220
 Val Leu Lys Ile His Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr
 225 230 235 240
 Cys Leu Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser
 245 250 255
 Tyr Gly Tyr Leu Leu Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys
 260 265 270
 Phe Ile Ser Leu Phe Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Met Glu Val Lys Gly Ala Leu Arg Arg Leu
 290 295 300
 Leu Gly Lys Gly Arg Glu Val Gly
 305 310

<210> 1551

<211> 82

<212> PRT

<213> Unknown (H38g468 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(82)

<223> Xaa = Any Amino Acid

<400> 1551

Gly Glu Arg Leu Lys Thr Leu Asn Thr Cys Val Ser His Ile Tyr Ala
 1 5 10 15
 Val Leu Ile Phe Tyr Val Pro Met Val Ser Val Ser Met Val His Arg
 20 25 30
 Phe Gly Arg His Ala Pro Glu Tyr Val His Lys Phe Met Ser Phe Val
 35 40 45
 Pro Pro Met Leu Tyr Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile
 50 55 60
 Arg Arg Arg Leu His Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Arg
 65 70 75 80
 Lys Thr

<210> 1552

<211> 312

<212> PRT

<213> Unknown (H38g469 protein)

<220>

<223> Synthetic construct

<400> 1552

Met Glu Val Gly Asn Cys Thr Ile Leu Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Ala Asp Ser Gln Trp Gln Pro Ile Leu Phe Gly Val Phe Leu


```

      20      25      30
Met Leu Tyr Leu Ile Thr Leu Ser Gly Asn Met Thr Leu Val Ile Leu
  35      40      45
Ile Arg Thr Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Ile Gly
  50      55      60
Asn Leu Ser Phe Leu Asp Phe Trp Tyr Thr Ser Val Tyr Thr Pro Lys
  65      70      75      80
Ile Leu Ala Ser Cys Val Ser Glu Asp Lys Arg Ile Ser Leu Ala Gly
      85      90      95
Cys Gly Ala Gln Leu Phe Phe Ser Cys Val Val Ala Tyr Thr Glu Cys
  100      105      110
Tyr Leu Leu Ala Ala Met Ala Tyr Asp Arg His Ala Ala Ile Cys Asn
  115      120      125
Pro Leu Leu Tyr Ser Gly Thr Met Ser Thr Ala Leu Cys Thr Gly Leu
  130      135      140
Val Ala Gly Ser Tyr Ile Gly Gly Phe Leu Asn Ala Ile Ala His Thr
  145      150      155      160
Ala Asn Thr Phe Arg Leu His Phe Cys Gly Lys Asn Ile Ile Asp His
      165      170      175
Phe Phe Cys Asp Ala Pro Pro Leu Val Lys Met Ser Cys Thr Asn Thr
      180      185      190
Arg Val Tyr Glu Lys Val Leu Leu Gly Val Val Gly Phe Thr Val Leu
  195      200      205
Ser Ser Ile Leu Ala Ile Leu Ile Ser Tyr Val Asn Ile Leu Leu Ala
  210      215      220
Ile Leu Arg Ile His Ser Ala Ser Gly Arg His Lys Ala Phe Ser Thr
  225      230      235      240
Cys Ala Ser His Leu Ile Ser Val Met Leu Phe Tyr Gly Ser Leu Leu
      245      250      255
Phe Met Tyr Ser Arg Pro Ser Ser Thr Tyr Ser Leu Glu Arg Asp Lys
      260      265      270
Val Ala Ala Leu Phe Tyr Thr Val Ile Asn Pro Leu Leu Asn Pro Leu
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Glu Ala Phe Arg Lys Ala
  290      295      300
Thr Gln Thr Ile Gln Pro Gln Thr
  305      310

```

<210> 1553

<211> 318

<212> PRT

<213> Unknown (H38g470 protein)

<220>

<223> Synthetic construct

<400> 1553

```

Met Pro Thr Val Asn His Ser Gly Thr Ser His Thr Val Phe His Leu
  1      5      10      15
Leu Gly Ile Pro Gly Leu Gln Asp Gln His Met Trp Ile Ser Ile Pro
      20      25      30
Phe Phe Ile Ser Tyr Val Thr Ala Leu Leu Gly Asn Ser Leu Leu Ile
      35      40      45
Phe Ile Ile Leu Thr Lys Arg Ser Leu His Glu Pro Met Tyr Leu Phe
      50      55      60
Leu Cys Met Leu Ala Gly Ala Asp Ile Val Leu Ser Thr Cys Thr Ile
  65      70      75      80
Pro Gln Ala Leu Ala Ile Phe Trp Phe Arg Ala Gly Asp Ile Ser Leu
      85      90      95
Asp Arg Cys Ile Thr Gln Leu Phe Phe Ile His Ser Thr Phe Ile Ser
      100      105      110

```

Glu Ser Gly Ile Leu Leu Val Met Ala Phe Asp His Tyr Ile Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Leu Ile Lys
 130 135 140
 Lys Ile Cys Val Thr Val Ser Leu Arg Ser Tyr Gly Thr Ile Phe Pro
 145 150 155 160
 Ile Ile Phe Leu Leu Lys Arg Leu Thr Phe Cys Gln Asn Asn Ile Ile
 165 170 175
 Pro His Thr Phe Cys Glu His Ile Gly Leu Ala Lys Tyr Ala Cys Asn
 180 185 190
 Asp Ile Arg Ile Asn Ile Trp Tyr Gly Phe Ser Ile Leu Met Ser Thr
 195 200 205
 Val Val Leu Asp Val Val Leu Ile Phe Ile Ser Tyr Met Leu Ile Leu
 210 215 220
 His Ala Val Phe His Met Pro Ser Pro Asp Ala Cys His Lys Ala Leu
 225 230 235 240
 Asn Thr Phe Gly Ser His Val Cys Ile Ile Ile Leu Phe Tyr Gly Ser
 245 250 255
 Gly Ile Phe Thr Ile Leu Thr Gln Arg Phe Gly Arg His Ile Pro Pro
 260 265 270
 Cys Ile His Ile Pro Leu Ala Asn Val Cys Ile Leu Ala Pro Pro Met
 275 280 285
 Leu Asn Pro Ile Ile Tyr Gly Ile Lys Thr Lys Gln Ile Gln Glu Gln
 290 295 300
 Val Val Gln Phe Leu Phe Ile Lys Gln Lys Ile Thr Leu Val
 305 310 315

<210> 1554

<211> 314

<212> PRT

<213> Unknown (H38g471 protein)

<220>

<223> Synthetic construct

<400> 1554

Met Glu Ala Ala Asn Glu Ser Ser Glu Gly Ile Ser Phe Val Leu Leu
 1 5 10 15
 Gly Leu Thr Thr Ser Pro Gly Gln Gln Arg Pro Leu Phe Val Leu Phe
 20 25 30
 Leu Leu Leu Tyr Val Ala Ser Leu Leu Gly Asn Gly Leu Ile Val Ala
 35 40 45
 Ala Ile Gln Ala Ser Pro Ala Leu His Ala Pro Met Tyr Phe Leu Leu
 50 55 60
 Ala His Leu Ser Phe Ala Asp Leu Cys Phe Ala Ser Val Thr Val Pro
 65 70 75 80
 Lys Met Leu Ala Asn Leu Leu Ala His Asp His Ser Ile Ser Leu Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Tyr Phe Phe Phe Ala Leu Gly Val Thr Asp
 100 105 110
 Ser Cys Leu Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Arg
 115 120 125
 His Pro Leu Pro Tyr Ala Thr Arg Met Ser Arg Ala Met Cys Ala Ala
 130 135 140
 Leu Val Gly Met Ala Trp Leu Val Ser His Val His Ser Leu Leu Tyr
 145 150 155 160
 Ile Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Ser His Gln Val Pro
 165 170 175
 His Phe Phe Cys Asp His Gln Pro Leu Leu Arg Leu Ser Cys Ser Asp
 180 185 190
 Thr His His Ile Gln Leu Leu Ile Phe Thr Glu Gly Ala Ala Val Val

```

      195      200      205
Val Thr Pro Phe Leu Leu Ile Leu Ala Ser Tyr Gly Ala Ile Ala Ala
  210      215      220
Ala Val L u Gln Leu Pro Ser Ala Ser Gly Arg Leu Arg Ala Val Ser
  225      230      235      240
Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Val
      245      250      255
Ile Ala Val Tyr Phe Gln Ala Thr Ser Arg Arg Glu Ala Glu Trp Gly
      260      265      270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275      280      285
Ile Ile Tyr Ser Leu Trp Asn Arg Asp Val Gln Gly Ala Leu Arg Ala
      290      295      300
Leu Leu Ile Gly Arg Arg Ile Ser Ala Ser
  305      310

```

<210> 1555

<211> 316

<212> PRT

<213> Unknown (H38g472 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1555

```

Ile Ser Met Phe Ser Cys Asn Thr Ser Thr Ser Gly Gln Ser Thr Phe
  1      5      10      15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Ser His His Trp Val Ser
      20      25      30
Ile Pro Ile Asn Leu Phe Cys Val Val Ser Ile Leu Gly Asn Asn Ile
      35      40      45
Ile Leu Phe Leu Ile His Thr Asp Pro Ala Leu His Glu Pro Met Tyr
      50      55      60
Ile Phe Leu Ser Met Leu Ala Ala Ser Asp Leu Gly Leu Cys Ala Ser
  65      70      75      80
Thr Phe Pro Thr Met Val Arg Leu Phe Trp Leu Gly Ala Arg Glu Leu
      85      90      95
Pro Phe Asp Leu Cys Ala Ala Gln Met Phe Phe Ile His Thr Phe Thr
      100      105      110
Tyr Val Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Ile
      115      120      125
Ala Ile Arg Asp Pro Leu His Tyr Ala Ile Ile Ile Thr Cys Ser Val
      130      135      140
Thr Ala Glu Val Gly Thr Ala Ile Leu Val Arg Ala Val Leu Leu Asn
  145      150      155      160
Leu Pro Gly Pro Ile Leu Leu Gln Gln Leu Leu Phe Pro Lys Ile Ser
      165      170      175
Ala Leu Cys His Cys Tyr Cys Leu His Cys Asp Leu Val Gly Leu Ala
      180      185      190
Cys Ser Asp Thr Gln Ile Asn Ser Leu Val Gly Leu Val Ser Ile Leu
      195      200      205
Phe Ser Leu Cys Leu Asp Ser Phe Leu Ile Met Leu Ser Tyr Ala Leu
      210      215      220
Ile Leu Xaa Thr Val Leu Gly Ile Ala Ser Pro Gly Glu Arg Leu Lys
  225      230      235      240
Ala Leu Asn Thr Cys Val Ser His Leu Cys Ile Val Leu Ile Phe Tyr
      245      250      255

```

Leu Pro Ile Ile Gly Leu Ser Val Leu His Arg Val Lys Lys His Asp
 260 265 270
 Tyr Pro Ala Leu Ala Val Leu Met Ala Asn Leu His Phe Leu Val Pro
 275 280 285
 Pro Phe Met Asn Pro Ile Val Tyr Cys Ile Lys Ser Arg Gln Ile Arg
 290 295 300
 Gln Ser Leu Leu Lys His Phe Gln Gln Lys Arg Ile
 305 310 315

<210> 1556

<211> 320

<212> PRT

<213> Unknown (H38g473 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1556

His Thr Glu Pro Trp Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
 20 25 30
 Arg Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 100 105 110
 Asp Met Leu Leu Thr Ala Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Ser Val Phe
 130 135 140
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
 180 185 190
 Ser Val Ile Asn Ser Ile Phe Leu Tyr Phe Asp Ser Thr Met Phe Gly
 195 200 205
 Phe Leu Pro Ile Ser Arg Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
 210 215 220
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
 245 250 255
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Ser Gly
 260 265 270
 Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg
 290 295 300
 Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser

305 310 315 320

<210> 1557
 <211> 329
 <212> PRT
 <213> Unknown (H38g474 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(329)
 <223> Xaa = Any Amino Acid

<400> 1557
 Met Lys Leu Ile Asn His Thr Asp Gln Asn Pro Thr Ser Phe Leu Leu
 1 5 10 15
 Met Gly Ile Pro Gly Pro Glu Ala Ser His Phe Trp Ile Ala Phe Pro
 20 25 30
 Phe Cys Ser Met Tyr Ala Leu Ala Val Leu Gly Asn Met Val Val Leu
 35 40 45
 Leu Val Val His Ser Glu Pro Val Leu His Gln Pro Met Tyr Leu Phe
 50 55 60
 Leu Cys Met Leu Ser Thr Ile Asp Leu Val Leu Cys Thr Ser Thr Val
 65 70 75 80
 Pro Lys Leu Leu Ala Leu Phe Trp Ala Lys Asp Ala Glu Ile Asn Phe
 85 90 95
 Gly Ala Cys Ala Ala Gln Met Phe Phe Ile His Gly Phe Ser Ala Val
 100 105 110
 Glu Ser Gly Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Leu Ala Ile
 115 120 125
 Cys Trp Pro Leu His Tyr Gly Ser Leu Leu Ser Pro Glu Ser Val Gly
 130 135 140
 Lys Leu Gly Ala Ala Ala Val Leu Arg Gly Leu Gly Leu Met Thr Pro
 145 150 155 160
 Leu Thr Cys Leu Leu Ala Arg Leu Ser Tyr Cys Ser Arg Val Val Ala
 165 170 175
 His Ser Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Gly
 180 185 190
 Thr Gln Pro Asn Asn Ile Tyr Gly Ile Thr Ala Ala Thr Leu Val Val
 195 200 205
 Gly Thr Asp Ser Ile Cys Ile Ala Val Ser Tyr Ala Leu Ile Leu Arg
 210 215 220
 Ala Val Leu Gly Leu Ser Ser Lys Glu Ala Arg Ala Lys Thr Phe Gly
 225 230 235 240
 Thr Cys Gly Ser His Leu Gly Val Ile Leu Leu Phe Tyr Thr Pro Gly
 245 250 255
 Leu Phe Ser Phe Tyr Thr Gln Arg Phe Gly Gln His Val Pro Arg His
 260 265 270
 Ile His Ile Leu Leu Ala Asp Leu Tyr Leu Val Val Pro Pro Met Leu
 275 280 285
 Asn Pro Ile Ile Tyr Gly Met Lys Thr Lys Gln Ile Trp Asp Gly Ala
 290 295 300
 Leu Arg Leu Leu Lys Trp Gly Pro Ala Gln Ser Xaa Ser Leu Gln Pro
 305 310 315 320
 His Pro Glu Thr Phe Ile Phe Phe Ala
 325

<210> 1558
 <211> 330
 <212> PRT

<213> Unknown (H38g475 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 1558

His	Thr	Glu	Pro	Arg	His	Leu	Thr	Gly	Val	Xaa	Glu	Phe	Leu	Leu	Val
1				5					10					15	
Gly	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Val	Leu	Gly	Gly	Val	Ser
		20					25						30		
Leu	Ser	Met	Tyr	Gly	Val	Thr	Val	Ile	Arg	Asn	Val	Leu	Ile	Ile	Leu
	35					40					45				
Gly	Val	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	Asn	Val	Trp	Trp	Ala	Asp	Ile	Ser	Phe	Thr	Ser	Ala	Gly	Val	Pro
65					70				75					80	
Lys	Met	Thr	Val	Asp	Met	Gln	Ser	His	Ser	Arg	Val	Ile	Tyr	Tyr	Ala
			85						90					95	
Gly	Cys	Met	Thr	Arg	Met	Ser	Phe	Phe	Val	Leu	Leu	Ala	Cys	Ile	Glu
		100					105						110		
Asp	Met	Leu	Val	Cys	Val	Met	Ala	Xaa	Glu	Cys	Phe	Val	Ala	Met	Cys
	115					120						125			
Arg	Pro	Val	Gln	Tyr	Thr	Val	Ile	Val	Asn	Pro	His	Leu	Cys	Val	Phe
	130					135					140				
Arg	Val	Gly	Val	Ser	Phe	Leu	Gln	Ser	Val	Leu	Tyr	Ser	Gln	Val	His
145					150					155				160	
Arg	Xaa	Ser	Val	Ser	Gln	Phe	Thr	Phe	Phe	Lys	Asn	Val	Glu	Ile	Ser
			165					170						175	
His	Phe	Val	Cys	Glu	Pro	Ser	Gln	Phe	Leu	His	Phe	Ala	Cys	Cys	Asp
		180						185					190		
Ser	Phe	Ile	Lys	Ser	Ile	Phe	Met	Tyr	Phe	Asp	Ser	Asn	Met	Phe	Gly
	195					200						205			
Phe	Leu	Pro	Ile	Thr	Gly	Ile	Phe	Leu	Ser	Xaa	Tyr	Lys	Ser	Val	Pro
	210					215						220			
Ser	Ile	Ile	Arg	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr	Lys	Ala	Phe	Ser
225					230					235				240	
Thr	Cys	Gly	Ser	His	Val	Ala	Val	Val	Cys	Leu	Leu	Tyr	Gly	Thr	Gly
				245					250					255	
Ile	Gly	Val	Tyr	Met	Thr	Ser	Gly	Val	Ala	Pro	Pro	Pro	Ser	Asn	Gly
		260					265						270		
Val	Val	Ala	Ser	Val	Lys	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu	Thr	Pro
		275					280						285		
Phe	Ile	Tyr	Ser	Val	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Pro	Leu	Trp	Ser
	290					295					300				
Val	Cys	Ser	Ser	Thr	Val	Lys	Ser	Phe	Asp	Val	Ser	His	Leu	Phe	Cys
305					310					315				320	
Val	Trp	Val	Arg	Lys	Gly	Thr	His	Ile	Lys						
				325					330						

<210> 1559

<211> 170

<212> PRT

<213> Unknown (H38g476 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(170)

<223> Xaa = Any Amino Acid

<400> 1559

```

His Thr Gln Pro Arg Gly Leu Thr Arg Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15
Gly Leu Ser Gln Asp Pro Gln Leu Gln Pro Val Leu Ser Gly Leu Ser
          20          25          30
Leu Cys Met Cys Leu Gly Thr Gln Leu Gly Asn Leu Leu Ile Ile Leu
          35          40          45
Gly Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Ser Phe Leu
          50          55          60
Ser Asn Leu Ser Gly Ala Asp Ile Ser Phe Thr Ser Thr Thr Gly Pro
65          70          75          80
Lys Leu Ile Val Asp Ile His Ser Tyr Thr Arg Asp Ile Ser Tyr Ala
          85          90          95
Arg Cys Leu Thr His Thr Pro Leu Phe Ala Ile Phe Gly Gly Val Glu
          100          105          110
Arg Asp Met Leu Leu Arg Val Met Gly Tyr Asp Arg Val Val Asp Ile
          115          120          125
Cys Asp Pro Leu Tyr His Ser His Ala Met Asn Pro Cys Val Cys Gly
          130          135          140
Ser Leu Asp Leu Trp Ser Leu Phe Phe Leu Thr Leu Leu Tyr Thr His
145          150          155          160
Leu His Asn Ser Ile Ala Leu His Met Thr
          165          170

```

<210> 1560

<211> 322

<212> PRT

<213> Unknown (H38g477 protein)

<220>

<223> Synthetic construct

<400> 1560

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
 1          5          10          15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
          20          25          30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
          35          40          45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
65          70          75          80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
          85          90          95
Arg Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
          100          105          110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
          130          135          140
Phe Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
          165          170          175
Phe Phe Cys Asp Leu Pro Leu Val Thr Lys Leu Ala Cys Ile Asp Thr
          180          185          190

```

Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser Gly Phe Leu Ser Leu
 195 200 205
 Ser Ser Phe Leu Leu Leu Val Val Ser Tyr Thr Val Ile L u Val Thr
 210 215 220
 Val Arg Asn Ser Ser Ser Val Ser Met Val Lys Ala Cys Ser Thr Leu
 225 230 235 240
 Thr Ala His Ile Thr Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Phe Ser Ser Tyr Ser Val Asp Lys Val Leu Ala
 260 265 270
 Val Phe Tyr Thr Ile Phe Thr Ser Ile Leu Asn Pro Val Ile Tyr Met
 275 280 285
 Leu Arg Asn Lys Glu Val Lys Ala Ala Met Ser Lys Leu Lys Ser Arg
 290 295 300
 Tyr Gln Lys Leu Gly Gln Val Ser Val Val Ile Arg Asn Val Leu Phe
 305 310 315 320
 Leu Glu

<210> 1561

<211> 314

<212> PRT

<213> Unknown (H38g478 protein)

<220>

<223> Synthetic construct

<400> 1561

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Phe Val Val Phe Ser
 20 25 30
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
 35 40 45
 Val Leu Ser Thr Ser His Leu His Ser Arg Thr Tyr Phe Leu Leu Ser
 50 55 60
 Asn Leu Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
 65 70 75 80
 Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly Cys
 85 90 95
 Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
 100 105 110
 Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
 115 120 125
 Leu Arg Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
 130 135 140
 Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
 145 150 155 160
 Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
 180 185 190
 Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Thr Ala Leu
 195 200 205
 Thr Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Thr
 210 215 220
 Ile Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser


```

                260                265                270
Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
      275                280                285
Leu Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Lys Leu Asn Ile
      290                295                300
Gln Tyr Phe Ser Leu Gly Lys Thr Ala Pro
305                310

```

<210> 1562
 <211> 198
 <212> PRT
 <213> Unknown (H38g479 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(198)
 <223> Xaa = Any Amino Acid

```

<400> 1562
Met Asn Pro Cys Leu Cys Gly Phe Arg Val Val Val Ser Phe Phe Phe
 1                5                10                15
His Ser Leu Leu Gly Ala Gln Val His Asn Leu Ser Ala Ser Gln Met
      20                25                30
Thr Cys Phe Glu Tyr Val Glu Ile His Asn Phe Leu Trp Ala Leu Ser
      35                40                45
Gln Leu Pro His Arg Ala Trp Cys Asp Thr Phe Pro Asn Asn Ile Ile
      50                55                60
Val Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ala Gly Thr
      65                70                75                80
Leu Phe Ser Xaa Tyr Glu Ser Val Ser Ser Ile Glu Arg Val Ser Ser
      85                90                95
Xaa Gly Gly Glu Tyr Lys Ala Phe Pro Thr Cys Gly Ser His Leu Ser
      100                105                110
Val Val Cys Xaa Leu Tyr Gly Thr Gly Val Gly Gly His Leu Ser Ser
      115                120                125
Asp Val Ser Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met Tyr
      130                135                140
Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Met Arg Asn
      145                150                155                160
Arg Asp Thr Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Xaa
      165                170                175
Phe Xaa Tyr Leu Leu Ile Cys Pro Ile Pro Phe Val Val Trp Val Lys
      180                185                190
Lys Gly Arg Lys Val Lys
      195

```

<210> 1563
 <211> 314
 <212> PRT
 <213> Unknown (H38g480 protein)

<220>
 <223> Synthetic construct

```

<400> 1563
Met Leu Gly Leu Asn Gly Thr Pro Phe Gln Pro Ala Thr Leu Gln Leu
 1                5                10                15
Thr Gly Ile Pro Gly Ile Gln Thr Gly Leu Thr Trp Val Ala Leu Ile
      20                25                30

```

Phe Cys Ile Leu Tyr Met Ile Ser Ile Val Gly Asn Leu Ser Ile Leu
 35 40 45
 Thr Leu Val Phe Trp Glu Pro Ala Leu His Gln Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Leu Asn Asp Leu Gly Val Ser Phe Ser Thr Leu
 65 70 75 80
 Pro Thr Val Ile Ser Thr Phe Cys Phe Asn Tyr Asn His Val Ala Phe
 85 90 95
 Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Ser Phe Met
 100 105 110
 Glu Ser Gly Ile Leu Leu Ala Met Ser Leu Asp Arg Phe Val Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg Tyr Val Thr Val Leu Thr His Asn Arg Ile Leu
 130 135 140
 Ala Met Gly Leu Gly Ile Leu Thr Lys Ser Phe Thr Thr Leu Phe Pro
 145 150 155 160
 Phe Pro Phe Val Val Lys Arg Leu Pro Phe Cys Lys Gly Asn Val Leu
 165 170 175
 His His Ser Tyr Cys Leu His Pro Asp Leu Met Lys Val Ala Cys Gly
 180 185 190
 Asp Ile His Val Asn Asn Ile Tyr Gly Leu Leu Val Ile Ile Phe Thr
 195 200 205
 Tyr Gly Met Asp Ser Thr Phe Ile Leu Leu Ser Tyr Ala Leu Ile Leu
 210 215 220
 Arg Ala Met Leu Val Ile Ile Ser Gln Glu Gln Arg Leu Lys Ala Leu
 225 230 235 240
 Asn Thr Cys Met Ser His Ile Cys Ala Val Leu Ala Phe Tyr Val Pro
 245 250 255
 Ile Ile Ala Val Ser Met Ile His Arg Phe Trp Lys Ser Ala Pro Pro
 260 265 270
 Val Val His Val Met Met Ser Asn Val Tyr Leu Phe Val Pro Pro Met
 275 280 285
 Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Glu Ile Arg Lys Gly
 290 295 300
 Ile Leu Lys Phe Phe His Lys Ser Gln Ala
 305 310

<210> 1564

<211> 312

<212> PRT

<213> Unknown (H38g481 protein)

<220>

<223> Synthetic construct

<400> 1564

Met Gly Leu Phe Asn Val Thr His Pro Ala Phe Phe Leu Leu Thr Gly
 1 5 10 15
 Ile Pro Gly Leu Glu Ser Ser His Ser Trp Leu Ser Gly Pro Leu Cys
 20 25 30
 Val Met Tyr Ala Val Ala Leu Gly Gly Asn Thr Val Ile Leu Gln Ala
 35 40 45
 Val Arg Val Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Met Leu Ser Phe Ser Asp Val Ala Ile Ser Met Ala Thr Leu Pro Thr
 65 70 75 80
 Val Leu Arg Thr Phe Cys Leu Asn Ala Arg Asn Ile Thr Phe Asp Ala
 85 90 95
 Cys Leu Ile Gln Met Phe Leu Ile His Phe Phe Ser Met Met Glu Ser
 100 105 110
 Gly Ile Leu Leu Ala Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Asp

```

      115              120              125
Pro Leu Arg Tyr Ala Thr Val Leu Thr Thr Glu Val Ile Ala Ala Met
      130              135              140
Gly Leu Gly Ala Ala Ala Arg Ser Phe Ile Thr Leu Phe Pro Leu Pro
145              150              155              160
Phe Leu Ile Lys Arg Leu Pro Ile Cys Arg Ser Asn Val Leu Ser His
      165              170              175
Ser Tyr Cys Leu His Pro Asp Met Met Arg Leu Ala Cys Ala Asp Ile
      180              185              190
Ser Ile Asn Ser Ile Tyr Gly Leu Phe Val Leu Val Ser Thr Phe Gly
      195              200              205
Met Asp Leu Phe Phe Ile Phe Leu Ser Tyr Val Leu Ile Leu Arg Ser
210              215              220
Val Met Ala Thr Ala Ser Arg Glu Glu Arg Leu Lys Ala Leu Asn Thr
225              230              235              240
Cys Val Ser His Ile Leu Ala Val Leu Ala Phe Tyr Val Pro Met Ile
      245              250              255
Gly Val Ser Thr Val His Arg Phe Gly Lys His Val Pro Cys Tyr Ile
      260              265              270
His Val Leu Met Ser Asn Val Tyr Leu Phe Val Pro Pro Val Leu Asn
275              280              285
Pro Leu Ile Tyr Ser Ala Lys Thr Lys Glu Ile Arg Arg Ala Ile Phe
290              295              300
Arg Met Phe His His Ile Lys Ile
305              310

```

<210> 1565

<211> 156

<212> PRT

<213> Unknown (H38g482 protein)

<220>

<223> Synthetic construct

<400> 1565

```

Met Glu Ser Asn Gln Thr Trp Ile Thr Glu Val Ile Leu Leu Gly Phe
  1              5              10              15
Gln Val Asp Pro Ala Leu Glu Leu Phe Leu Phe Gly Phe Phe Leu Leu
      20              25              30
Phe Tyr Ser Leu Thr Leu Met Gly Asn Gly Ile Ile Leu Gly Leu Ile
      35              40              45
Tyr Leu Asp Ser Arg Leu His Thr Pro Met Tyr Val Phe Leu Ser His
      50              55              60
Leu Ala Ile Val Asp Met Ser Tyr Ala Ser Ser Thr Val Pro Lys Met
      65              70              75              80
Leu Ala Asn Leu Val Met His Lys Lys Val Ile Ser Phe Ala Pro Cys
      85              90              95
Ile Leu Gln Thr Phe Leu Tyr Leu Ala Phe Ala Ile Thr Glu Cys Leu
      100              105              110
Ile Leu Val Met Met Cys Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
      115              120              125
Leu Ala Tyr Thr Pro Ile Ile Met Asn Trp Arg Val Cys Thr Val Leu
      130              135              140
Ala Ser Thr Cys Trp Ile Phe Ser Phe Leu Leu Ala
145              150              155

```

<210> 1566

<211> 329

<212> PRT

<213> Unknown (H38g483 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1566

```

Met Glu Cys Asn Gln Thr Trp Ile Thr Asp Ile Thr Leu Leu Gly Phe
 1           5           10           15
Gln Val Gly Pro Ala Leu Ala Ile Leu Ile Tyr Glu Leu Phe Ser Val
 20           25           30
Phe Tyr Thr Leu Thr Leu Leu Gly Asn Gly Val Ile Phe Gly Ile Ile
 35           40           45
Cys Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
 50           55           60
Leu Ala Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met
 65           70           75           80
Leu Ala Asn Leu Met Asn Gln Lys Arg Thr Ile Ser Phe Val Pro Cys
 85           90           95
Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Glu Cys Leu
100           105           110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
115           120           125
Phe Gln Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Val
130           135           140
Leu Thr Ser Trp Ser Cys Gly Phe Ala Leu Ser Leu Val His Glu Ile
145           150           155           160
Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Arg Asp Val Asn His Leu
165           170           175
Phe Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp
180           185           190
Val Asn Gln Val Val Ile Phe Ala Thr Cys Val Phe Val Leu Val Gly
195           200           205
Pro Leu Ser Leu Ile Leu Val Ser Tyr Met His Ile Leu Gly Ala Ile
210           215           220
Leu Lys Ile Gln Thr Lys Glu Gly Arg Ile Lys Ala Phe Ser Thr Cys
225           230           235           240
Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ile Ala Met Val
245           250           255
Val Tyr Met Val Pro Asp Ser Asn Gln Arg Glu Glu Gln Glu Lys Met
260           265           270
Leu Ser Leu Phe His Ser Val Leu Asn Pro Met Leu Asn Pro Leu Ile
275           280           285
Tyr Ser Leu Arg Asn Ala Gln Leu Lys Gly Ala Leu His Arg Ala Leu
290           295           300
Gln Arg Lys Arg Ser Met Arg Thr Val Tyr Gly Leu Cys Leu Xaa Asn
305           310           315           320
Met Trp Phe Ala Glu Ala Arg Ile Leu
325

```

<210> 1567

<211> 313

<212> PRT

<213> Unknown (H38g484 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1567

```

Met Gly Val Asn Gln Ser Trp Ser Pro Glu Phe Ile Leu Val Glu Ser
 1          5          10          15
Gln Leu Ser Ala Glu Met Glu Val Leu Leu Phe Xaa Ile Phe Ser Leu
 20          25          30
Leu Tyr Ile Phe Ser Leu Leu Ala Asn Gly Met Ile Leu Gly Leu Ile
 35          40          45
Cys Leu Asp His Ile Leu Pro Thr Pro Met Tyr Phe Phe Leu Ser His
 50          55          60
Leu Ala Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met
 65          70          75          80
Leu Ala Asn Leu Met Asn Lys Lys Arg Thr Ile Ser Phe Leu Pro Cys
 85          90          95
Ile Met Gln Thr Tyr Leu Tyr Phe Ser Phe Ala Ala Thr Glu Cys Leu
100          105          110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
115          120          125
Leu Gln Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Ala
130          135          140
Leu Thr Ser Trp Ser Cys Gly Phe Ala Leu Ser Leu Val His Ala Ile
145          150          155          160
Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Arg Asp Val Asn His Leu
165          170          175
Phe Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ser Asp Thr Trp
180          185          190
Val Asn Gln Val Val Ile Phe Ala Thr Cys Val Phe Val Leu Val Gly
195          200          205
Pro Leu Cys Leu Met Leu Val Ser Tyr Met His Ile Leu Leu Ala Ile
210          215          220
Leu Lys Ile Gln Thr Lys Glu Gly Arg Ile Lys Ala Phe Ser Thr Cys
225          230          235          240
Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ile Ala Met Val
245          250          255
Val Tyr Ile Val Pro Asp Ser Asn Gln Arg Glu Glu Gln Glu Lys Met
260          265          270
Leu Ser Leu Phe His Ser Val Leu Asn Pro Ile Leu Asn Pro Leu Ile
275          280          285
Tyr Ser Leu Arg Asn Ala Gln Val Lys Gly Ala Leu His Arg Ala Leu
290          295          300
Gln Arg Thr Leu Ser Met Xaa Gly Val
305          310

```

<210> 1568

<211> 334

<212> PRT

<213> Unknown (H38g485 protein)

<220>

<223> Synthetic construct

<400> 1568

```

Met Cys Tyr Leu Ser Gln Leu Cys Leu Ser Leu Gly Glu His Thr Leu
 1          5          10          15
His Met Gly Met Val Arg His Thr Asn Glu Ser Asn Leu Ala Gly Phe
 20          25          30
Ile Leu Leu Gly Phe Ser Asp Tyr Pro Gln Leu Gln Lys Val Leu Phe
 35          40          45
Val Leu Ile Leu Ile Leu Tyr Leu Leu Thr Ile Leu Gly Asn Thr Thr
 50          55          60

```

```

Ile Ile Leu Val Ser Arg Leu Glu Pro Lys Leu His Met Pro Met Tyr
65          70          75          80
Phe Phe Leu Ser His Leu Ser Phe Leu Tyr Arg Cys Phe Thr Ser Ser
          85          90          95
Val Ile Pro Gln Leu Leu Val Asn Leu Trp Glu Pro Met Lys Thr Ile
          100          105          110
Ala Tyr Gly Gly Cys Leu Val His Leu Tyr Asn Ser His Ala Leu Gly
          115          120          125
Ser Thr Glu Cys Val Leu Pro Ala Val Met Ser Cys Asp Arg Tyr Val
          130          135          140
Ala Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Ile His Leu
145          150          155          160
Cys Met Ala Leu Ala Ser Met Ala Trp Leu Ser Gly Ile Ala Thr Thr
          165          170          175
Leu Val Gln Ser Thr Leu Thr Leu Gln Leu Pro Phe Cys Gly His Arg
          180          185          190
Gln Val Asp His Phe Ile Cys Glu Val Pro Val Leu Ile Lys Leu Ala
          195          200          205
Cys Val Gly Thr Thr Phe Asn Glu Ala Glu Leu Phe Val Ala Ser Ile
          210          215          220
Leu Phe Leu Ile Val Pro Val Ser Phe Ile Leu Val Ser Ser Gly Tyr
225          230          235          240
Ile Ala His Ala Val Leu Arg Ile Lys Ser Ala Thr Arg Arg Gln Lys
          245          250          255
Ala Phe Gly Thr Cys Phe Ser His Leu Thr Val Val Thr Ile Phe Tyr
          260          265          270
Gly Thr Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Arg Ser Arg
          275          280          285
Asp Gln Gly Lys Phe Val Ser Leu Phe Tyr Thr Val Val Thr Arg Met
          290          295          300
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Ile Lys Glu Val Lys Gly Ala
305          310          315          320
Leu Lys Lys Val Leu Ala Lys Ala Leu Gly Val Asn Ile Leu
          325          330

```

<210> 1569

<211> 170

<212> PRT

<213> Unknown (H38g486 protein)

<220>

<223> Synthetic construct

<400> 1569

```

Met Glu Gly Asn Lys Thr Trp Ile Thr Asp Ile Thr Leu Pro Arg Phe
1          5          10          15
Gln Val Gly Pro Ala Leu Glu Ile Leu Leu Cys Gly Leu Phe Ser Ala
          20          25          30
Phe Tyr Thr Leu Thr Leu Leu Gly Asn Gly Val Ile Phe Gly Ile Ile
          35          40          45
Cys Leu Asp Cys Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
          50          55          60
Leu Ala Ile Val Asp Ile Ser Tyr Ala Ser Asn Tyr Val Pro Lys Met
65          70          75          80
Leu Thr Asn Leu Met Asn Gln Glu Ser Thr Ile Ser Phe Phe Pro Cys
          85          90          95
Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala His Val Glu Cys Leu
          100          105          110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Asp Ile Cys His Pro
          115          120          125
Leu Arg Tyr Asn Ile Leu Met Ser Trp Arg Val Cys Thr Val Leu Ala

```

130	135	140
Val Ala Ser Trp Val Phe Ser Phe Leu Leu Ala Leu Val Pro Phe Ser		
145	150	155
Ser Gln Ser Leu Arg Cys Met Asn Val Leu		160
165	170	

<210> 1570

<211> 308

<212> PRT

<213> Unknown (H38g487 protein)

<220>

<223> Synthetic construct

<400> 1570

Met Asp Thr Gly Asn Lys Thr Leu Pro Gln Asp Phe Leu Leu Leu Gly		
1	5	10
Phe Pro Gly Ser Gln Thr Leu Gln Leu Ser Leu Phe Met Leu Phe Leu		15
20	25	30
Val Met Tyr Ile Leu Thr Val Ser Gly Asn Val Ala Ile Leu Met Leu		35
35	40	45
Val Ser Thr Ser His Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser		50
50	55	60
Asn Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Ala Val Pro Lys		65
65	70	75
Ala Leu Ala Ile Leu Leu Gly Arg Ser Gln Thr Ile Ser Phe Thr Ser		80
85	90	95
Cys Leu Leu Gln Met Tyr Phe Val Phe Ser Leu Gly Cys Thr Glu Tyr		100
100	105	110
Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Cys Leu Ala Ile Cys Tyr		115
115	120	125
Pro Leu His Tyr Gly Ala Ile Met Ser Ser Leu Leu Ser Ala Gln Leu		130
130	135	140
Ala Leu Gly Ser Trp Val Cys Gly Phe Val Ala Ile Ala Val Pro Thr		145
145	150	155
Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro Arg Ala Ile Asn His		160
165	170	175
Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu Ala Cys Thr Asn Thr		180
180	185	190
Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala Val Val Ile Leu		195
195	200	205
Ser Ser Cys Leu Ile Thr Phe Val Ser Tyr Val Tyr Ile Ile Ser Thr		210
210	215	220
Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser Lys Ala Phe Ser Thr		225
225	230	235
Cys Ser Ser His Leu Thr Val Val Leu Ile Trp Tyr Gly Ser Thr Val		240
245	250	255
Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala Leu Asp Leu Ile Lys		260
260	265	270
Ala Val His Val Leu Asn Thr Val Val Thr Pro Val Leu Asn Pro Phe		275
275	280	285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Glu Thr Leu Leu Lys Lys		290
290	295	300
Trp Lys Gly Lys		
305		

<210> 1571

<211> 223

<212> PRT

<213> Unknown (H38g488 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(223)

<223> Xaa = Any Amino Acid

<400> 1571

```

Lys Glu Met Gly Cys His Gln Ser Met Val Thr Glu Phe Ile Leu Val
 1           5           10           15
Gly Phe Gln Leu Ser Ala Glu Met Glu Val Leu Leu Phe Trp Ser Phe
           20           25           30
Ser Leu Gly Ile Ala Leu Glu Leu Ile Cys Leu Asp His Ser Leu His
 35           40           45
Thr Pro Tyr Phe Phe Leu Ser His Leu Ala Val Ile Asp Met Ala Tyr
 50           55           60
Ala Ser Asn Asn Val Pro Lys Met Leu Val Asp Leu Ala Asn Xaa Lys
 65           70           75           80
Ser Thr Met Cys Phe Phe Pro Cys Ile Met Gln Thr Phe Leu Tyr Leu
           85           90           95
Ala Phe Ala His Ile Glu Cys Leu Ile Leu Val Val Leu Ser Tyr Asp
           100          105          110
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Asn Val Leu Met Ser
 115          120          125
Trp Arg Glu Cys Thr Val Leu Ala Val Ala Ser Trp Val Phe Ser Phe
 130          135          140
Leu Leu Ala Leu Val His Leu Val Leu Ile Leu Arg Leu Pro Phe Ser
 145          150          155          160
Gly Pro His Glu Ile Asn His Tyr Cys Glu Ile Leu Ser Val Leu Lys
           165          170          175
Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val Ile Phe Ala Ser
           180          185          190
Cys Met Phe Ile Leu Val Gly Xaa Leu Cys Leu Val Leu Val Ser Tyr
 195          200          205
Leu Gly Ile Trp Arg His Leu Arg Ser Val Ala Lys Pro Lys Arg
 210          215          220

```

<210> 1572

<211> 309

<212> PRT

<213> Unknown (H38g489 protein)

<220>

<223> Synthetic construct

<400> 1572

```

Met Gly Leu Gly Asn Glu Ser Ser Leu Met Asp Phe Ile Leu Leu Gly
 1           5           10           15
Phe Ser Asp His Pro Arg Leu Glu Ala Val Leu Phe Val Phe Val Leu
           20           25           30
Phe Phe Tyr Leu Leu Thr Leu Val Gly Asn Phe Thr Ile Ile Ile Ile
 35           40           45
Ser Tyr Leu Asp Pro Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50           55           60
Asn Leu Ser Leu Leu Asp Ile Cys Phe Thr Thr Ser Leu Ala Pro Gln
 65           70           75           80
Thr Leu Val Asn Leu Gln Arg Pro Lys Lys Thr Ile Thr Tyr Gly Gly
           85           90           95
Cys Val Ala Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys
           100          105          110
Ile Leu Leu Ala Asp Met Ala Leu Asp Arg Tyr Ile Ala Val Cys Lys

```



```

      115      120      125
Pro Leu His Tyr Val Val Ile Met Asn Pro Arg Leu Cys Gln Gln Leu
  130      135      140
Ala Ser Ile Ser Trp Leu Ser Gly Leu Ala Ser Ser Leu Ile His Ala
 145      150      155      160
Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly Asn His Arg Leu Asp His
      165      170      175
Phe Ile Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Val Asp Thr
      180      185      190
Thr Val Asn Glu Leu Val Leu Phe Val Val Ser Val Leu Phe Val Val
      195      200      205
Ile Pro Pro Ala Leu Ile Ser Ile Ser Tyr Gly Phe Ile Thr Gln Ala
      210      215      220
Val Leu Arg Ile Lys Ser Val Glu Ala Arg His Lys Ala Phe Ser Thr
 225      230      235      240
Cys Ser Ser His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Ile
      245      250      255
Tyr Val Tyr Leu Gln Pro Ser Asp Ser Tyr Ala Gln Asp Gln Gly Lys
      260      265      270
Phe Ile Ser Leu Phe Tyr Thr Met Val Thr Pro Thr Leu Asn Pro Ile
      275      280      285
Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Arg Lys Leu
      290      295      300
Leu Ser Gly Lys Leu
305

```

<210> 1573

<211> 337

<212> PRT

<213> Unknown (H38g490 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(337)

<223> Xaa = Any Amino Acid

<400> 1573

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Val Phe Leu Leu Leu
 1      5      10      15
Gly Thr Thr Glu Asp Pro Glu Arg Gln Pro Val Leu Thr Gly Leu Phe
      20      25      30
Leu Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Ile Ser Pro Asp Ser His Leu His Ile Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
      100      105      110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
      115      120      125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
      130      135      140
Phe Leu Val Leu Leu Ser Phe Phe Ser Val Leu Ser Leu Leu Asp Ser
 145      150      155      160
Gln Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val
      165      170      175

```

Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
 180 185 190
 Cys Cys Asp Thr Phe Thr Asn Lys Ile Ile Met Tyr Phe Pro Ala Ala
 195 200 205
 Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys
 210 215 220
 Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Val Tyr
 245 250 255
 Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Asp Val Ser Ser Ser
 260 265 270
 Pro Arg Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
 275 280 285
 Met Pro Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser
 290 295 300
 Val Leu Arg Arg Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Leu
 305 310 315 320
 Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Arg Lys Val
 325 330 335
 Lys

<210> 1574

<211> 293

<212> PRT

<213> Unknown (H38g491 protein)

<220>

<223> Synthetic construct

<400> 1574

Met Gly Phe Ser Asn Ser Trp Asp Ile Gln Ile Val His Ala Ala Leu
 1 5 10 15
 Phe Phe Leu Val Tyr Leu Ala Ala Val Ile Gly Asn Leu Leu Ile Ile
 20 25 30
 Ile Leu Thr Thr Leu Asp Val His Leu Gln Thr Pro Met Tyr Phe Phe
 35 40 45
 Leu Arg Asn Leu Ser Phe Leu Asp Phe Cys Tyr Ile Ser Val Thr Ile
 50 55 60
 Pro Lys Ser Ile Val Ser Ser Leu Thr His Asp Thr Ser Ile Ser Phe
 65 70 75 80
 Phe Gly Cys Ala Leu Gln Ala Phe Phe Phe Met Asp Leu Ala Thr Thr
 85 90 95
 Glu Val Ala Ile Leu Thr Val Met Ser Tyr Asp Arg Tyr Met Ala Ile
 100 105 110
 Cys Arg Pro Leu His Tyr Glu Val Ile Ile Asn Gln Gly Val Cys Leu
 115 120 125
 Arg Met Met Ala Met Ser Trp Leu Ser Gly Val Ile Cys Gly Phe Met
 130 135 140
 His Val Ile Ala Thr Phe Ser Leu Pro Phe Cys Gly Arg Asn Arg Ile
 145 150 155 160
 Arg Gln Phe Phe Cys Asn Ile Pro Gln Leu Leu Ser Leu Leu Asp Pro
 165 170 175
 Lys Val Ile Thr Ile Glu Ile Gly Val Met Val Phe Gly Thr Ser Leu
 180 185 190
 Val Ile Ile Ser Phe Val Val Ile Thr Leu Ser Tyr Met Tyr Ile Phe
 195 200 205
 Ser Val Ile Met Arg Ile Pro Ser Lys Glu Gly Arg Ser Lys Thr Phe
 210 215 220
 Ser Thr Cys Ile Pro His Leu Val Val Val Thr Leu Phe Met Ile Ser

<210> 1575
<211> 341
<212> PRT
<213> Unknown (H38g492 protein)

<220>
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(341)
<223> Xaa = Any Amino Acid
```

838

Tyr Ala Gln Lys Xaa Leu Ser Ala Gln Lys Asn Glu Xaa Glu Asn Ser
 305 310 315 320
 Xaa Met Cys Val Leu Ser Ile Ser Met Leu Asn Ala Xaa Arg Ile Leu
 325 330 335
 Met Arg Trp Phe Pro
 340

<210> 1576
 <211> 311
 <212> PRT
 <213> Unknown (H38g493 protein)

<220>
 <223> Synthetic construct

<400> 1576
 Met Lys Trp Ala Asn Gln Thr Ala Val Thr Glu Tyr Val Leu Met Gly
 1 5 10 15
 Leu His Glu His Cys Asn Leu Glu Val Val Leu Phe Val Phe Cys Leu
 20 25 30
 Gly Ile Tyr Ser Val Asn Val Leu Gly Asn Ala Leu Leu Ile Gly Leu
 35 40 45
 Asn Val Leu His Pro Arg Leu His Asn Pro Met Tyr Phe Phe Ser Asn
 50 55 60
 Leu Ser Leu Met Asp Ile Cys Gly Thr Ser Ser Phe Val Pro Leu Met
 65 70 75 80
 Leu Asp Asn Phe Leu Glu Thr Gln Arg Thr Ile Ser Phe Pro Gly Cys
 85 90 95
 Ala Leu Gln Met Tyr Leu Thr Leu Ala Leu Gly Ser Thr Glu Cys Leu
 100 105 110
 Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Pro
 115 120 125
 Leu Arg Tyr Pro Glu Leu Met Ser Gly Gln Thr Cys Met Gln Met Ala
 130 135 140
 Ala Leu Ser Trp Gly Thr Gly Phe Ala Asn Ser Leu Leu Gln Ser Ile
 145 150 155 160
 Leu Val Trp His Leu Pro Phe Cys Gly His Val Ile Asn Tyr Phe Tyr
 165 170 175
 Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Gly Asp Ile Ser Leu Asn
 180 185 190
 Ala Leu Ala Leu Met Val Ala Thr Ala Val Leu Thr Leu Ala Pro Leu
 195 200 205
 Leu Leu Ile Cys Leu Ser Tyr Leu Phe Ile Leu Ser Ala Ile Leu Arg
 210 215 220
 Val Pro Ser Ala Ala Gly Arg Cys Lys Ala Phe Ser Thr Cys Ser Ala
 225 230 235 240
 His Arg Thr Val Val Val Phe Tyr Gly Thr Ile Ser Phe Met Tyr
 245 250 255
 Phe Lys Pro Lys Ala Lys Asp Pro Asn Val Asp Lys Thr Val Ala Leu
 260 265 270
 Phe Tyr Gly Val Val Thr Pro Ser Leu Asn Pro Ile Ile Tyr Ser Leu
 275 280 285
 Arg Asn Ala Glu Val Lys Ala Ala Val Leu Thr Leu Leu Arg Gly Gly
 290 295 300
 Leu Leu Ser Arg Lys Ala Ser
 305 310

<210> 1577
 <211> 319
 <212> PRT
 <213> Unknown (H38g494 protein)

<220>

<223> Synthetic construct

<400> 1577

```

Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
 1          5          10          15
Gly Phe Ser Thr Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
          20          25          30
Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu
          35          40          45
Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ala Asn Leu Pro Phe Leu Asp Met Ser Phe Thr Ser Ile Val Pro
65          70          75          80
Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
          85          90          95
Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
          100          105          110
Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys
          115          120          125
Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly
          130          135          140
Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly
145          150          155          160
Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp
          165          170          175
His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp
          180          185          190
Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val
          195          200          205
Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg
          210          215          220
Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn
225          230          235          240
Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile
          245          250          255
Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly
          260          265          270
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro
          275          280          285
Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His
          290          295          300
Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln
305          310          315

```

<210> 1578

<211> 264

<212> PRT

<213> Unknown (H38g495 protein)

<220>

<223> Synthetic construct

<400> 1578

```

Met Met Val Leu Ser Ile Val Leu Thr Ser Leu Phe Gly Asn Ser Leu
 1          5          10          15
Met Ile L u Leu Ile His Trp Asp His Arg Phe His Thr Pro Met Tyr
          20          25          30
Phe Leu Leu Ser Gln Leu Ser Leu Met Asp Val Met Leu Val Ser Thr
          35          40          45

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```

Thr Val Pro Lys Met Ala Ala Asp Tyr Leu Thr Gly Ser Lys Ala Ile
 50          55          60
Ser Arg Ala Gly Cys Gly Ala Gln Ile Phe Phe Leu Pro Thr Leu Gly
65          70          75          80
Gly Gly Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala
          85          90          95
Ala Val Cys His Pro Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln Leu
          100          105          110
Cys Leu Arg Met Asn Leu Ser Cys Trp Leu Leu Gly Ala Ala Asp Gly
          115          120          125
Leu Leu Gln Ala Val Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala His
130          135          140
Glu Ile Asp His Phe Phe Cys Glu Thr Pro Val Leu Val Arg Leu Ala
145          150          155          160
Cys Ala Asp Thr Ser Val Phe Glu Asn Ala Met Tyr Ile Cys Cys Val
          165          170          175
Leu Met Leu Leu Val Pro Phe Ser Leu Ile Leu Ser Ser Tyr Gly Leu
          180          185          190
Ile Leu Ala Ala Val Leu His Met Arg Ser Thr Glu Ala Arg Lys Lys
          195          200          205
Ala Phe Ala Thr Cys Ser Ser His Val Ala Val Val Gly Leu Phe Tyr
210          215          220
Gly Ala Ala Ile Phe Thr Tyr Met Arg Pro Lys Ser His Arg Ser Thr
225          230          235          240
Asn His Asp Lys Val Val Ser Ala Phe Tyr Thr Met Phe Thr Pro Leu
          245          250          255
Leu Asn Pro Leu Ile Tyr Ser Val
          260

```

<210> 1579

<211> 220

<212> PRT

<213> Unknown (H38g496 protein)

<220>

<223> Synthetic construct

<400> 1579

```

Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ala Ser Ile Ala Pro Gln
 1          5          10          15
Leu Leu Trp Asn Leu Gly Gly Pro Glu Lys Thr Ile Thr Tyr His Gly
          20          25          30
Cys Val Ala Gln Leu Tyr Ile Tyr Met Met Leu Gly Ser Thr Glu Cys
          35          40          45
Val Leu Leu Val Val Met Ser His Asp Arg Tyr Val Ala Val Cys Arg
50          55          60
Ser Leu His Tyr Met Ala Val Met Arg Pro His Leu Cys Leu Gln Leu
65          70          75          80
Val Thr Val Ala Trp Cys Cys Gly Phe Leu Asn Ser Phe Ile Met Cys
          85          90          95
Pro Gln Thr Met Gln Leu Ser Arg Cys Gly Arg Arg Arg Val Asp His
          100          105          110
Phe Leu Cys Glu Met Pro Ala Leu Ile Ala Met Ser Cys Glu Glu Thr
          115          120          125
Met Leu Val Glu Ala Ile Thr Phe Ala Leu Gly Val Ala Leu Leu Leu
130          135          140
Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr Gly Val Ile Ala Ala Ala
145          150          155          160
Val Leu Arg Met Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe His Thr
          165          170          175
Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ile Ile

```

```
<210> 1581
<211> 314
<212> PRT
<213> Unknown (H38g498 protein)
```

<220>

<223> Synthetic construct

<400> 1581

```

Met Glu Arg Gly Asn Trp Thr Leu Val Thr Glu Phe Ile Leu Val Gly
 1           5           10           15
Ile Pro Thr Thr Arg Ala Leu Gly Gly Leu Leu Phe Val Ile Phe Tyr
           20           25           30
Pro Ala Tyr Leu Val Thr Val Leu Gly Asn Thr Leu Ile Ile Ile Leu
 35           40           45
Ile Leu Val Asp Tyr Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser
 50           55           60
Asn Leu Ser Phe Ser Glu Thr Leu Thr Ile Thr Cys Ala Val Pro Lys
 65           70           75           80
Met Leu Glu Gly Phe Pro Ser Glu Arg Lys Ser Ile Thr Ser Gly Glu
           85           90           95
Cys Ser Ala Gln Ser Tyr Phe Tyr Phe Leu Ser Gly Cys Thr Glu Phe
           100           105           110
Ile Pro Phe Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Ser
 115           120           125
Pro Leu Gln Tyr Pro Ala Ile Met Thr Ser Ser Leu Cys Ala His Leu
 130           135           140
Val Ile Leu Ser Trp Val Gly Gly Phe Leu Leu Met Leu Pro Ser Thr
 145           150           155           160
Ile Leu Lys Ala Gly Leu Pro His Cys Gly Pro Asn Val Ile Glu His
           165           170           175
Phe Phe Cys Asp Ser Ala Pro Leu Leu His Leu Ala Cys Ala Asp Ile
 180           185           190
Arg Ala Ile Glu Leu Leu Asp Phe Leu Ser Ser Leu Val Leu Ile Leu
 195           200           205
Ser Ser Leu Ser Leu Thr Val Val Ser Tyr Val Tyr Ile Ile Ser Thr
 210           215           220
Ile Leu Lys Ile Pro Ser Gly Gln Gly Gln Arg Lys Ala Phe Ala Thr
 225           230           235           240
Cys Ala Ser His Phe Thr Val Val Ser Val Gly Tyr Gly Ile Ser Ile
           245           250           255
Phe Val Tyr Val His Pro Ser Gln Lys Ser Ser Leu His Leu Asn Lys
 260           265           270
Ile Leu Phe Ile Leu Ser Ser Ile Ile Thr Pro Leu Leu Asn Pro Phe
 275           280           285
Val Phe Ser Leu Trp Asn Glu Pro Met Lys Asp Ala Leu Lys Asp Ala
 290           295           300
Val Gly Arg Arg Thr Glu Leu Ala Gln Arg
 305           310

```

<210> 1582

<211> 309

<212> PRT

<213> Unknown (H38g499 protein)

<220>

<223> Synthetic construct

<400> 1582

```

Met Ala Asn Leu Thr Ile Val Thr Glu Phe Ile Leu Met Gly Phe Ser
 1           5           10           15
Thr Asn Lys Asn Met Cys Ile Leu His Ser Ile Leu Phe Leu Leu Ile
           20           25           30
Tyr Leu Cys Ala Leu Met Gly Asn Val Leu Ile Ile Met Ile Thr Thr
 35           40           45
Leu Asp His His Leu His Thr Pro Val Tyr Phe Phe Leu Lys Asn Leu

```


50 55 60
 Ser Phe Leu Asp Leu Cys Leu Ile Ser Val Thr Ala Pro Lys Ser Ile
 65 70 75 80
 Ala Asn Ser Leu Ile His Asn Asn Ser Ile Ser Phe Leu Gly Cys Val
 85 90 95
 Ser Gln Val Phe Leu Leu Leu Ser Ser Ala Ser Ala Glu Leu Leu Leu
 100 105 110
 Leu Thr Val Met Ser Phe Asp Arg Tyr Thr Ala Ile Cys His Pro Leu
 115 120 125
 His Tyr Asp Val Ile Met Asp Arg Ser Thr Cys Val Gln Arg Ala Thr
 130 135 140
 Val Ser Trp Leu Tyr Gly Gly Leu Ile Ala Val Met His Thr Ala Gly
 145 150 155 160
 Thr Phe Ser Leu Ser Tyr Cys Gly Ser Asn Met Val His Gln Phe Phe
 165 170 175
 Cys Asp Ile Pro Gln Leu Leu Ala Ile Ser Cys Ser Glu Asn Leu Ile
 180 185 190
 Arg Glu Ile Ala Leu Ile Leu Ile Asn Val Val Leu Asp Phe Cys Cys
 195 200 205
 Phe Ile Val Ile Ile Ile Thr Tyr Val His Val Phe Ser Thr Val Lys
 210 215 220
 Lys Ile Pro Ser Thr Glu Gly Gln Ser Lys Ala Tyr Ser Ile Cys Leu
 225 230 235 240
 Pro His Leu Leu Val Val Leu Phe Leu Ser Thr Gly Phe Ile Ala Tyr
 245 250 255
 Leu Lys Pro Ala Ser Glu Ser Pro Ser Ile Leu Asp Ala Val Ile Ser
 260 265 270
 Val Phe Tyr Thr Met Leu Pro Pro Thr Phe Asn Pro Ile Ile Tyr Ser
 275 280 285
 Leu Arg Asn Lys Ala Ile Lys Val Ala Leu Gly Met Leu Ile Lys Gly
 290 295 300
 Lys Leu Thr Lys Lys
 305

<210> 1583

<211> 314

<212> PRT

<213> Unknown (H38g500 protein)

<220>

<223> Synthetic construct

<400> 1583

Met Gly Asp Val Asn Gln Ser Val Ala Ser Asp Phe Ile Leu Val Gly
 1 5 10 15
 Leu Phe Ser His Ser Gly Ser Arg Gln Leu Leu Phe Ser Leu Val Ala
 20 25 30
 Val Met Phe Val Ile Gly Leu Leu Gly Asn Thr Val Leu Leu Phe Leu
 35 40 45
 Ile Arg Val Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Gln Leu Ser Leu Phe Asp Ile Gly Cys Pro Met Val Thr Ile Pro Lys
 65 70 75 80
 Met Ala Ser Asp Phe Leu Arg Gly Glu Gly Ala Thr Ser Tyr Gly Gly
 85 90 95
 Gly Ala Ala Gln Ile Phe Phe Leu Thr Leu Met Gly Val Ala Glu Gly
 100 105 110
 Val Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Gln
 115 120 125
 Pro Leu Gln Tyr Pro Val Leu Met Arg Arg Gln Val Cys Leu Leu Met
 130 135 140

Met Gly Ser Ser Trp Val Val Gly Val Leu Asn Ala Ser Ile Gln Thr
 145 150 155 160
 Ser Ile Thr Leu His Phe Pro Tyr Cys Ala Ser Arg Ile Val Asp His
 165 170 175
 Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
 180 185 190
 Cys Ala Tyr Glu Met Ala Leu Ser Thr Ser Gly Val Leu Ile Leu Met
 195 200 205
 Leu Pro Leu Ser Leu Ile Ala Thr Ser Tyr Gly His Val Leu Gln Ala
 210 215 220
 Val Leu Ser Met Arg Ser Glu Glu Ala Arg His Lys Ala Val Thr Thr
 225 230 235 240
 Cys Ser Ser His Ile Thr Val Val Gly Leu Phe Tyr Gly Ala Ala Val
 245 250 255
 Phe Met Tyr Met Val Pro Cys Ala Tyr His Ser Pro Gln Gln Asp Asn
 260 265 270
 Val Val Ser Leu Phe Tyr Ser Leu Val Thr Pro Thr Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Pro Glu Val Trp Met Ala Leu Val Lys Val
 290 295 300
 Leu Ser Arg Ala Gly Leu Arg Gln Met Cys
 305 310

<210> 1584

<211> 312

<212> PRT

<213> Unknown (H38g501 protein)

<220>

<223> Synthetic construct

<400> 1584

Met Asp Leu Lys Asn Gly Ser Leu Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Phe Gly Arg Trp Glu Leu Gln Ile Phe Phe Phe Val Thr Phe Ser
 20 25 30
 Leu Ile Tyr Gly Ala Thr Val Met Gly Asn Ile Leu Ile Met Val Thr
 35 40 45
 Val Thr Cys Arg Ser Thr Leu His Ser Pro Leu Tyr Phe Leu Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Met Cys Leu Ser Thr Ala Thr Thr Pro Lys
 65 70 75 80
 Met Ile Ile Asp Leu Thr Asp His Lys Thr Ile Ser Val Trp Gly
 85 90 95
 Cys Val Thr Gln Met Phe Phe Met His Phe Phe Gly Gly Ala Glu Met
 100 105 110
 Thr Leu Leu Ile Ile Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Arg Thr Ile Met Ser His Lys Leu Leu Lys Gly Phe
 130 135 140
 Ala Ile Leu Ser Trp Ile Ile Gly Phe Leu His Ser Ile Ser Gln Ile
 145 150 155 160
 Val Leu Thr Met Asn Leu Pro Phe Cys Gly His Asn Val Ile Asn Asn
 165 170 175
 Ile Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Ile Glu Thr
 180 185 190
 Tyr Thr Leu Glu Leu Phe Val Ile Ala Asp Ser Gly Leu Leu Ser Phe
 195 200 205
 Thr Cys Phe Ile Leu Leu Leu Val Ser Tyr Ile Val Ile Leu Val Ser
 210 215 220
 Val Pro Lys Lys Ser Ser His Gly Leu Ser Lys Ala Leu Ser Thr Leu

<210> 1585
<211> 325
<212> PRT
<213> Unknown (H38g502 protein)

<220>
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(325)
<223> Xaa = Any Amino Acid
```

846

Asn Asn Asp Met Lys Lys Ala Leu Arg Lys Met Lys Ile Asn Phe Val
 290 295 300
 Ser Ser Arg Ser Thr Xaa Xaa Leu Lys Tyr Tyr Asn His Xaa Lys His
 305 310 315 320
 His His Tyr Cys Cys
 325

<210> 1586

<211> 312

<212> PRT

<213> Unknown (H38g503 protein)

<220>

<223> Synthetic construct

<400> 1586

Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1 5 10 15
 Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Leu Phe Leu Phe Phe Ser
 20 25 30
 Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr
 35 40 45
 Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly
 85 90 95
 Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe
 130 135 140
 Leu Val Ile Ser Trp Ile Ile Gly Ile Ile His Ser Val Ile Gln Leu
 145 150 155 160
 Ala Phe Val Val Asp Leu Leu Phe Cys Gly Pro Asn Glu Leu Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Ile Glu Thr
 180 185 190
 Tyr Thr Leu Gly Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu
 195 200 205
 Ala Ser Phe Leu Ile Leu Ile Ser Tyr Ile Phe Ile Leu Val Thr
 210 215 220
 Val Gln Lys Lys Ser Ser Gly Gly Ile Phe Lys Ala Phe Ser Met Leu
 225 230 235 240
 Ser Ala His Val Ile Val Val Val Leu Val Phe Gly Pro Leu Ile Phe
 245 250 255
 Phe Tyr Ile Phe Pro Phe Pro Thr Ser His Leu Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Ile Thr Pro Val Leu Asn Pro Val Ile Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Met Val Ala Met Arg Arg Arg Cys Ser Gln
 290 295 300
 Phe Val Asn Tyr Ser Lys Ile Phe
 305 310

<210> 1587

<211> 322

<212> PRT

<213> Unknown (H38g504 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1587

```

Met Asn Arg Asp Asn Gln Ser Val Val Ser Glu Phe Val Leu Leu Gly
 1           5           10           15
Leu Ser Asn Ser Trp Glu Ile Lys Ile Phe Leu Phe Cys Phe Ser Cys
          20           25           30
Leu Phe Tyr Val Ser Gly Val Met Ala Asn Leu Ile Val Val Val Ile
          35           40           45
Val Thr Ser Asp Pro Tyr Leu His Ser Ser Leu Tyr Ile Leu Leu Ala
          50           55           60
Asn Leu Ser Val Ile Asp Leu Thr Phe Cys Ser Ile Ala Ala Arg Lys
65           70           75           80
Met Ile Cys Asp Ile Phe Arg Lys Gln Lys Val Ile Ser Phe Trp Gly
          85           90           95
Cys Val Ala Gln Ile Phe Phe Ser His Ala Val Gly Gly Thr Glu Met
          100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Val Cys Lys
          115          120          125
Pro Leu His Tyr Leu Thr Ile Met His Pro Arg Met Cys Ile Leu Ile
          130          135          140
Leu Val Ala Ser Trp Ala Ile Gly Leu Ile His Ser Leu Val Gln Leu
145          150          155          160
Ser Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
          165          170          175
Phe Tyr Cys Asp Ile Pro Gln Leu Ile Lys Leu Ala Cys Thr Asn Thr
          180          185          190
Tyr Lys Leu Gln Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu
          195          200          205
Ser Ala Phe Phe Leu Leu Ile Leu Ser Tyr Ile Phe Ile Leu Ala Thr
          210          215          220
Leu Gln Lys His Ser Ser Gly Gly Ser Ser Lys Ala Val Ser Thr Leu
225          230          235          240
Ser Ala His Ile Thr Val Val Val Leu Phe Phe Gly Pro Leu Ile Phe
          245          250          255
Phe Tyr Val Trp Pro Ser Pro Pro Thr His Leu Asn Lys Phe Leu Ala
          260          265          270
Ile Phe Asp Ala Ile Phe Thr Pro Phe Leu Asn Pro Val Ile Tyr Thr
          275          280          285
Phe Arg Asn Arg Glu Met Lys Ile Ala Ile Arg Arg Val Phe Gly Gln
          290          295          300
Phe Met Gly Phe Arg Lys Thr Thr Xaa Val Ala Leu Leu Lys His Arg
305          310          315          320
Ile Ser

```

<210> 1588

<211> 291

<212> PRT

<213> Unknown (H38g505 protein)

<220>

<223> Synthetic construct

<400> 1588

```

Met Val Gly Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1          5          10          15
Leu Thr Asn Ser Trp Glu Ile Arg Leu Leu Leu Val Phe Ser Ser
          20          25          30
Met Phe Tyr Met Ala Ser Met Met Gly Asn Ser Leu Ile Leu Leu Thr
          35          40          45
Val Thr Ser Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Asn Leu Ser Phe Ile Asp Leu Gly Val Ser Ser Val Thr Ser Pro Lys
65          70          75          80
Met Ile Tyr Asp Leu Phe Arg Lys His Glu Val Ile Ser Phe Gly Gly
          85          90          95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
          100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Leu Gln Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Met Phe Phe
          130          135          140
Leu Val Ala Ala Trp Val Thr Gly Leu Ile His Ser Val Val Gln Leu
145          150          155          160
Val Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Ser Asp Ser
          165          170          175
Phe Tyr Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Thr Asp Ser
          180          185          190
Tyr Arg Leu Glu Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu
          195          200          205
Gly Ser Phe Phe Ile Leu Ile Ile Ser Tyr Val Val Ile Ile Leu Thr
          210          215          220
Val Leu Lys His Ser Ser Ala Gly Leu Ser Lys Ala Leu Ser Thr Leu
225          230          235          240
Ser Ala His Val Ser Val Val Val Leu Phe Phe Gly Pro Leu Ile Phe
          245          250          255
Val Tyr Thr Trp Pro Ser Pro Ser Thr His Leu Asp Lys Phe Leu Ala
          260          265          270
Ile Phe Asp Ala Val Leu Thr Pro Val Leu Asn Pro Ile Ile Tyr Thr
          275          280          285
Phe Arg Asn
          290

```

<210> 1589

<211> 312

<212> PRT

<213> Unknown (H38g506 protein)

<220>

<223> Synthetic construct

<400> 1589

```

Met Asn Gly Met Asn His Ser Val Val Ser Glu Phe Val Phe Met Gly
 1          5          10          15
Leu Thr Asn Ser Arg Glu Ile Gln Leu Leu Phe Val Phe Ser Leu
          20          25          30
Leu Phe Tyr Phe Ala Ser Met Met Gly Asn Leu Val Ile Val Phe Thr
          35          40          45
Val Thr Met Asp Ala His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Asn Leu Ser Ile Ile Asp Met Ala Phe Cys Ser Ile Thr Ala Pro Lys
65          70          75          80
Met Ile Cys Asp Ile Phe Lys Lys His Lys Ala Ile Ser Phe Arg Gly
          85          90          95
Cys Ile Thr Gln Ile Phe Phe Ser His Ala Leu Gly Gly Thr Glu Met

```

```

      100      105      110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Cys Lys
      115      120      125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Tyr Phe
      130      135      140
Leu Ala Thr Ser Ser Ile Ile Gly Leu Ile His Ser Leu Val Gln Leu
145      150      155      160
Val Phe Val Val Asp Leu Pro Phe Cys Gly Pro Asn Ile Phe Asp Ser
      165      170      175
Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asn Thr
      180      185      190
Gln Glu Leu Glu Phe Met Val Thr Val Asn Ser Gly Leu Ile Ser Val
      195      200      205
Gly Ser Phe Val Leu Leu Val Ile Ser Tyr Ile Phe Ile Leu Phe Thr
210      215      220
Val Trp Lys His Ser Ser Gly Gly Leu Ala Lys Ala Leu Ser Thr Leu
225      230      235      240
Ser Ala His Val Thr Val Val Ile Leu Phe Phe Gly Pro Leu Met Phe
      245      250      255
Phe Tyr Thr Trp Pro Ser Pro Thr Ser His Leu Asp Lys Tyr Leu Ala
260      265      270
Ile Phe Asp Ala Phe Ile Thr Pro Phe Leu Asn Pro Val Ile Tyr Thr
275      280      285
Phe Arg Asn Lys Asp Met Lys Val Ala Met Arg Arg Leu Cys Ser Arg
290      295      300
Leu Ala His Phe Thr Lys Ile Leu
305      310

```

<210> 1590

<211> 327

<212> PRT

<213> Unknown (H38g507 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1590

```

Met Glu Gln Arg Lys Asn Val Thr Glu Phe Val Leu Val Gly Leu Thr
1      5      10      15
Gln Ser Pro Gln Gly Gln Lys Ile Leu Phe Leu Val Phe Leu Leu Ile
      20      25      30
Tyr Val Val Thr Met Val Gly Asn Ile Phe Ile Val Val Thr Val Val
35      40      45
Val Ser Pro Thr Leu Gly Cys Pro Met Tyr Phe Phe Leu Gly Tyr Leu
50      55      60
Ser Phe Met Asp Ala Val His Ser Thr Thr Val Thr Pro Asn Met Ile
65      70      75      80
Ile Asp Leu Leu Tyr Glu Lys Lys Thr Ile Ser Phe Gln Ala Cys Ile
      85      90      95
Thr Gln Ile Phe Ile Gly His Leu Phe Gly Gly Ala Glu Ile Leu Leu
100      105      110
Leu Val Val Met Ala Tyr Asp Gly Tyr Val Thr Ile Cys Lys Pro Leu
115      120      125
His Tyr Leu Thr Ile Met Asn Gln Arg Val Cys Ile Leu Leu Leu Leu
130      135      140
Leu Ala Trp Ala Gly Gly Phe Leu His Ala Val Val Gln Leu Leu Phe
145      150      155      160

```

```

Val Tyr Asn Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile
      165                      170                      175
Cys Asp Met Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asp Thr Tyr Val
      180                      185                      190
Thr Gly Leu Thr Val Val Ala Asn Asp Gly Ala Ile Cys Val Val Ile
      195                      200                      205
Phe Met Leu Leu Leu Phe Ser Tyr Gly Val Ile Leu His Ser Leu Lys
      210                      215                      220
Asn Leu Ser Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Gly Ser
      225                      230                      235                      240
His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
      245                      250                      255
Val Arg Pro Pro Leu Thr Leu Pro Ile Asp Lys Ser Leu Thr Val Phe
      260                      265                      270
Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
      275                      280                      285
Asn Ala Glu Met Lys Asn Ala Met Lys Lys Leu Trp Thr Arg Lys Arg
      290                      295                      300
Lys Xaa Gly Gly Asp Lys Cys Ile Ile Tyr Phe Gln Xaa Arg Val Ala
      305                      310                      315                      320
Pro Ser Arg Lys Ala Ile Cys
      325

```

<210> 1591

<211> 306

<212> PRT

<213> Unknown (H38g508 protein)

<220>

<223> Synthetic construct

<400> 1591

```

Met Asn Leu Lys Asn Gly Ser Leu Val Thr Glu Phe Ile Leu Leu Gly
  1                      5                      10                      15
Phe Phe Gly Arg Trp Glu Leu Gln Ile Phe Phe Phe Val Thr Phe Ser
      20                      25                      30
Leu Ile Tyr Gly Ala Thr Val Val Gly Asn Ile Leu Ile Met Val Thr
      35                      40                      45
Val Thr Cys Ser Ser Thr Leu His Ser Pro Leu Tyr Phe Leu Leu Gly
      50                      55                      60
Asn Leu Ser Phe Leu Asp Met Cys Leu Ser Thr Ala Thr Thr Pro Lys
      65                      70                      75                      80
Met Asp His Lys Thr Ile Ser Val Trp Gly Cys Val Thr Gln Lys Phe
      85                      90                      95
Phe Met His Phe Phe Gly Ser Ala Glu Met Thr Leu Leu Ile Ile Met
      100                      105                      110
Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His Tyr Arg Thr
      115                      120                      125
Ile Met Ser His Lys Leu Leu Lys Gly Phe Ala Ile Leu Ser Trp Ile
      130                      135                      140
Ile Gly Phe Leu His Ser Ile Ser Gln Ile Val Leu Thr Met Asn Leu
      145                      150                      155                      160
Pro Phe Cys Gly His Asn Val Ile Asn Asn Ile Phe Cys Asp Leu Pro
      165                      170                      175
Leu Val Ile Lys Leu Ala Cys Ile Glu Thr Tyr Thr Leu Glu Leu Phe
      180                      185                      190
Val Ile Ala Asp Ser Gly Leu Leu Ser Phe Thr Cys Phe Ile Leu Leu
      195                      200                      205
Leu Val Ser Tyr Ile Val Ile Leu Val Ser Val Pro Lys Lys Ser Ser
      210                      215                      220
His Gly Leu Ser Lys Ala Leu Ser Thr Leu Ser Ala His Ile Ile Val

```


<400> 1592																
Ser	Thr	Asp	Pro	Gln	Asn	Leu	Thr	Asp	Val	Ser	Ile	Phe	Leu	Leu	Leu	
1				5					10					15		
Gly	Thr	Ser	Glu	Asp	Pro	Glu	Xaa	Gln	Pro	Val	Leu	Ala	Gly	Leu	Phe	
			20					25					30			
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	
		35					40					45				
Ala	Val	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Ile	Phe	Phe	
		50				55					60					
Ser	Asn	Leu	Ser	Leu	Pro	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro	
65					70				75						80	
Lys	Met	Thr	Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala	
				85					90					95		
Gly	Cys	Leu	Thr	Gln	Met	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Met	Glu	
			100					105					110			
Glu	Asn	Met	Phe	Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	
		115				120						125				
Cys	His	Pro	Leu	Tyr	His	Ser	Ala	Ile	Met	Asn	Pro	Cys	Phe	Cys	Gly	
	130					135				140						
Phe	Leu	Val	Leu	Leu	Ser	Phe	Phe	Phe	Ser	Leu	Ser	Leu	Leu	Asp	Val	
145					150				155						160	
Gln	Leu	Arg	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Lys	Asp	Val	
			165						170					175		
Glu	Ile	Pro	Asn	Phe	Phe	Trp	Asp	Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	
		180					185					190				
Cys	Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Leu	Tyr	Phe	Pro	Ala	Ala	
		195				200						205				
Ile	Phe	Gly	Phe	Leu	Pro	Ile	Leu	Gly	Thr	Leu	Phe	Ser	Tyr	Tyr	Lys	
	210					215					220					
Ile	Val	Phe	Ser	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly	Lys	Tyr	Lys	
225				230					235						240	
Ala	Phe	Ser	Thr	Cys	Val	Ser	His	Leu	Ser	Val	Val	Cys	Xaa	Phe	Tyr	
			245						250					255		
Gly	Thr	Gly	Val	Gly	Gly	Tyr	Leu	Ser	Ser	Asp	Val	Ser	Ser	Ser	Pro	
		260					265						270			
Arg	Lys	Ala	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	
	275					280						285				

Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val
 290 295 300
 Leu Arg Arg Pro His Ser Ser Thr Val Xaa Ser Xaa Tyr Leu Leu Ile
 305 310 315 320
 Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
 325 330 335

<210> 1593

<211> 319

<212> PRT

<213> Unknown (H38g510 protein)

<220>

<223> Synthetic construct

<400> 1593

Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
 1 5 10 15
 Gly Phe Ser Thr Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
 20 25 30
 Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Leu
 35 40 45
 Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ala Asn Leu Pro Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro
 65 70 75 80
 Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
 85 90 95
 Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
 100 105 110
 Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly
 130 135 140
 Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly
 145 150 155 160
 Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp
 165 170 175
 His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp
 180 185 190
 Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val
 195 200 205
 Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg
 210 215 220
 Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile
 245 250 255
 Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly
 260 265 270
 Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro
 275 280 285
 Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His
 290 295 300
 Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln
 305 310 315

<210> 1594

<211> 304

<212> PRT

<213> Unknown (H38g511 protein)

<220>

<223> Synthetic construct

<400> 1594

```

Met Glu Arg Ala Asn His Ser Val Val Ser Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Ser Lys Ser Gln Asn Leu Gln Ile Leu Phe Phe Leu Gly Phe Ser
      20          25          30
Val Val Phe Val Gly Ile Val Leu Gly Asn Leu Leu Ile Leu Val Thr
      35          40          45
Val Thr Phe Asp Ser Leu Leu His Thr Pro Met Tyr Phe Leu Leu Ser
      50          55          60
Asn Leu Ser Cys Ile Asp Met Ile Leu Ala Ser Phe Ala Thr Pro Lys
      65          70          75          80
Met Ile Val Asp Phe Leu Arg Glu Arg Lys Thr Ile Ser Trp Trp Gly
      85          90          95
Cys Tyr Ser Gln Met Phe Phe Met His Leu Leu Gly Gly Ser Glu Met
      100          105          110
Met Leu Leu Val Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Lys
      115          120          125
Pro Leu His Tyr Met Thr Ile Met Ser Pro Arg Val Leu Thr Gly Leu
      130          135          140
Leu Leu Ser Ser Tyr Ala Val Gly Phe Val His Ser Ser Ser Gln Met
      145          150          155          160
Ala Phe Met Leu Thr Leu Pro Phe Cys Gly Pro Asn Val Ile Asp Ser
      165          170          175
Phe Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Lys Asp Thr
      180          185          190
Tyr Ile Leu Gln Leu Leu Val Ile Ala Asp Ser Gly Leu Leu Ser Leu
      195          200          205
Val Cys Phe Leu Leu Leu Leu Val Ser Tyr Gly Val Ile Ile Phe Ser
      210          215          220
Val Arg Tyr Arg Ala Ala Ser Arg Ser Ser Lys Ala Phe Ser Thr Leu
      225          230          235          240
Ser Ala His Ile Thr Val Val Thr Leu Phe Phe Ala Pro Cys Val Phe
      245          250          255
Ile Tyr Val Trp Pro Phe Ser Arg Tyr Ser Val Asp Lys Ile Leu Ser
      260          265          270
Val Phe Tyr Thr Ile Phe Thr Pro Leu Leu Asn Pro Ile Ile Tyr Thr
      275          280          285
Leu Arg Asn Gln Glu Val Lys Ala Ala Ile Lys Lys Arg Leu Cys Ile
      290          295          300

```

<210> 1595

<211> 321

<212> PRT

<213> Unknown (H38g512 protein)

<220>

<223> Synthetic construct

<400> 1595

```

Met Val Asn Leu Thr Ser Met Ser Gly Phe Leu Leu Met Gly Phe Ser
 1          5          10          15
Asp Glu Arg Lys Leu Gln Ile Leu His Ala Leu Val Phe Leu Val Thr
      20          25          30
Tyr Leu Leu Ala Leu Thr Gly Asn Leu Leu Ile Ile Thr Ile Ile Thr
      35          40          45
Val Asp Arg Arg Leu His Ser Pro Met Tyr Tyr Phe Leu Lys His Leu
      50          55          60

```

Ser Leu Leu Asp Leu Cys Phe Ile Ser Val Thr Val Pro Gln Ser Ile
 65 70 75 80
 Ala Asn Ser Leu Met Gly Asn Gly Tyr Ile Ser Leu Val Gln Cys Ile
 85 90 95
 Leu Gln Val Phe Phe Phe Ile Ala Leu Ala Ser Ser Glu Val Ala Ile
 100 105 110
 Leu Thr Val Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu
 115 120 125
 His Tyr Glu Thr Ile Met Asp Pro Arg Ala Cys Arg His Ala Val Ile
 130 135 140
 Ala Val Trp Ile Ala Gly Gly Leu Ser Gly Leu Met His Ala Ala Ile
 145 150 155 160
 Asn Phe Ser Ile Pro Leu Cys Gly Lys Arg Val Ile His Gln Phe Phe
 165 170 175
 Cys Asp Val Pro Gln Met Leu Lys Leu Ala Cys Ser Tyr Glu Phe Ile
 180 185 190
 Asn Glu Ile Ala Leu Ala Ala Phe Thr Thr Ser Ala Ala Phe Ile Cys
 195 200 205
 Leu Ile Ser Ile Val Leu Ser Tyr Ile Arg Ile Phe Ser Thr Val Leu
 210 215 220
 Arg Ile Pro Ser Ala Glu Gly Arg Thr Lys Val Phe Ser Thr Cys Leu
 225 230 235 240
 Pro His Leu Phe Val Ala Thr Phe Phe Leu Ser Ala Ala Gly Phe Glu
 245 250 255
 Phe Leu Arg Leu Pro Ser Asp Ser Ser Ser Thr Val Asp Leu Val Phe
 260 265 270
 Ser Val Phe Tyr Thr Val Ile Pro Pro Thr Leu Asn Pro Val Ile Tyr
 275 280 285
 Ser Leu Arg Asn Asp Ser Met Lys Ala Ala Leu Arg Lys Met Leu Ser
 290 295 300
 Lys Glu Glu Leu Pro Gln Arg Lys Met Cys Leu Lys Ala Met Phe Lys
 305 310 315 320
 Leu

<210> 1596

<211> 310

<212> PRT

<213> Unknown (H38g513 protein)

<220>

<223> Synthetic construct

<400> 1596

Met Asp Pro Gln Asn Tyr Ser Leu Val Ser Glu Phe Val Leu His Gly
 1 5 10 15
 Leu Cys Thr Ser Arg His Leu Gln Asn Phe Phe Phe Ile Phe Phe Phe
 20 25 30
 Gly Val Tyr Val Ala Ile Met Leu Gly Asn Leu Leu Ile Leu Val Thr
 35 40 45
 Val Ile Ser Asp Pro Cys Leu His Ser Ser Pro Met Tyr Phe Leu Leu
 50 55 60
 Gly Asn Leu Ala Phe Leu Asp Met Trp Leu Ala Ser Phe Ala Thr Pro
 65 70 75 80
 Lys Met Ile Arg Asp Phe Leu Ser Asp Gln Lys Leu Ile Ser Phe Gly
 85 90 95
 Gly Cys Met Ala Gln Ile Phe Phe Leu His Phe Thr Gly Gly Ala Glu
 100 105 110
 Met Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Lys Pro Leu His Tyr Met Thr Leu Met Ser Trp Gln Thr Cys Ile Arg

```

      130              135              140
Leu Val Leu Ala Ser Trp Val Val Gly Phe Val His Ser Ile Ser Gln
145              150              155              160
Val Ala Phe Thr Val Asn Leu Pro Tyr Cys Gly Pro Asn Glu Val Asp
      165              170              175
Ser Phe Phe Cys Asp Leu Pro Leu Val Ile Lys Leu Ala Cys Met Asp
      180              185              190
Thr Tyr Val Leu Gly Ile Ile Met Ile Ser Asp Ser Gly Leu Leu Ser
      195              200              205
Leu Ser Cys Phe Leu Leu Leu Leu Ile Ser Tyr Thr Val Ile Leu Leu
      210              215              220
Ala Ile Arg Gln Arg Ala Ala Gly Ser Thr Ser Lys Ala Leu Ser Thr
225              230              235              240
Cys Ser Ala His Ile Met Val Val Thr Leu Phe Phe Gly Pro Cys Ile
      245              250              255
Phe Val Tyr Val Arg Pro Phe Ser Arg Phe Ser Val Asp Lys Leu Leu
      260              265              270
Ser Val Phe Tyr Thr Ile Phe Thr Pro Leu Leu Asn Pro Ile Ile Tyr
      275              280              285
Thr Leu Arg Asn Glu Glu Met Lys Ala Ala Met Lys Lys Leu Gln Asn
      290              295              300
Arg Arg Val Thr Phe Gln
305              310

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<210> 1597

<211> 319

<212> PRT

<213> Unknown (H38g514 protein)

<220>

<223> Synthetic construct

<400> 1597

```

Met Glu Arg Lys Asn Gln Thr Ala Ile Thr Glu Phe Ile Ile Leu Gly
1      5      10      15
Phe Ser Asn Leu Asn Glu Leu Gln Phe Leu Leu Phe Thr Ile Phe Phe
      20      25      30
Leu Thr Tyr Phe Cys Thr Leu Gly Gly Asn Ile Leu Ile Ile Leu Thr
      35      40      45
Thr Val Thr Asp Pro His Leu His Thr Pro Met Tyr Tyr Phe Leu Gly
      50      55      60
Asn Leu Ala Phe Ile Asp Ile Cys Tyr Thr Thr Ser Asn Val Pro Gln
65      70      75      80
Met Met Val His Leu Leu Ser Lys Lys Lys Ser Ile Ser Tyr Val Gly
      85      90      95
Cys Val Val Gln Leu Phe Ala Phe Val Phe Phe Val Gly Ser Glu Cys
      100      105      110
Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Asn
      115      120      125
Pro Leu Arg Tyr Ser Val Ile Leu Ser Lys Val Leu Cys Asn Gln Leu
      130      135      140
Ala Ala Ser Cys Trp Ala Ala Gly Phe Leu Asn Ser Val Val His Thr
145      150      155      160
Val Leu Thr Phe Cys Leu Pro Phe Cys Gly Asn Asn Gln Ile Asn Tyr
      165      170      175
Phe Phe Cys Asp Ile Pro Pro Leu Leu Ile Leu Ser Cys Gly Asn Thr
      180      185      190
Ser Val Asn Glu Leu Ala Leu Leu Ser Thr Gly Val Phe Ile Gly Trp
      195      200      205
Thr Pro Phe Leu Cys Ile Val Leu Ser Tyr Ile Cys Ile Ile Ser Thr
      210      215      220

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```

Ile Leu Arg Ile Gln Ser Ser Glu Gly Arg Arg Lys Ala Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Ala Ile Val Phe Leu Phe Tyr Gly Ser Ala Ile
          245          250          255
Phe Thr Tyr Val Arg Pro Ile Ser Thr Tyr Ser Leu Lys Lys Asp Arg
          260          265          270
Leu Val Ser Val Leu Tyr Ser Val Val Thr Pro Met Leu Asn Pro Ile
          275          280          285
Ile Tyr Thr Leu Arg Asn Lys Asp Ile Lys Glu Ala Val Lys Thr Ile
          290          295          300
Gly Ser Lys Trp Gln Pro Pro Ile Ser Ser Leu Asp Ser Lys Leu
305          310          315

```

<210> 1598

<211> 303

<212> PRT

<213> Unknown (H38g515 protein)

<220>

<223> Synthetic construct

<400> 1598

```

Met Arg Glu Phe Phe Leu Ser Gly Phe Ser Gln Thr Pro Ser Ile Glu
1          5          10          15
Ala Gly Leu Phe Val Leu Phe Leu Phe Phe Tyr Met Ser Ile Trp Val
          20          25          30
Gly Asn Val Leu Ile Met Val Thr Val Ala Ser Asp Lys Tyr Leu Asn
          35          40          45
Ser Ser Pro Met Tyr Phe Leu Leu Gly Asn Leu Ser Phe Leu Asp Leu
          50          55          60
Cys Tyr Ser Thr Val Thr Thr Pro Lys Leu Leu Ala Asp Phe Phe Asn
65          70          75          80
His Glu Lys Leu Ile Ser Tyr Asp Gln Cys Ile Val Gln Leu Phe Phe
          85          90          95
Leu His Phe Val Gly Ala Ala Glu Met Phe Leu Leu Thr Val Met Ala
          100          105          110
Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His Tyr Thr Thr Val
          115          120          125
Met Ser Arg Gly Leu Cys Cys Val Leu Val Ala Ala Ser Trp Met Gly
          130          135          140
Gly Phe Val His Ser Thr Val Gln Thr Ile Leu Thr Val His Leu Pro
145          150          155          160
Phe Cys Gly Pro Asn Gln Val Glu Asn Phe Phe Cys Asp Val Pro Pro
          165          170          175
Val Ile Lys Leu Ala Cys Ala Asp Thr Phe Val Ile Glu Leu Leu Met
          180          185          190
Val Ser Asn Ser Gly Leu Ile Ser Thr Ile Ser Phe Val Val Leu Ile
          195          200          205
Ser Ser Tyr Thr Thr Ile Leu Val Lys Ile Arg Ser Lys Glu Gly Arg
          210          215          220
Arg Lys Ala Leu Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu
225          230          235          240
Phe Phe Gly Pro Cys Ile Phe Ile Tyr Ala Arg Pro Phe Ser Thr Phe
          245          250          255
Ser Val Asp Lys Met Val Ser Val Leu Tyr Asn Val Ile Thr Pro Met
          260          265          270
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Ser Ala
          275          280          285
Met Gln Lys Leu Trp Val Arg Asn Gly Leu Thr Trp Lys Lys Gln
290          295          300

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<210> 1599
 <211> 315
 <212> PRT
 <213> Unknown (H38g516 protein)

<220>
 <223> Synthetic construct

<400> 1599
 Met Glu Asn Val Thr Thr Met Asn Glu Phe Leu Leu Leu Gly Leu Thr
 1 5 10 15
 Gly Val Gln Glu Leu Gln Pro Phe Phe Phe Gly Ile Phe Leu Ile Ile
 20 25 30
 Tyr Leu Ile Asn Leu Ile Gly Asn Gly Ser Ile Leu Val Met Val Val
 35 40 45
 Leu Glu Pro Gln Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu
 50 55 60
 Ser Cys Leu Asp Ile Ser Tyr Ser Ser Val Thr Leu Pro Lys Leu Leu
 65 70 75 80
 Val Asn Leu Val Cys Ser Arg Arg Ala Ile Ser Phe Leu Gly Cys Ile
 85 90 95
 Thr Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Ile Leu
 100 105 110
 Leu Ala Ile Met Ala Phe Asp Arg Phe Val Ala Ile Cys Asn Pro Leu
 115 120 125
 Arg Tyr Thr Val Ile Met Asn Pro Gln Val Cys Ile Leu Leu Ala Ala
 130 135 140
 Ala Ala Trp Leu Ile Ser Phe Phe Tyr Ala Leu Met His Ser Val Met
 145 150 155 160
 Thr Ala His Leu Ser Phe Cys Gly Ser Gln Lys Leu Asn His Phe Phe
 165 170 175
 Tyr Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Ser Asp Thr Leu Leu
 180 185 190
 Asn Gln Trp Leu Leu Ser Ile Val Thr Gly Ser Ile Ser Met Gly Ala
 195 200 205
 Phe Phe Leu Thr Leu Leu Ser Cys Phe Tyr Val Ile Gly Phe Leu Leu
 210 215 220
 Phe Lys Asn Arg Ser Cys Arg Ile Leu His Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Ala Ser His Phe Met Val Val Cys Leu Phe Tyr Gly Pro Val Gly Phe
 245 250 255
 Thr Tyr Ile Arg Pro Ala Ser Ala Thr Ser Met Ile Gln Asp Arg Ile
 260 265 270
 Met Ala Ile Met Tyr Ser Ala Val Thr Pro Val Leu Asn Pro Leu Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Met Met Ala Leu Lys Lys Ile Phe
 290 295 300
 Gly Arg Lys Leu Phe Lys Asp Trp Gln Gln His
 305 310 315

<210> 1600
 <211> 322
 <212> PRT
 <213> Unknown (H38g517 protein)

<220>
 <223> Synthetic construct

<400> 1600
 Met Asn Glu Thr Asn His Ser Arg Val Thr Glu Phe Val Leu Leu Gly
 1 5 10 15

Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Thr Phe Ser
 20 25 30
 Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
 35 40 45
 Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Phe Ala Thr Pro Lys
 65 70 75 80
 Met Ile Ala Asp Phe Leu Val Glu Arg Lys Thr Ile Ser Phe Asp Ala
 85 90 95
 Cys Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
 100 105 110
 Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Met Thr Val Met Ser Arg Arg Val Cys Val Val Leu
 130 135 140
 Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
 145 150 155 160
 Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Leu Val Thr Lys Leu Ala Cys Ile Asp Thr
 180 185 190
 Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser Gly Phe Leu Ser Leu
 195 200 205
 Ser Ser Phe Leu Leu Leu Val Val Ser Tyr Thr Val Ile Leu Val Thr
 210 215 220
 Val Arg Asn Arg Ser Ser Ala Ser Met Ala Lys Ala Arg Ser Thr Leu
 225 230 235 240
 Thr Ala His Ile Thr Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Phe Ser Ser Tyr Ser Val Asp Lys Val Leu Ala
 260 265 270
 Val Phe Tyr Thr Ile Phe Thr Leu Ile Leu Asn Pro Val Ile Tyr Thr
 275 280 285
 Leu Arg Asn Lys Glu Val Lys Ala Ala Met Ser Lys Leu Lys Ser Arg
 290 295 300
 Tyr Leu Lys Pro Ser Gln Val Ser Val Val Ile Arg Asn Val Leu Phe
 305 310 315 320
 Leu Glu

<210> 1601

<211> 197

<212> PRT

<213> Unknown (H38g518 protein)

<220>

<223> Synthetic construct

<400> 1601

Glu Arg Leu Leu Leu Pro Met Tyr Cys Phe Leu Thr Ile Leu Ser Ala
 1 5 10 15
 Thr Asp Leu Gly Leu Ser Ile Ser Thr Leu Val Thr Met Leu Ser Ile
 20 25 30
 Phe Trp Phe Asn Val Arg Glu Ile Ser Phe Asn Ala Cys Leu Ser His
 35 40 45
 Met Phe Phe Ile Lys Phe Phe Thr Val Met Glu Ser Ser Val Leu Leu
 50 55 60
 Ala Met Ala Phe Asp Arg Phe Val Ala Val Ser Asn Pro Leu Arg Tyr
 65 70 75 80
 Ala Met Ile Leu Thr Asp Ser Arg Ile Ala Gln Ile Gly Val Ala Ser

<400> 1602																
Met	Ser	Pro	Glu	Asn	Gln	Ser	Ser	Val	Ser	Glu	Phe	Leu	Leu	Leu	Gly	
1				5					10					15		
Leu	Pro	Ile	Arg	Pro	Glu	Gln	Gln	Ala	Val	Phe	Phe	Thr	Leu	Phe	Leu	
			20					25					30			
Gly	Met	Tyr	Leu	Thr	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Met	Leu	Leu	
		35				40						45				
Ile	Gln	Leu	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	
	50					55					60					
His	Leu	Ala	Leu	Thr	Asp	Ile	Ser	Phe	Ser	Ser	Val	Thr	Val	Pro	Lys	
65					70				75					80		
Met	Leu	Met	Asp	Met	Arg	Thr	Lys	Tyr	Lys	Ser	Ile	Leu	Tyr	Glu	Glu	
			85						90					95		
Cys	Ile	Ser	Gln	Met	Tyr	Phe	Phe	Ile	Phe	Phe	Thr	Asp	Leu	Asp	Ser	
			100					105					110			
Phe	Leu	Ile	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	
		115				120						125				
Pro	Leu	His	Tyr	Thr	Val	Ile	Met	Arg	Glu	Glu	Leu	Cys	Val	Phe	Leu	
	130					135					140					
Val	Ala	Val	Ser	Trp	Ile	Leu	Ser	Cys	Ala	Ser	Ser	Leu	Ser	His	Thr	
145					150				155					160		
Leu	Leu	Leu	Thr	Arg	Leu	Ser	Phe	Cys	Ala	Ala	Asn	Thr	Ile	Pro	His	
			165					170						175		
Val	Phe	Cys	Asp	Leu	Ala	Ala	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Ile	
			180					185					190			
Phe	Leu	Asn	Glu	Leu	Val	Met	Phe	Thr	Val	Gly	Val	Val	Val	Ile	Thr	
	195					200						205				
Leu	Pro	Phe	Met	Cys	Ile	Leu	Val	Ser	Tyr	Gly	Tyr	Ile	Gly	Ala	Thr	
	210					215						220				
Ile	Leu	Arg	Val	Pro	Ser	Thr	Lys	Gly	Ile	His	Lys	Ala	Leu	Ser	Thr	
225					230				235					240		
Cys	Gly	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Tyr	Tyr	Gly	Ser	Ile	Phe	
			245					250						255		
Gly	Gln	Tyr	Leu	Phe	Pro	Thr	Val	Ser	Ser	Ser	Ile	Asp	Lys	Asp	Val	
			260					265					270			
Ile	Val	Ala	Leu	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	
	275						280					285				

Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu
 290 295 300
 Phe Ser Arg Ala Thr Phe Phe Ser Trp
 305 310

<210> 1603
 <211> 196
 <212> PRT
 <213> Unknown (H38g520 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(196)
 <223> Xaa = Any Amino Acid

<400> 1603
 Arg Leu Leu Leu Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Leu Leu
 1 5 10 15
 Asp Leu Cys Leu Pro Ser Ile Pro Val Pro Lys Met Leu Gln Asn Leu
 20 25 30
 Leu Thr Gln Arg Xaa Thr Ile Ser Met Trp Tyr Cys Ile Val Gln Ser
 35 40 45
 Phe Phe Leu Ile Phe Ser Gly Ser Thr Glu Ala Cys Leu Leu Leu Ala
 50 55 60
 Met Ala Cys Asp His Ser Thr Ser Asn Cys His Pro Arg Leu Asn Asp
 65 70 75 80
 Val Val Met Asn Gln Pro Val Cys Val Arg Met Val Ile Ala Ala Trp
 85 90 95
 Ala Val Gly Phe Leu Asn Ser Leu Thr Lys Asn Leu Phe Ile Tyr Asn
 100 105 110
 Leu His Phe Cys Gly Pro Ser Val Ile Pro His Phe Cys Cys Glu Leu
 115 120 125
 Pro Ser Leu Phe Pro Leu Ser Cys Ile Asp Pro Ala Ala Ser Glu Val
 130 135 140
 Leu Pro Ala Gly Ser Cys Thr Leu Leu Gly Phe Val Thr Cys Arg Cys
 145 150 155 160
 Val Leu Phe Ser Tyr Ser Asn Thr Ile Ser Ala Val Leu Ala Ile Trp
 165 170 175
 Phe Ser Glu Gly Gln Gly Lys Ala Phe Ser Thr Cys Ser Ser His Leu
 180 185 190
 Thr Val Val Leu
 195

<210> 1604
 <211> 306
 <212> PRT
 <213> Unknown (H38g521 protein)

<220>
 <223> Synthetic construct

<400> 1604
 Met Ser Pro Glu Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Arg Pro Glu Gln Gln Ala Val Phe Phe Ala Leu Phe Leu
 20 25 30
 Gly Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Leu Ile Met Leu Leu
 35 40 45
 Ile Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser

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      50              55              60
His Leu Ala Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys
65              70              75              80
Met Leu Met Asn Met Gln Thr Gln His Leu Ala Val Phe Tyr Lys Gly
      85              90              95
Cys Ile Ser Gln Thr Tyr Phe Phe Ile Phe Phe Ala Asp Leu Asp Ser
      100              105              110
Phe Leu Ile Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115              120              125
Pro Leu His Tyr Ala Thr Ile Met Thr Gln Ser Gln Cys Val Met Leu
      130              135              140
Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys Ala Leu Leu His Thr
145              150              155              160
Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp His Ile Ile Pro His
      165              170              175
Tyr Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr
      180              185              190
Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Ala Leu Thr Ala Ile Met
      195              200              205
Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly His Ile Gly Val Thr
      210              215              220
Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys Lys Ala Leu Ser Thr
225              230              235              240
Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr Tyr Arg Thr Ile Ile
      245              250              255
Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr Asn Asp Lys Asn Ile
      260              265              270
Ile Ala Ser Val Ile Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu
      290              295              300
Leu Ser
305

```

<210> 1605

<211> 197

<212> PRT

<213> Unknown (H38g522 protein)

<220>

<223> Synthetic construct

<400> 1605

```

Leu Leu Leu Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Leu Met Asp
1              5              10              15
Ile Cys Gly Thr Ser Ser Phe Val Pro Leu Ile Leu Asp Asn Phe Leu
      20              25              30
Glu Thr Gln Arg Thr Ile Ser Phe Pro Gly Cys Ala Leu Gln Met Tyr
      35              40              45
Leu Thr Leu Ala Leu Gly Ser Thr Glu Cys Leu Leu Ala Val Met
      50              55              60
Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Pro Glu
65              70              75              80
Leu Met Ser Gly Gln Thr Cys Met Gln Met Ala Ala Leu Ser Trp Gly
      85              90              95
Thr Gly Phe Ala Asn Ser Leu Leu Gln Ser Ile Leu Val Trp His Leu
      100              105              110
Pro Phe Cys Gly His Val Ile Asn Tyr Phe Tyr Glu Ile Leu Ala Val
      115              120              125
Leu Lys Leu Ala Cys Gly Asp Ile Ser Leu Asn Ala Leu Ala Leu Met
130              135              140

```

Val Ala Thr Ala Val Leu Thr Leu Ala Pro Leu Leu Leu Ile Cys Leu
 145 150 155 160
 Ser Tyr Leu Phe Ile Leu Ser Ala Ile Leu Arg Val Pro Ser Ala Ala
 165 170 175
 Gly Arg Cys Lys Ala Phe Ser Thr Cys Ser Ala His Arg Thr Val Val
 180 185 190
 Val Val Phe Tyr Gly
 195

<210> 1606

<211> 328

<212> PRT

<213> Unknown (H38g523 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1606

Val Asn Gly Trp Ser Asn Lys Ser Val Val Thr Glu Phe Asn Leu Leu
 1 5 10 15
 Gly Leu Ser Ser Ser Trp Glu Leu Gln Val Phe Phe Phe Phe Ile Phe
 20 25 30
 Ser Val Phe Tyr Gly Ala Ala Val Leu Gly Asn Ile Leu Ile Ile Ile
 35 40 45
 Thr Val Ile Ile Asp Ser His Leu His Ser Pro Met Tyr Phe Leu Leu
 50 55 60
 Ser Asn Leu Ser Ser Ile Asp Val Cys Gln Ala Thr Phe Ala Thr Pro
 65 70 75 80
 Lys Met Ile Ala Asp Phe Leu Asn Glu His Lys Thr Thr Thr Phe Gln
 85 90 95
 Gly Cys Met Ser Gln Ile Phe Phe Leu His Val Phe Gly Gly Ser Glu
 100 105 110
 Met Val Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys
 115 120 125
 Lys Pro Leu His Tyr Met Thr Ile Met Asn Arg Arg Val Xaa Thr Val
 130 135 140
 Leu Val Gly Val Ser Trp Ala Ile Gly Ile Ser His Ser Ala Thr His
 145 150 155 160
 Leu Ala Phe Lys Val Asn Leu Pro Phe Cys Gly Pro Asn Arg Val Asp
 165 170 175
 Asn Phe Phe Cys Asp Leu Leu Leu Val Ile Lys Leu Ala Cys Leu Asp
 180 185 190
 Thr Tyr Gly Phe Glu Ile Leu Val Leu Thr Asn Ser Gly Leu Leu Ser
 195 200 205
 Leu Met Cys Phe Leu Leu Leu Ile Ser Asp Thr Ile Ile Leu Ala
 210 215 220
 Thr Val His Arg Gln Ala Ser Asp Gly Met Ser Lys Ala Leu Ser Thr
 225 230 235 240
 Leu Ser Ala His Ile Thr Val Val Leu Leu Phe Phe Gly Pro Leu Ile
 245 250 255
 Phe Ile Tyr Ile Trp Pro Phe Glu Ser Phe Pro Ile Asp Lys Phe Ile
 260 265 270
 Ser Val Phe Phe Thr Val Phe Thr Pro Leu Leu Asn Pro Met Ile Tyr
 275 280 285
 Thr Leu Arg Asn Lys Asp Ile Lys Glu Ala Met Arg Lys Leu Arg Arg
 290 295 300
 Xaa His Val Gly Ser Lys Gln Gly Phe Xaa Thr Thr Thr Lys Lys Xaa

305 310 315 320

Tyr Lys Phe Leu Leu Leu Gly Phe
325

<210> 1607
<211> 260
<212> PRT
<213> Unknown (H38g524 protein)

<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(260)
<223> Xaa = Any Amino Acid

<400> 1607

Met Tyr Phe Phe Leu Ser Phe Leu Ser Leu Thr Asp Ile Cys Phe Thr
1 5 10 15
Thr Ser Val Val Pro Lys Met Leu Met Asn Phe Leu Ser Glu Lys Lys
20 25 30
Thr Ile Ser Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Leu Tyr Ala
35 40 45
Leu Gly Asn Ser Asp Ser Cys Leu Leu Ser Xaa Met Ala Phe Asp Arg
50 55 60
Tyr Val Ala Val Cys Asp Pro Phe His Tyr Val Thr Thr Met Ser His
65 70 75 80
His His Cys Val Leu Leu Val Ala Phe Ser Cys Ser Phe Thr Tyr Leu
85 90 95
His Ser Leu Leu His Thr Leu Leu Leu Asn Arg Leu Thr Phe Cys Asp
100 105 110
Ser Asn Val Ile His His Phe Leu Cys Asp Leu Ser Pro Val Leu Lys
115 120 125
Leu Ser Cys Ser Ser Ile Phe Val Asn Glu Ile Val Gln Met Thr Glu
130 135 140
Ala Pro Ile Val Leu Val Thr Arg Phe Leu Cys Ile Ala Phe Ser Tyr
145 150 155 160
Ile Arg Ile Leu Thr Thr Val Leu Lys Ile Pro Ser Thr Ser Gly Lys
165 170 175
Arg Lys Ala Phe Ser Thr Cys Gly Phe Tyr Leu Thr Val Val Thr Leu
180 185 190
Phe Tyr Gly Ser Ile Phe Cys Val Tyr Leu Gln Pro Pro Ser Thr Tyr
195 200 205
Ala Val Lys Asp His Val Ala Thr Ile Val Tyr Thr Val Leu Ser Ser
210 215 220
Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Leu Lys Gln
225 230 235 240
Gly Leu Arg Lys Leu Met Ser Lys Arg Ser Xaa Glu Ala Pro Ser Xaa
245 250 255
Lys Thr Arg Lys
260

<210> 1608
<211> 192
<212> PRT
<213> Unknown (H38g525 protein)

<220>
<223> Synthetic construct

<400> 1608

Tyr Tyr Tyr Tyr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Phe Leu
 1 5 10 15
 Asp Met Ser Phe Thr Thr Ser Ile Val Pro Gln Leu Leu Ala Asn Leu
 20 25 30
 Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly Cys Val Val Gln Phe
 35 40 45
 Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys Val Leu Leu Ala Thr
 50 55 60
 Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg Pro Leu His Tyr Thr
 65 70 75 80
 Val Ile Met His Pro Gln Leu Cys Leu Gly Leu Ala Leu Ala Ser Trp
 85 90 95
 Leu Gly Gly Leu Thr Thr Ser Met Val Gly Ser Thr Leu Thr Met Leu
 100 105 110
 Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His Phe Phe Cys Glu Met
 115 120 125
 Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr Ser Leu Asn Glu Met
 130 135 140
 Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val Leu Pro Leu Gly Leu
 145 150 155 160
 Ile Leu Val Ser Tyr Gly His Ile Ala Glu Ala Gly Leu Lys Asn Lys
 165 170 175
 Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Ser Phe His Val
 180 185 190

<210> 1609

<211> 310

<212> PRT

<213> Unknown (H38g526 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1609

Met Asp Ile Arg Asn Ser Ser Ile Ile Thr Glu Phe Val Leu Leu Glu
 1 5 10 15
 Phe Ile Ser Thr Trp Glu Leu Glu Ile Leu Phe Leu Ile Ile Phe Leu
 20 25 30
 Leu Ala Tyr Ala Ala Ile Met Ala Gly Asn Leu Thr Ala Ile Ala Val
 35 40 45
 Thr Ser Asn Pro Pro Leu Cys Ser Thr Pro Met Tyr Phe Leu Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Ser Met Phe Ile Ser Thr Val Thr Ile Ser Lys
 65 70 75 80
 Met Val Leu Asp Val Leu Arg Glu Asn Lys Thr Thr Ser Ser Trp Gly
 85 90 95
 Cys Met Ala Gln Met Leu His Phe Leu Gly Gly Ser Glu Met Thr Leu
 100 105 110
 Leu Ile Phe Met Ala Val Asp Gln His Ile Ala Ile Cys Arg Pro Leu
 115 120 125
 His Cys Arg Thr Ile Thr Asn Cys Arg Val Leu Met Ala Thr His Gly
 130 135 140
 Leu Cys Val Leu Ser Arg Ala Val Gly Phe Val His Thr Ile Ser Gln
 145 150 155 160
 Ile Val Phe Ile Ile Thr Leu Pro Phe Cys Gly Pro Ser Val Val Asp
 165 170 175
 Asn Leu Phe Xaa Asp Leu Pro Leu Val Leu Lys Leu Ala Cys Thr Glu

```

      180      185      190
Thr Tyr Asp Leu Glu Leu Leu Val Ile Ala Lys Ser Gly Gln Leu Ser
      195      200      205
Phe Ile Cys Phe Ile Val Leu Leu Ile Phe Tyr Thr Ile Ile Leu Val
      210      215      220
Thr Val Gln His Arg Ser Ser Asp Ala Leu Ser Lys Ala Leu Ser Thr
225      230      235      240
Leu Ser Ala His Ile Thr Ala Val Thr Leu Phe Phe Glu Pro Cys Val
      245      250      255
Tyr Ile Tyr Thr Trp Pro Phe Arg Ser Phe Ser Val Asp Thr Phe Leu
      260      265      270
Ser Val Phe Tyr Ser Val Thr Pro Leu Leu Asn Pro Ile Thr Tyr Ser
      275      280      285
Leu Arg Xaa Lys His Ala Ile His Gln Leu Arg Thr Gln His Ile Ile
      290      295      300
Ser Arg Gln Thr Phe Ser
305      310

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<210> 1610

<211> 198

<212> PRT

<213> Unknown (H38g527 protein)

<220>

<223> Synthetic construct

<400> 1610

```

Leu Leu Leu Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Leu Val Asp
1      5      10      15
Phe Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Met Val Gly Phe Leu
      20      25      30
Thr Gly Asp Lys Phe Ile Leu Tyr Asn Ala Cys Ala Thr Gln Phe Phe
      35      40      45
Phe Phe Val Ala Phe Ile Thr Ala Glu Ser Phe Leu Leu Ala Ser Met
      50      55      60
Ala Tyr Asp Arg Tyr Ala Ala Leu Cys Lys Pro Leu His Tyr Thr Thr
65      70      75      80
Thr Met Thr Thr Asn Val Cys Ala Arg Leu Ala Ile Gly Ser Tyr Ile
      85      90      95
Cys Gly Phe Leu Asn Ala Ser Ile His Thr Gly Asn Thr Phe Arg Leu
      100      105      110
Ser Phe Cys Arg Ser Asn Val Val Glu His Phe Phe Cys Asp Ala Pro
      115      120      125
Pro Leu Leu Thr Leu Ser Cys Ser Asp Asn Tyr Ile Ser Glu Met Val
      130      135      140
Ile Phe Phe Val Val Gly Phe Asn Asp Leu Phe Ser Ile Leu Val Ile
145      150      155      160
Leu Ile Ser Tyr Leu Phe Ile Phe Ile Thr Ile Met Lys Met Arg Ser
      165      170      175
Pro Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr
      180      185      190
Ala Val Ser Ile Phe Tyr
      195

```

<210> 1611

<211> 315

<212> PRT

<213> Unknown (H38g528 protein)

<220>

<223> Synthetic construct

<400> 1611

```

Met Glu Ala Met Lys Leu Leu Asn Gln Ser Gln Val Ser Glu Phe Ile
 1          5          10          15
Leu Leu Gly Leu Thr Ser Ser Gln Asp Val Glu Phe Leu Leu Phe Ala
 20          25          30
Leu Phe Ser Val Ile Tyr Val Val Thr Val Leu Gly Asn Leu Leu Ile
 35          40          45
Ile Val Thr Val Phe Asn Thr Pro Asn Leu Asn Thr Pro Met Tyr Phe
 50          55          60
Leu Leu Gly Asn Leu Ser Phe Val Asp Met Thr Leu Ala Ser Phe Ala
 65          70          75          80
Thr Pro Lys Val Ile Leu Asn Leu Leu Lys Lys Gln Lys Val Ile Ser
 85          90          95
Phe Ala Gly Cys Phe Thr Gln Ile Phe Leu Leu His Leu Leu Gly Gly
100          105          110
Val Glu Met Val Leu Leu Val Ser Met Ala Phe Asp Arg Tyr Val Ala
115          120          125
Ile Cys Lys Pro Leu His Tyr Met Thr Ile Met Asn Lys Lys Val Cys
130          135          140
Val Leu Leu Val Val Thr Ser Trp Leu Leu Gly Leu Leu His Ser Gly
145          150          155          160
Phe Gln Ile Pro Phe Ala Val Asn Leu Pro Phe Cys Gly Pro Asn Val
165          170          175
Val Asp Ser Ile Phe Cys Asp Leu Pro Leu Val Thr Lys Leu Ala Cys
180          185          190
Ile Asp Ile Tyr Phe Val Gln Val Val Ile Val Ala Asn Ser Gly Ile
195          200          205
Ile Ser Leu Ser Cys Phe Ile Ile Leu Leu Ile Ser Tyr Ser Leu Ile
210          215          220
Leu Ile Thr Ile Lys Asn His Ser Pro Thr Gly Gln Ser Lys Ala Arg
225          230          235          240
Ser Thr Leu Thr Ala His Ile Thr Val Val Ile Leu Phe Phe Gly Pro
245          250          255
Cys Ile Phe Ile Tyr Ile Trp Pro Phe Gly Asn His Ser Val Asp Lys
260          265          270
Phe Leu Ala Val Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Ile
275          280          285
Ile Tyr Thr Leu Arg Asn Lys Glu Met Lys Ile Ser Met Lys Lys Leu
290          295          300
Trp Arg Ala Phe Val Asn Ser Arg Glu Asp Thr
305          310          315

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<210> 1612

<211> 317

<212> PRT

<213> Unknown (H38g529 protein)

<220>

<223> Synthetic construct

<400> 1612

```

Met Glu Pro Gln Asn Thr Ser Thr Val Thr Asn Phe Gln Leu Leu Gly
 1          5          10          15
Phe Gln Asn Leu Leu Glu Trp Gln Ala Leu Leu Phe Val Ile Phe Leu
 20          25          30
Leu Ile Tyr Cys Leu Thr Ile Ile Gly Asn Val Val Ile Ile Thr Val
 35          40          45
Val Ser Gln Gly Leu Arg Leu His Ser Pro Met Tyr Met Phe Leu Gln
 50          55          60
His Leu Ser Phe Leu Glu Val Trp Tyr Thr Ser Thr Thr Val Pro Leu

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65          70          75          80
Leu Leu Ala Asn Leu Leu Ser Trp Gly Gln Ala Ile Ser Phe Ser Ala
      85          90          95
Cys Met Ala Gln Leu Tyr Phe Phe Val Phe Leu Gly Ala Thr Glu Cys
      100          105          110
Phe Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Ser
      115          120          125
Pro Leu Arg Tyr Pro Phe Leu Met His Arg Gly Leu Cys Ala Arg Leu
      130          135          140
Val Val Val Ser Trp Cys Thr Gly Val Ser Thr Gly Phe Leu His Ser
145          150          155          160
Met Met Ile Ser Arg Leu Asp Phe Cys Gly Arg Asn Gln Ile Asn His
      165          170          175
Phe Phe Cys Asp Leu Pro Pro Leu Met Gln Leu Ser Cys Ser Arg Val
      180          185          190
Tyr Ile Thr Glu Val Thr Ile Phe Ile Leu Ser Ile Ala Val Leu Cys
      195          200          205
Ile Cys Phe Phe Leu Thr Leu Gly Pro Tyr Val Phe Ile Val Ser Ser
      210          215          220
Ile Leu Arg Ile Pro Ser Thr Ser Gly Arg Arg Lys Thr Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Ala Val Val Thr Leu Tyr Tyr Gly Thr Met Ile
      245          250          255
Ser Met Tyr Val Cys Pro Ser Pro His Leu Leu Pro Glu Ile Asn Lys
      260          265          270
Ile Ile Ser Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Phe Lys Glu Ala Val Arg Lys Val
      290          295          300
Met Arg Arg Lys Cys Gly Ile Leu Trp Ser Thr Ser Lys
305          310          315

```

<210> 1613

<211> 335

<212> PRT

<213> Unknown (H38g530 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1613

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Gly Ser Ser Glu Asp Pro Glu Trp Gln Pro Val Leu Thr Gly Leu Cys
      20          25          30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35          40          45
Ala Val Ser Pro Asp Ser His Leu His Ile Pro Met Tyr Phe Phe Leu
      50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
      100          105          110
Glu Asn Met Leu Leu Ser Val Ile Ala Tyr Glu Arg Phe Val Ala Ile
      115          120          125

```

Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
 130 135 140
 Phe Leu Val Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln
 145 150 155 160
 Leu His Asn Leu Ile Ala Leu Gln Arg Thr Cys Phe Lys Asp Val Glu
 165 170 175
 Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Tyr
 180 185 190
 Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile
 210 215 220
 Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
 245 250 255
 Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
 260 265 270
 Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Ile Pro Met Pro
 275 280 285
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Ser Val Leu
 290 295 300
 Gln Arg Pro His Gly Ser Thr Ile Ser Ser Gln Tyr Leu Leu Ile Cys
 305 310 315 320
 Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
 325 330 335

<210> 1614

<211> 330

<212> PRT

<213> Unknown (H38g531 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 1614

His Thr Glu Pro Gln Asn Leu Thr Gly Ile Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Thr Leu
 35 40 45
 Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Ile Val Pro
 65 70 75 80
 Lys Met Thr Val Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 100 105 110
 Asp Met Phe Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu Tyr Tyr Pro Val Ile Ile Asn Pro His Leu Cys Val Phe
 130 135 140
 Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Ser Trp Ile Val Xaa Gln Phe Thr Phe Ser Lys Asn Val Glu Ile Ser

Asn	Phe	Val	Cys	Glu	Pro	Ser	Gln	Leu	Leu	Tyr	Leu	Ala	Cys	Ser	Asp
			180					185					190		
Ser	Ile	Ile	Asn	Ser	Ile	Phe	Ile	Tyr	Phe	Asp	Ser	Thr	Met	Phe	Gly
		195					200					205			
Phe	Leu	Pro	Ile	Ser	Arg	Ile	Leu	Leu	Ser	Tyr	Tyr	Lys	Ile	Val	Pro
	210					215					220				
Ser	Ile	Leu	Arg	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr	Lys	Ala	Phe	Thr
	225				230					235					240
Thr	Cys	Gly	Ser	His	Leu	Ala	Val	Val	Cys	Leu	Phe	Asp	Gly	Thr	Gly
			245					250						255	
Ile	Gly	Met	Tyr	Leu	Thr	Ser	Ala	Val	Ala	Pro	Pro	Pro	Arg	Asn	Gly
		260						265					270		
Val	Val	Ala	Ser	Val	Met	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu	Asn	Pro
	275						280					285			
Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Asn	Thr	Leu	Trp	Arg
	290					295					300				
Leu	Arg	Ser	Arg	Arg	Val	Glu	Ser	His	Asp	Leu	Phe	His	Pro	Phe	Phe
	305				310					315					320
Val	Trp	Val	Arg	Lys	Gly	Asn	His	Ile	Lys						
			325						330						

<210> 1615

<211> 335

<212> PRT

<213> Unknown (H38g532 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1615

Ser	Thr	Asp	Pro	Gln	Asn	Leu	Ile	Asp	Val	Phe	Val	Phe	Leu	Leu	Leu
1					5				10					15	
Gly	Thr	Ser	Glu	Asp	Pro	Glu	Arg	Gln	Leu	Val	Leu	Ala	Gly	Leu	Phe
			20					25					30		
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu
		35					40					45			
Ala	Val	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	Asn	Leu	Ser	Leu	Pro	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro
	65				70				75					80	
Lys	Leu	Ile	Val	Asp	Ile	Gln	Ser	Tyr	Ser	Arg	Val	Ile	Ser	Tyr	Ala
			85					90						95	
Gly	Cys	Leu	Thr	Gln	Thr	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Met	Glu
		100						105					110		
Glu	Asn	Met	Leu	Leu	Ser	Val	Met	Val	Tyr	Asp	Arg	Phe	Val	Ala	Ile
	115					120						125			
Cys	His	Pro	Leu	Tyr	His	Ser	Ala	Val	Met	Asn	Pro	Cys	Phe	Cys	Gly
	130					135					140				
Phe	Leu	Val	Leu	Leu	Ser	Phe	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ala	Gln
	145				150				155					160	
Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Lys	Asp	Val	Glu
			165					170					175		
Ile	Pro	Asn	Phe	Phe	Trp	Asp	Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	Cys
		180					185						190		
Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Met	Tyr	Phe	Pro	Ala	Ala	Ile
		195					200					205			

```

Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Glu Ile
 210                215                220
Val Ser Ser Ile Leu Arg Val Ser Ser Xaa Gly Gly Lys Tyr Lys Ala
225                230                235                240
Phe Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
                245                250                255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
                260                265                270
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
                275                280                285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Thr Lys Ser Val Leu
                290                295                300
Arg Arg Pro His Gly Ser Thr Val Xaa Ser Xaa Tyr Leu Leu Ile Cys
305                310                315                320
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Arg Lys Val Lys
                325                330                335

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<210> 1616

<211> 320

<212> PRT

<213> Unknown (H38g533 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1616

```

His Thr Glu Pro Arg His Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1                5                10                15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
                20                25                30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
                35                40                45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
                50                55                60
Ser Asn Leu Cys Trp Ala Asp Ile Ser Phe Thr Ser Ala Thr Val Pro
65                70                75                80
Lys Met Thr Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala
                85                90                95
Gly Cys Leu Thr Arg Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu
                100                105                110
Asp Met Leu Leu Thr Val Met Ala Xaa Asp Cys Phe Val Ala Ile Cys
                115                120                125
Arg Pro Leu His Tyr Ala Val Ile Val Asn Pro His Leu Cys Val Phe
130                135                140
Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
145                150                155                160
Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
                165                170                175
His Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
                180                185                190
Ser Phe Ile Asn Ser Ile Phe Met Tyr Phe Asp Ser Thr Met Phe Gly
195                200                205
Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
210                215                220
Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser
225                230                235                240
Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly

```

<A00> 1617															
Ile	Ser	Leu	Leu	Phe	Trp	Val	Leu	Leu	Leu	Val	Ile	Ser	Arg	Val	Leu
1				5					10					15	
Val	Ala	Met	Ala	Xaa	Gly	Asn	Ser	Thr	Glu	Val	Thr	Glu	Phe	Cys	Leu
			20					25					30		
Leu	Gly	Phe	Gly	Ala	Xaa	Gln	Glu	Phe	Trp	Cys	Ile	Leu	Phe	Ile	Ile
		35					40					45			
Phe	Leu	Leu	Ile	Tyr	Val	Thr	Ser	Ile	Met	Gly	Asn	Ser	Gly	Ile	Ile
	50					55					60				
Leu	Leu	Ile	Asn	Thr	Asp	Ser	Arg	Phe	Gln	Thr	Pro	Met	Tyr	Phe	Phe
65					70					75					80
Leu	Gln	His	Leu	Ala	Phe	Val	Asp	Ile	Cys	Tyr	Thr	Ser	Ala	Ile	Thr
				85					90					95	
Pro	Lys	Met	Leu	Gln	Ser	Phe	Thr	Glu	Glu	Lys	Asn	Leu	Ile	Ser	Phe
			100					105					110		
Trp	Gly	Cys	Met	Ile	Gln	Leu	Leu	Val	Tyr	Ala	Thr	Phe	Ala	Thr	Ser
		115					120					125			
Asp	Cys	Tyr	Leu	Leu	Ala	Met	Ile	Ala	Val	Asp	His	Tyr	Val	Ala	Ile
	130					135					140				
Cys	Lys	Pro	Leu	His	Tyr	Thr	Val	Ile	Thr	Ser	Gln	Thr	Val	Cys	Ile
145					150					155					160
His	Leu	Val	Ala	Gly	Ser	Tyr	Ile	Met	Gly	Ser	Ile	Asn	Ala	Ser	Val
				165					170					175	
His	Thr	Gly	Phe	Ala	Phe	Ser	Leu	Ser	Phe	Cys	Lys	Ser	Asn	Asn	Ile
			180					185					190		
Asn	His	Phe	Phe	Cys	Asp	Gly	Pro	Pro	Ile	Leu	Ala	Leu	Ser	Cys	Ser
		195					200					205			
Asn	Ile	Asp	Ile	Asn	Ile	Met	Leu	Leu	Val	Val	Phe	Val	Gly	Phe	Asn
	210					215					220				
Leu	Met	Phe	Thr	Gly	Leu	Val	Val	Ile	Phe	Ser	Tyr	Ile	Tyr	Ile	Met
225				230						235					240
Ala	Thr	Ile	Leu	Lys	Met	Ser	Ser	Ser	Ala	Gly	Arg	Lys	Lys	Ser	Phe
				245					250					255	
Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Thr	Val	Ala	Ile	Phe	Tyr	Gly	Thr
			260					265					270		
Leu	Ser	Tyr	Met	His	Leu	Gln	Ser	His	Ser	Asn	Asn	Ser	Gln	Glu	Asn
		275					280					285			
Met	Lys	Val	Ala	Ser	Ile	Phe	Tyr	Gly	Thr	Val	Ile	Pro	Met	Leu	Asn
	290					295					300				

Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys
 305 310 315 320
 Leu Ile Gly Lys Lys Phe Phe
 325

<210> 1618

<211> 309

<212> PRT

<213> Unknown (H38g535 protein)

<220>

<223> Synthetic construct

<400> 1618

Met Thr Leu Gly Asn Ser Thr Glu Val Thr Glu Phe Tyr Leu Leu Gly
 1 5 10 15
 Phe Gly Ala Gln His Glu Phe Trp Cys Ile Leu Phe Ile Val Phe Leu
 20 25 30
 Leu Ile Tyr Val Thr Ser Ile Met Gly Asn Ser Gly Ile Ile Leu Leu
 35 40 45
 Ile Asn Thr Asp Ser Arg Phe Gln Thr Leu Thr Tyr Phe Phe Leu Gln
 50 55 60
 His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
 65 70 75 80
 Met Leu Gln Ser Phe Thr Glu Glu Lys Asn Leu Met Leu Phe Gln Gly
 85 90 95
 Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys
 100 105 110
 Tyr Leu Leu Ala Met Met Ala Val Asp Pro Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Thr Val Ile Met Ser Arg Thr Val Cys Ile Arg Leu
 130 135 140
 Val Ala Gly Ser Tyr Ile Met Gly Ser Ile Asn Ala Ser Val Gln Thr
 145 150 155 160
 Gly Phe Thr Cys Ser Leu Ser Phe Cys Lys Ser Asn Ser Ile Asn His
 165 170 175
 Phe Phe Cys Asp Val Pro Pro Ile Leu Ala Leu Ser Cys Ser Asn Val
 180 185 190
 Asp Ile Asn Ile Met Leu Leu Val Val Phe Val Gly Ser Asn Leu Ile
 195 200 205
 Phe Thr Gly Leu Val Val Ile Phe Ser Tyr Ile Tyr Ile Met Ala Thr
 210 215 220
 Ile Leu Lys Met Ser Ser Ser Ala Gly Arg Lys Lys Ser Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
 245 250 255
 Tyr Met Tyr Leu Gln Ser His Ser Asn Asn Ser Gln Glu Asn Met Lys
 260 265 270
 Val Ala Phe Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Lys Val Ile
 290 295 300
 Gly Lys Lys Leu Phe
 305

<210> 1619

<211> 298

<212> PRT

<213> Unknown (H38g536 protein)

<220>

<223> Synthetic construct

<400> 1619

```

Met Gly Arg Gly Asn Ser Thr Glu Val Thr Glu Phe His Leu Leu Gly
 1           5           10           15
Phe Gly Val Gln His Glu Phe Gln His Val Leu Phe Ile Val Leu Leu
 20           25           30
Leu Ile Tyr Val Thr Ser Leu Ile Gly Asn Ile Gly Met Ile Leu Leu
 35           40           45
Ile Lys Thr Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Pro Gln
 50           55           60
His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro Lys
 65           70           75
Met Leu Gln Ser Phe Thr Glu Glu Asn Asn Leu Ile Thr Phe Arg Gly
 85           90           95
Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser Asp Cys
100           105           110
Tyr Leu Leu Ala Ile Met Ala Met Asp Cys Tyr Val Ala Ile Cys Lys
115           120           125
Pro Leu Arg Tyr Pro Met Ile Met Ser Gln Thr Val Tyr Ile Gln Leu
130           135           140
Val Ala Gly Ser Tyr Ile Ile Gly Ser Ile Asn Ala Ser Val His Thr
145           150           155
Gly Phe Thr Phe Ser Leu Ser Phe Cys Lys Ser Asn Lys Ile Asn His
165           170           175
Phe Phe Cys Asp Gly Leu Pro Ile Leu Ala Leu Ser Cys Ser Asn Ile
180           185           190
Asp Ile Asn Ile Ile Leu Asp Val Val Phe Val Gly Phe Asp Leu Met
195           200           205
Phe Thr Glu Leu Val Ile Ile Phe Ser Tyr Ile Tyr Ile Met Val Thr
210           215           220
Ile Leu Lys Met Ser Ser Thr Ala Gly Arg Lys Lys Ser Phe Ser Thr
225           230           235
Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly Thr Leu Ser
245           250           255
Tyr Met Tyr Leu Gln Pro Gln Ser Asn Asn Ser Gln Glu Asn Met Lys
260           265           270
Val Ala Ser Ile Phe Tyr Gly Thr Val Ile Pro Met Leu Asn Pro Leu
275           280           285
Ile Tyr Ser Leu Arg Asn Lys Glu Gly Lys
290           295

```

<210> 1620

<211> 148

<212> PRT

<213> Unknown (H38g537 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(148)

<223> Xaa = Any Amino Acid

<400> 1620

```

Thr Tyr Asp Gly Ala Arg Ala Gly Leu Cys Ile Val Ser Tyr Asn Thr
 1           5           10           15
Cys Lys Ser Thr Met Met Ser Ile Lys Ile Gln Leu Lys Tyr Met Xaa
 20           25           30
Xaa Lys Xaa Leu Leu Ile Tyr Ala Gly Val Tyr Leu Asn Val Thr Met
 35           40           45

```

Leu Ile Val Thr Phe Lys Tyr Thr His Ile Phe His His Pro Glu Leu
 50 55 60
 Ala Leu Cys Tyr Val Ser Phe Ser Ala Val Val Phe His Leu Thr Ala
 65 70 75 80
 Val Thr Ile Phe Phe Gly Ala Leu Ser Tyr Met Asp Leu Gln Pro Glu
 85 90 95
 Ser Thr Val Phe Gln Glu Gln Glu Lys Pro Ala Ser Ile Phe Cys Gly
 100 105 110
 Ile Met Thr Leu Val Leu Asn Phe Leu Ile Tyr Cys Leu Xaa Asn Xaa
 115 120 125
 Glu Val Lys Glu Ala Leu Gln Leu Thr Arg Lys Lys Tyr Xaa Tyr Met
 130 135 140
 Xaa Thr Glu Gly
 145

<210> 1621

<211> 296

<212> PRT

<213> Unknown (H38g538 protein)

<220>

<223> Synthetic construct

<400> 1621

Met Leu Val Ser Gln Gln Glu Gln Pro Leu Leu Phe Gly Ile Phe Leu
 1 5 10 15
 Gly Met Tyr Leu Val Thr Met Val Gly Asn Leu Leu Ile Ile Leu Ala
 20 25 30
 Ile Ser Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 35 40 45
 Asn Leu Ser Leu Thr Asp Ala Cys Phe Thr Ser Ala Ser Ile Pro Lys
 50 55 60
 Met Leu Ala Asn Ile His Thr Gln Ser Gln Ile Ile Ser Tyr Ser Gly
 65 70 75 80
 Cys Leu Ala Gln Leu Tyr Phe Leu Leu Met Phe Gly Gly Leu Asp Asn
 85 90 95
 Cys Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln
 100 105 110
 Pro Leu His Tyr Ser Thr Ser Met Ser Pro Gln Leu Cys Ala Leu Met
 115 120 125
 Leu Gly Val Cys Trp Val Leu Thr Asn Cys Pro Ala Leu Met His Thr
 130 135 140
 Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln Lys Ala Ile Pro His
 145 150 155 160
 Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 165 170 175
 His Val Asn Glu Leu Met Ile Ile Thr Met Gly Leu Leu Phe Leu Thr
 180 185 190
 Val Pro Leu Leu Ile Val Phe Ser Tyr Val Arg Ile Phe Trp Ala
 195 200 205
 Val Phe Val Ile Ser Ser Pro Gly Gly Arg Trp Lys Ala Phe Ser Thr
 210 215 220
 Cys Gly Ser His Leu Thr Val Val Leu Leu Phe Tyr Gly Ser Leu Met
 225 230 235 240
 Gly Val Tyr Leu Leu Pro Pro Ser Thr Tyr Ser Thr Glu Arg Glu Ser
 245 250 255
 Arg Ala Ala Val Leu Tyr Met Val Ile Ile Pro Thr Leu Asn Pro Phe
 260 265 270
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Gly Lys Leu
 275 280 285
 Phe Val Ser Gly Lys Thr Phe Phe

290

295

<210> 1622
 <211> 313
 <212> PRT
 <213> Unknown (H38g539 protein)

<220>
 <223> Synthetic construct

<400> 1622
 Met Lys Arg Glu Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Asp
 1 5 10 15
 Leu Pro Ile Trp Pro Glu Gln Gln Ala Val Phe Phe Thr Leu Phe Leu
 20 25 30
 Gly Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Phe Phe Phe Leu Ser
 50 55 60
 His Leu Ala Leu Thr Asp Ile Ser Leu Ser Ser Val Thr Val Pro Lys
 65 70 75 80
 Met Leu Leu Ser Met Gln Thr Gln Asp Gln Ser Ile Leu Tyr Ala Gly
 85 90 95
 Cys Val Thr Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Asn
 100 105 110
 Phe Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Thr Thr Ile Met Lys Glu Gly Leu Cys Asn Leu Leu
 130 135 140
 Val Thr Val Ser Trp Ile Leu Ser Cys Thr Asn Ala Leu Ser His Thr
 145 150 155 160
 Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His
 165 170 175
 Phe Phe Cys Asp Leu Val Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile
 180 185 190
 Ser Leu Asn Glu Leu Val Ile Phe Thr Val Gly Gln Ala Val Ile Thr
 195 200 205
 Leu Pro Leu Ile Cys Ile Leu Ile Ser Tyr Gly His Ile Gly Val Thr
 210 215 220
 Ile Leu Lys Ala Pro Ser Thr Lys Gly Ile Phe Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr Gly Thr Ile Ile
 245 250 255
 Gly Leu Tyr Phe Leu Pro Ser Ser Ser Ala Ser Ser Asp Lys Asp Val
 260 265 270
 Ile Ala Ser Val Met Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Ala Leu Glu Arg Leu
 290 295 300
 Phe Asn Arg Ala Thr Val Leu Ser Gln
 305 310

<210> 1623
 <211> 311
 <212> PRT
 <213> Unknown (H38g540 protein)

<220>
 <223> Synthetic construct

<400> 1623

```

Met Glu Asn Gln Ser Ser Ile Ser Glu Phe Phe Leu Arg Gly Ile Ser
 1          5          10          15
Ala Pro Pro Glu Gln Gln Gln Ser Leu Phe Gly Ile Phe Leu Cys Met
          20          25          30
Tyr Leu Val Thr Leu Thr Gly Asn Leu Leu Ile Ile Leu Ala Ile Gly
          35          40          45
Ser Asp Leu His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu
          50          55          60
Ser Phe Val Asp Met Gly Leu Thr Ser Ser Thr Val Thr Lys Met Leu
          65          70          75          80
Val Asn Ile Gln Thr Arg His His Thr Ile Ser Tyr Thr Gly Cys Leu
          85          90          95
Thr Gln Met Tyr Phe Phe Leu Met Phe Gly Asp Leu Asp Ser Phe Phe
          100          105          110
Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
          115          120          125
Cys Tyr Ser Thr Val Met Arg Pro Gln Val Cys Ala Leu Met Leu Ala
          130          135          140
Leu Cys Trp Val Leu Thr Asn Ile Val Ala Leu Thr His Thr Phe Leu
          145          150          155          160
Met Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe
          165          170          175
Cys Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile
          180          185          190
Asn Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro
          195          200          205
Phe Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu
          210          215          220
Arg Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser
          225          230          235          240
Ser His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala
          245          250          255
Tyr Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala
          260          265          270
Ala Ala Met Tyr Thr Ile Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
          275          280          285
Ser Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Lys Arg Leu Phe Ser
          290          295          300
His Arg Ser Ile Val Ser Ser
          305          310

```

<210> 1624

<211> 314

<212> PRT

<213> Unknown (H38g541 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1624

```

Met Gly Gly Lys Gln Pro Trp Val Thr Glu Phe Ile Leu Val Gly Phe
 1          5          10          15
Gln Val Gly Pro Ala Leu Ala Ile Leu Leu Cys Gly Leu Phe Ser Val
          20          25          30
Phe Tyr Thr Leu Thr Leu Leu Gly Asn Gly Val Ile Phe Gly Ile Ile
          35          40          45
Cys Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His

```

```

      50              55              60
Leu Ala Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met
65              70              75              80
Leu Ala Asn Leu Met Asn Gln Lys Ser Thr Ile Ser Phe Val Pro Cys
      85              90              95
Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Glu Cys Leu
      100              105              110
Ile Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
      115              120              125
Phe Gln Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Ala
      130              135              140
Ser Thr Cys Trp Ile Ile Ser Phe Leu Met Ala Leu Val His Ile Thr
145              150              155              160
His Ile Leu Arg Pro Pro Phe Cys Gly Pro Gln Lys Ile Asn His Phe
      165              170              175
Ile Cys Gln Ile Met Ser Val Phe Lys Leu Ala Cys Ala Gly Pro Arg
      180              185              190
Leu Asn Gln Val Val Leu Tyr Ala Gly Ser Ala Phe Ile Val Glu Gly
      195              200              205
Pro Leu Cys Leu Glu Leu Val Ser Asn Leu His Ile Leu Ser Ala Ile
      210              215              220
Leu Arg Ile Gln Asn Gly Glu Gly Arg Arg Pro Thr Tyr Ser Ser Cys
225              230              235              240
Ser Ser His Leu Cys Met Val Gly Leu Leu Phe Gly Ser Thr Met Val
      245              250              255
Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val
      260              265              270
Leu Ser Leu Phe Tyr Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
      275              280              285
Tyr Ser Leu Arg Asn Ala Glu Val Lys Gly Ala Leu Lys Arg Val Leu
      290              295              300
Trp Lys Gln Arg Ser Lys Xaa Gly Met Pro
305              310

```

<210> 1625

<211> 193

<212> PRT

<213> Unknown (H38g542 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(193)

<223> Xaa = Any Amino Acid

<400> 1625

```

Leu Lys Val Tyr Xaa Lys Ala Ile Xaa Val Gln Lys Gln Gly Lys Phe
1      5      10      15
Phe Val Ile Ile Phe Cys Xaa Xaa Cys Glu Met Xaa Gly Lys Asn Ile
      20      25      30
Gln Leu Xaa Gly Cys Leu Thr Val Leu Leu Glu Thr Ser Phe Ala Leu
      35      40      45
Gln Arg Pro Leu Cys Gly Asn Leu Ile Asp Asp Thr Cys Glu Ile Leu
      50      55      60
Glu Val Leu Lys Leu Val Cys Ser Ser Ser Leu Leu Met Asp Met Ile
65              70              75              80
Met Met Val Val Asn Ile Leu Leu Leu Pro Ile Pro Met Tyr Leu Phe
      85              90              95
Ile Thr Met Cys Ser Val Ile Leu Phe Leu Lys Arg Ser Tyr Gly Asn
      100              105              110

```

Leu Pro Arg Glu Phe Ser Phe Cys Ile Ser Trp Ser Ile Trp Val Phe
 115 120 125
 Val Tyr Cys Leu Ala Ile Ile Phe Arg Ala Leu Tyr Lys Leu Thr Lys
 130 135 140
 Ile Trp Gly Ser Thr Met Asn Glu Ile Val Arg Trp Met Tyr Xaa Tyr
 145 150 155 160
 Xaa Thr Tyr Xaa Tyr Xaa Ile Val Xaa His Lys Leu Ala Leu Lys Tyr
 165 170 175
 Asn His Lys Leu Val Ser Thr Met Leu Gln Ala Leu Leu Ser Phe Leu
 180 185 190
 Lys

<210> 1626

<211> 314

<212> PRT

<213> Unknown (H38g543 protein)

<220>

<223> Synthetic construct

<400> 1626

Met Ala Glu Glu Asn His Thr Met Lys Asn Glu Phe Ile Leu Thr Gly
 1 5 10 15
 Phe Thr Asp His Pro Glu Leu Lys Thr Leu Leu Phe Val Val Phe Phe
 20 25 30
 Ala Ile Tyr Leu Ile Thr Val Val Gly Asn Ile Ser Leu Val Ala Leu
 35 40 45
 Ile Phe Thr His Arg Arg Leu His Thr Pro Met Tyr Ile Phe Leu Gly
 50 55 60
 Asn Leu Ala Leu Val Asp Ser Cys Cys Ala Cys Ala Ile Thr Pro Lys
 65 70 75 80
 Met Leu Glu Asn Phe Phe Ser Glu Asn Lys Arg Ile Ser Leu Tyr Glu
 85 90 95
 Cys Ala Val Gln Phe Tyr Phe Leu Cys Thr Val Glu Thr Ala Asp Cys
 100 105 110
 Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Gln Tyr His Ile Met Met Ser Lys Lys Leu Cys Ile Gln Met
 130 135 140
 Thr Thr Gly Ala Phe Ile Ala Gly Asn Leu His Ser Met Ile His Val
 145 150 155 160
 Gly Leu Val Phe Arg Leu Val Phe Cys Gly Ser Asn His Ile Asn His
 165 170 175
 Phe Tyr Cys Asp Ile Leu Pro Leu Tyr Arg Leu Ser Cys Val Asp Pro
 180 185 190
 Tyr Ile Asn Glu Leu Val Leu Phe Ile Phe Ser Gly Ser Val Gln Val
 195 200 205
 Phe Thr Ile Gly Ser Val Leu Ile Ser Tyr Leu Tyr Ile Leu Leu Thr
 210 215 220
 Ile Phe Lys Met Lys Ser Lys Glu Gly Arg Ala Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Phe Leu Ser Val Ser Leu Phe Tyr Gly Ser Leu Phe
 245 250 255
 Phe Met Tyr Val Arg Pro Asn Leu Leu Glu Glu Gly Asp Lys Asp Ile
 260 265 270
 Pro Ala Ala Ile Leu Phe Thr Ile Val Val Pro Leu Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Glu Val Ile Ser Val Leu Arg Lys Ile
 290 295 300
 Leu Met Lys Glu Ile Ile Ser Arg Arg Trp

305

310

<210> 1627

<211> 316

<212> PRT

<213> Unknown (H38g544 protein)

<220>

<223> Synthetic construct

<400> 1627

```

Met Gln Gly Glu Asn Phe Thr Ile Trp Ser Ile Phe Phe Leu Glu Gly
 1           5           10           15
Phe Ser Gln Tyr Pro Gly Leu Glu Val Val Leu Phe Val Phe Ser Leu
 20           25           30
Val Met Tyr Leu Thr Thr Leu Leu Gly Asn Ser Thr Leu Ile Leu Ile
 35           40           45
Thr Ile Leu Asp Ser Arg Leu Lys Thr Pro Met Tyr Leu Phe Leu Gly
 50           55           60
Asn Leu Ser Phe Met Asp Ile Cys Tyr Thr Ser Ala Ser Val Pro Thr
 65           70           75           80
Leu Leu Val Asn Leu Ser Ser Gln Lys Thr Ile Ile Phe Ser Gly
 85           90           95
Cys Ala Val Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
 100          105          110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115          120          125
Pro Leu Arg Tyr Ser Ile Ile Met Asn Arg Cys Val Cys Ala Arg Met
 130          135          140
Ala Thr Val Ser Trp Val Thr Gly Cys Leu Thr Ala Leu Leu Glu Thr
 145          150          155          160
Ser Phe Ala Leu Gln Ile Pro Leu Cys Gly Asn Leu Ile Asp His Phe
 165          170          175
Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Thr Ser Ser Leu
 180          185          190
Leu Met Asn Thr Ile Met Leu Val Val Ser Ile Leu Leu Leu Pro Ile
 195          200          205
Pro Met Leu Leu Val Cys Ile Ser Tyr Ile Phe Ile Leu Ser Thr Ile
 210          215          220
Leu Arg Ile Thr Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser Thr Cys
 225          230          235          240
Gly Ala His Leu Thr Val Val Ile Leu Tyr Tyr Gly Ala Ala Leu Ser
 245          250          255
Met Tyr Leu Lys Pro Ser Ser Ser Asn Ala Gln Lys Ile Asp Lys Ile
 260          265          270
Ile Ser Leu Leu Tyr Gly Val Leu Thr Pro Met Leu Asn Pro Ile Ile
 275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Met Lys Lys Leu Leu
 290          295          300
Gly Lys Ile Thr Leu His Gln Thr His Glu His Leu
305           310           315

```

<210> 1628

<211> 312

<212> PRT

<213> Unknown (H38g545 protein)

<220>

<223> Synthetic construct

<400> 1628

Met Met Gly Arg Arg Asn Asn Thr Asn Val Ala Asp Phe Ile Leu Met
 1 5 10 15
 Gly Leu Thr Leu Ser Glu Glu Ile Gln Met Ala Leu Phe Met Leu Phe
 20 25 30
 Leu Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu
 35 40 45
 Ile Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Thr His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Val Thr Pro
 65 70 75 80
 Lys Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Thr Gly
 85 90 95
 Cys Phe Ala Gln Met Phe Phe Phe Ala Phe Leu Gly Thr Ala Glu Cys
 100 105 110
 Tyr Leu Leu Ser Ser Met Ala His Asp Arg Tyr Ala Ala Ile Cys Ser
 115 120 125
 Pro Leu His Tyr Thr Val Ile Met Ser Lys Arg Leu Cys Leu Ala Leu
 130 135 140
 Ile Thr Gly Pro Tyr Val Ile Gly Phe Ile Asp Ser Phe Val Asn Val
 145 150 155 160
 Val Ser Met Ser Arg Leu His Phe Tyr Asp Ser Asn Val Ile His His
 165 170 175
 Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Thr Asp Thr
 180 185 190
 Tyr Asn Thr Glu Ile Leu Ile Phe Ile Ile Val Gly Ser Thr Leu Met
 195 200 205
 Val Ser Leu Phe Thr Ile Ser Ala Ser Tyr Val Phe Ile Leu Phe Thr
 210 215 220
 Ile Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Val Ser His Leu Leu Gly Val Thr Ile Phe Tyr Ser Thr Leu Ile
 245 250 255
 Phe Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln
 260 265 270
 Val Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Val Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Val Ile Arg Val
 290 295 300
 Met Gln Arg Arg Gln Asp Ser Arg
 305 310

<210> 1629

<211> 212

<212> PRT

<213> Unknown (H38g546 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1629

Thr Met Phe Tyr Lys Ile Ser Ala Leu Phe Xaa Cys Leu Cys Ile Thr
 1 5 10 15
 Leu Phe Xaa Xaa Lys Leu Ser Lys Gln Lys Ile Tyr Trp Val Leu Thr
 20 25 30
 Ile Phe Gly Phe Leu Glu Ala Phe Ile Ala Met Asn Lys Leu Xaa Lys
 35 40 45
 Leu Tyr Ser Ser Leu Ile Cys Leu Tyr Phe Ile Ile Xaa Ile Phe Lys

```

      50              55              60
Phe Ser Asn Met Phe Ile Phe Tyr Asn Met Asn Ile Ser Val His Tyr
65              70              75              80
Phe Leu Lys Cys Ile Phe Phe Phe Cys Ile Cys Cys Leu Xaa Leu Leu
      85              90              95
Ile Phe Asp Ser Phe Ser Thr His Pro Pro Leu Pro Leu Leu Xaa Glu
      100              105              110
Ala Asp Ile Cys Ala Asn Ser Xaa Pro Cys Tyr Thr Asn Thr Thr Ala
      115              120              125
Ser Xaa Xaa His Phe Tyr Ile Ile Leu Asn Phe Cys Leu Ser Tyr Xaa
      130              135              140
Pro Ser Val Ser Ser Met Leu Tyr Gly Arg Leu Phe Leu Met Tyr Leu
145              150              155              160
Met Pro Glu Asn Ser Leu Asp Thr Asp Arg Met Ala Ser Val Phe Tyr
      165              170              175
Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Trp Ser Pro Arg Asn
      180              185              190
Lys Asp Val Thr Ser Ala Leu Arg Lys Val Met Val Asn Arg Lys Gln
      195              200              205
Ala Leu Phe Cys
210

```

<210> 1630

<211> 228

<212> PRT

<213> Unknown (H38g547 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(228)

<223> Xaa = Any Amino Acid

<400> 1630

```

Cys Met Phe Ser Phe Tyr Phe Asn Phe Tyr His Phe Phe Ser Thr Xaa
1              5              10              15
Lys Val Leu Gln Ser Leu Arg Asn Ala Glu Ile Asn Xaa Leu Val Xaa
      20              25              30
Ser Lys Val Ser Asp Xaa Xaa Asn Leu Leu Xaa Asn Xaa Leu Ala Phe
      35              40              45
Ser Trp Thr Ile Arg Leu Cys Thr Thr Thr Ser Tyr Ser Asn Met Gln
      50              55              60
Phe Ser Phe Gln Cys Cys Met Thr Gln Tyr Pro Ala Leu Gln Ser Thr
65              70              75              80
Phe Phe Phe Leu Gly Arg Ser Gln Val Phe Leu Leu Leu Leu Met Ala
      85              90              95
Tyr Asp Asn Tyr Arg Ala Ile Xaa Lys Ser Leu Gln Tyr Leu Val Val
      100              105              110
Met Lys Gln Trp Leu Cys Val Val Leu Leu Val Val Pro Trp Ala Gly
      115              120              125
Gly Phe Leu His Thr Val Ile Gln Leu Gly Leu Ile His Gly Leu Pro
      130              135              140
Ser Tyr Asp Pro Asn Val Ile Gly Arg Phe Val Cys Asp Met Asp Pro
145              150              155              160
Leu Met Lys Leu Val Cys Asp Tyr Thr Leu Asn Arg Phe Val Tyr Phe
      165              170              175
Ala Gly His Asp Leu Asn Tyr Xaa Val Leu Tyr Ile Ser Phe Ile Phe
      180              185              190
Arg Leu Asp Cys Phe Leu Leu Val Ile Xaa L u Trp Tyr Pro Phe Val
195              200              205

```

Ile Phe Ser Leu Glu Arg His Asp Ser Ile Asn Leu Val Ile His Ser
 210 215 220
 Tyr Tyr Pro Cys
 225

<210> 1631

<211> 299

<212> PRT

<213> Unknown (H38g548 protein)

<220>

<223> Synthetic construct

<400> 1631

Met Glu Pro Arg Lys Asn Val Thr Asp Phe Val Leu Leu Gly Phe Thr
 1 5 10 15
 Gln Asn Pro Lys Glu Gln Lys Val Leu Phe Val Met Phe Leu Leu Phe
 20 25 30
 Tyr Ile Leu Thr Met Val Gly Asn Leu Leu Ile Val Val Thr Val Thr
 35 40 45
 Val Ser Glu Thr Leu Gly Ser Pro Met Ser Phe Phe Leu Ala Gly Leu
 50 55 60
 Thr Phe Ile Asp Ile Ile Tyr Ser Ser Ser Ile Ser Pro Arg Leu Ile
 65 70 75 80
 Ser Asp Leu Phe Phe Gly Asn Asn Ser Ile Ser Phe Gln Ser Phe Met
 85 90 95
 Ala Gln Leu Phe Ile Glu His Leu Phe Gly Gly Ser Glu Val Phe Leu
 100 105 110
 Leu Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Leu Val Ile Met Arg Gln Trp Val Cys Val Leu Leu Leu Val
 130 135 140
 Val Ser Trp Val Gly Gly Phe Leu Gln Ser Val Phe Gln Leu Ser Ile
 145 150 155 160
 Ile Tyr Gly Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Phe
 165 170 175
 Cys Asp Met Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asp Thr His Val
 180 185 190
 Ile Gly Leu Leu Val Val Ala Asn Gly Gly Leu Ser Cys Thr Ile Ala
 195 200 205
 Phe Leu Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu His Ser Leu Lys
 210 215 220
 Lys Leu Ser Gln Lys Gly Arg Gln Lys Ala His Ser Thr Cys Ser Ser
 225 230 235 240
 His Ile Thr Val Val Val Phe Phe Phe Val Pro Cys Ile Phe Met Cys
 245 250 255
 Ala Arg Pro Ala Arg Thr Phe Ser Ile Asp Lys Ser Val Ser Val Phe
 260 265 270
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ser Glu Met Thr Ser Ala Met Lys Lys Leu
 290 295

<210> 1632

<211> 315

<212> PRT

<213> Unknown (H38g549 protein)

<220>

<223> Synthetic construct

<400> 1632

```

Met Ser Pro Asp Gly Asn His Ser Ser Asp Pro Thr Glu Phe Val Leu
 1          5          10          15
Ala Gly Leu Pro Asn Leu Asn Ser Ala Arg Val Glu Leu Phe Ser Val
          20          25          30
Phe Leu Leu Val Tyr Leu Leu Asn Leu Thr Gly Asn Val Leu Ile Val
          35          40          45
Gly Val Val Arg Ala Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe
          50          55          60
Leu Gly Asn Leu Ser Cys Leu Glu Ile Leu Leu Thr Ser Val Ile Ile
65          70          75          80
Pro Lys Met Leu Ser Asn Phe Leu Ser Arg Gln His Thr Ile Ser Phe
          85          90          95
Ala Ala Cys Ile Thr Gln Phe Tyr Phe Tyr Phe Phe Leu Gly Ala Ser
          100          105          110
Glu Phe Leu Leu Leu Ala Val Met Ser Ala Asp Arg Tyr Leu Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Pro Leu Leu Met Ser Gly Ala Val Cys Phe
          130          135          140
Arg Val Ala Leu Ala Cys Trp Val Gly Gly Leu Val Pro Val Leu Gly
145          150          155          160
Pro Thr Val Ala Val Ala Leu Leu Pro Phe Cys Lys Gln Gly Ala Val
          165          170          175
Val Gln His Phe Phe Cys Asp Ser Gly Pro Leu Leu Arg Leu Ala Cys
          180          185          190
Thr Asn Thr Lys Lys Leu Glu Glu Thr Asp Phe Val Leu Ala Ser Leu
          195          200          205
Val Ile Val Ser Ser Leu Leu Ile Thr Ala Val Ser Tyr Gly Leu Ile
          210          215          220
Val Leu Ala Val Leu Ser Ile Pro Ser Ala Ser Gly Arg Gln Lys Ala
225          230          235          240
Phe Ser Thr Cys Thr Ser His Leu Ile Val Val Thr Leu Phe Tyr Gly
          245          250          255
Ser Ala Ile Phe Leu Tyr Val Arg Pro Ser Gln Ser Gly Ser Val Asp
          260          265          270
Thr Asn Trp Ala Val Thr Val Ile Thr Thr Phe Val Thr Pro Leu Leu
          275          280          285
Asn Pro Phe Ile Tyr Ala Leu Arg Asn Glu Gln Val Lys Glu Ala Leu
          290          295          300
Lys Asp Met Phe Arg Lys Val Val Ala Gly Val
305          310          315

```

<210> 1633

<211> 260

<212> PRT

<213> Unknown (H38g550 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(260)

<223> Xaa = Any Amino Acid

<400> 1633

```

Val Leu Cys Val Ile Phe Cys Lys Xaa Asn His His Ile Ser Leu Leu
 1          5          10          15
Ser Phe Phe Glu Tyr Leu Met Thr Xaa Xaa Lys Lys Tyr Gly Ser Ile
          20          25          30
Cys Ser Thr Met Leu Val Ser Ile Arg Ile Lys Tyr Leu Glu Val Phe
          35          40          45

```

Ala Glu Asn Leu Phe Gly Ala Ala Glu Ile Ile Pro Leu Met Trp Met
 50 55 60
 Val His Gly Cys Tyr Val Thr Val Cys Asn Tyr Met Thr Ile Val Asn
 65 70 75 80
 Gln Tyr Arg Cys Ser His Leu Thr Gly Met Ala Trp Thr Glu Ser Phe
 85 90 95
 Ile His Gly Thr Val Xaa Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr
 100 105 110
 Asp Pro Asn Val Ile Ala His Phe Met Cys Asp Leu Asn Thr Phe Leu
 115 120 125
 Lys Leu Leu Cys Met Gly Thr Thr Asn Thr Ile Gly Phe Phe Val Ala
 130 135 140
 Ala Asn Gly Gly Phe Asn Tyr Leu Leu Asn Ile Ile Phe Leu Met Val
 145 150 155 160
 Ser Xaa Val Ala Ile Leu Cys Thr Leu Lys Thr His Ser Leu Glu Glu
 165 170 175
 Arg Cys Xaa Ser Leu Ser Thr Cys Ile Ser His Thr Thr Met Val Ile
 180 185 190
 Leu Phe Phe Glu Phe Cys Ile Ser Val Tyr Leu Cys Pro Val Thr Leu
 195 200 205
 Leu Pro Ile Asn Lys Ala Met Ala Val Phe His Thr Val Ile Asn Pro
 210 215 220
 Met Leu Lys Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser
 225 230 235 240
 Ala Leu Arg Lys Val Trp Val Lys Arg Xaa Pro Glu Glu Arg Asn Asn
 245 250 255
 Leu Asn Ile Arg
 260

<210> 1634

<211> 318

<212> PRT

<213> Unknown (H38g551 protein)

<220>

<223> Synthetic construct

<400> 1634

Met Glu Trp Glu Asn His Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1 5 10 15
 Leu Ser Gly His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
 20 25 30
 Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
 35 40 45
 Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
 65 70 75 80
 Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Leu Ser Gly
 85 90 95
 Cys Ala Val Gln Met Phe Leu Ser Leu Ala Met Gly Thr Thr Glu Cys
 100 105 110
 Val Leu Leu Gly Val Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asp Ala Tyr Val Pro Met
 130 135 140
 Ala Ala Gly Ser Trp Ile Ile Gly Ala Val Asn Ser Ala Val Gln Thr
 145 150 155 160
 Val Phe Val Val Gln Leu Pro Phe Cys Arg Asn Asn Ile Ile Asn His
 165 170 175
 Phe Thr Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile

<210> 1635
<211> 333
<212> PRT
<213> Unknown (H38g552 protein)

```
<220>  
<223> Synthetic construct  
  
<221> VARIANT  
<222> (1)...(333)  
<223> Xaa = Any Amino Acid
```

<400> 1635															
Met	Glu	Arg	Thr	Asn	Trp	Thr	Glu	Ile	Glu	Phe	Ile	Leu	Gln	Gly	Leu
1				5					10					15	
Ser	Gly	Tyr	Pro	Arg	Ala	Glu	Lys	Phe	Leu	Phe	Val	Met	Cys	Leu	Val
			20					25					30		
Met	Tyr	Leu	Val	Ile	Leu	Leu	Gly	Asn	Gly	Thr	Leu	Ile	Ile	Leu	Thr
		35					40					45			
Leu	Leu	Asp	Ala	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly	Asn
		50				55					60				
Leu	Ser	Phe	Leu	Asp	Ile	Trp	Tyr	Thr	Ser	Ser	Ile	Pro	Ser	Met	
65					70				75					80	
Leu	Ile	His	Phe	Leu	Ser	Glu	Lys	Lys	Thr	Ile	Ser	Phe	Thr	Arg	Cys
				85					90					95	
Val	Ile	Gln	Met	Ser	Val	Ser	Tyr	Thr	Met	Gly	Ser	Thr	Glu	Cys	Val
			100					105					110		
Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Asn	Pro
		115					120					125			
Leu	Arg	Tyr	Pro	Ile	Ile	Met	Gly	Lys	Ala	Leu	Cys	Ile	Gln	Met	Val
		130				135					140				
Ala	Val	Ser	Trp	Gly	Leu	Gly	Phe	Leu	Asn	Ser	Leu	Thr	Glu	Thr	Val
145					150				155					160	
Leu	Ala	Ile	Arg	Leu	Pro	Phe	Cys	Gly	Lys	Asn	Val	Ile	Asn	His	Phe
				165					170					175	
Val	Cys	Glu	Ile	Leu	Ala	Phe	Val	Lys	Leu	Ala	Cys	Thr	Asp	Thr	Ser
			180					185					190		
Leu	Asn	Glu	Ile	Ile	Ile	Met	Leu	Gly	Asn	Val	Ile	Phe	Leu	Phe	Ser
		195					200					205			
Pro	Leu	Leu	Leu	Ile	Cys	Ile	Ser	Tyr	Ile	Phe	Ile	Leu	Ser	Thr	Val
		210				215					220				
Leu	Arg	Ile	Asn	Ser	Ala	Glu	Gly	Arg	Lys	Lys	Ala	Phe	Ser	Thr	Cys
225					230					235					240

```

Ser Ala His Met Thr Val Val Ile Val Phe Tyr Gly Thr Ile Leu Phe
                245                250                255
Met Tyr Met Lys Ala Lys Ser Lys Asp Ser Ala Phe Asp Lys Leu Ile
                260                265                270
Ala Leu Phe Tyr Gly Ile Val Thr Pro Met Leu Asn Pro Ile Ile Tyr
                275                280                285
Ser Leu Arg Asn Thr Glu Val His Gly Ala Met Arg Lys Leu Met Ser
                290                295                300
Arg His Leu Val Leu Glu Glu Met Met Thr His Xaa His Leu Xaa Val
305                310                315                320
Tyr Ala Gln Asn Thr Leu Thr Ser Leu Arg Gln His Phe
                325                330

```

<210> 1636

<211> 322

<212> PRT

<213> Unknown (H38g553 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1636

```

His Thr Glu Pro Trp Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
1                5                10                15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
                20                25                30
Leu Ser Leu Ser Met Cys Leu Val Met Val Leu Arg Asn Leu Leu Ser
35                40                45
Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Val Tyr Phe
50                55                60
Phe Leu Ser Lys Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr
65                70                75                80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
85                90                95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Phe Ile Leu Phe Ala Cys
100               105               110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
115               120               125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
130               135               140
Val Ser Phe Leu Leu Val Ser Phe Phe Leu Ser Met Leu Asp Ser Gln
145               150               155               160
Leu His Ser Xaa Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
165               170               175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
180               185               190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asn Ser Thr Met
195               200               205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Cys Lys Ile
210               215               220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225               230               235               240
Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Arg
245               250               255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
260               265               270
Asn Gly Val Val Ala Ser Ala Met Phe Ser Val Val Thr Pro Met Leu

```

275 280 285
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
 290 295 300
 Arg Arg Leu Leu Ser Arg Thr Val Glu Ser Tyr Asp Leu Phe His Pro
 305 310 315 320
 Phe Ser

<210> 1637
 <211> 312
 <212> PRT
 <213> Unknown (H38g554 protein)

<220>
 <223> Synthetic construct

<400> 1637
 Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu
 20 25 30
 Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu
 35 40 45
 Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg
 65 70 75 80
 Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln
 85 90 95
 Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu
 100 105 110
 Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala
 130 135 140
 Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His
 145 150 155 160
 Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro
 165 170 175
 His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly
 180 185 190
 Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile
 195 200 205
 Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly
 210 215 220
 Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg Lys Val Phe Ser
 225 230 235 240
 Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Phe Gly Thr Ala
 245 250 255
 Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser Val Thr Thr Asp
 260 265 270
 Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro
 275 280 285
 Ile Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Arg Ala Leu Arg His
 290 295 300
 Leu Val Lys Arg Gln Arg Pro Ser
 305 310

<210> 1638
 <211> 310
 <212> PRT

<213> Unknown (H38g555 protein)

<220>

<223> Synthetic construct

<400> 1638

```

Met Ala Gly Asn Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly
 1           5           10          15
Phe Ala Asn His Pro Glu Leu Gln Val Ser Leu Phe Leu Met Phe Leu
          20          25          30
Phe Ile Tyr Leu Phe Thr Val Leu Gly Asn Leu Gly Leu Ile Thr Leu
          35          40          45
Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50          55          60
Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Thr Val Thr Pro Lys
          65          70          75          80
Ala Leu Val Asn Phe Gln Ser Asn Arg Arg Ser Ile Ser Phe Val Gly
          85          90          95
Cys Phe Val Gln Met Tyr Phe Phe Val Gly Leu Val Cys Cys Glu Cys
          100         105         110
Phe Leu Leu Gly Ser Met Ala Tyr Asn Arg Tyr Ile Ala Ile Cys Asn
          115         120         125
Pro Leu Leu Tyr Ser Val Val Met Ser Gln Lys Val Ser Asn Trp Leu
          130         135         140
Gly Val Met Pro Tyr Val Ile Gly Phe Thr Ser Ser Leu Ile Ser Val
          145         150         155         160
Trp Val Ile Ser Ser Leu Ala Phe Cys Asp Ser Ser Ile Asn His Phe
          165         170         175
Phe Cys Asp Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Thr Phe
          180         185         190
Gly Thr Glu Met Val Ser Phe Val Leu Ala Gly Phe Thr Leu Leu Ser
          195         200         205
Ser Leu Leu Ile Ile Thr Val Thr Tyr Ile Ile Ile Ser Ala Ile
          210         215         220
Leu Arg Ile Gln Ser Ala Ala Gly Arg Gln Lys Ala Phe Ser Thr Cys
          225         230         235         240
Ala Ser His Leu Met Ala Val Thr Ile Phe Tyr Gly Ser Leu Ile Phe
          245         250         255
Thr Tyr Leu Gln Pro Asp Asn Thr Ser Ser Leu Thr Gln Ala Gln Val
          260         265         270
Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
          275         280         285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Val Ile
          290         295         300
His Arg Lys Leu Phe Pro
          305         310

```

<210> 1639

<211> 157

<212> PRT

<213> Unknown (H38g556 protein)

<220>

<223> Synthetic construct

<400> 1639

```

Ile Cys Ser Pro Leu Leu Tyr Ser Val Ile Ile Ser Asn Lys Ala Cys
 1           5           10          15
Phe Ser Leu Ile Leu Gly Val Tyr Ile Ile Gly Leu Val Cys Ala Ser
          20          25          30
Val His Thr Gly Cys Met Phe Arg Val Gln Phe Cys Lys Phe Asp Leu

```

<210> 1640
<211> 178
<212> PRT
<213> Unknown (H38g557' protein)

<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(178)
<223> Xaa = Any Amino Acid

[illegible]

<210> 1641
<211> 314
<212> PRT
<213> Unknown (H38g558 protein)

<220>
<223> Synthetic construct

<400> 1641

```

Met Thr Arg Lys Asn Tyr Thr Ser Leu Thr Glu Phe Val Leu Leu Gly
 1          5          10          15
Leu Ala Asp Thr Leu Glu Leu Gln Ile Ile Leu Phe Leu Phe Phe Leu
 20          25          30
Val Ile Tyr Thr Leu Thr Val Leu Gly Asn Leu Gly Met Ile Leu Leu
 35          40          45
Ile Arg Ile Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50          55          60
Asn Leu Ser Phe Val Asp Val Cys Asn Ser Thr Thr Ile Thr Pro Lys
 65          70          75          80
Met Leu Ala Asp Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly
 85          90          95
Cys Phe Leu Gln Met Tyr Phe Phe Ile Ser Leu Ala Thr Thr Glu Cys
100          105          110
Ile Leu Phe Gly Leu Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg
115          120          125
Pro Leu Leu Tyr Ser Leu Ile Met Ser Arg Thr Val Tyr Leu Lys Met
130          135          140
Ala Ala Gly Ala Phe Ala Ala Gly Leu Leu Asn Phe Met Val Asn Thr
145          150          155          160
Ser His Val Ser Ser Leu Ser Phe Cys Asp Ser Asn Val Ile His His
165          170          175
Phe Phe Cys Asp Ser Pro Pro Leu Phe Lys Leu Ser Cys Ser Asp Thr
180          185          190
Ile Leu Lys Glu Ser Ile Ser Ser Ile Leu Ala Gly Val Asn Ile Val
195          200          205
Gly Thr Leu Leu Val Ile Leu Ser Ser Tyr Ser Tyr Val Leu Phe Ser
210          215          220
Ile Phe Ser Met His Ser Gly Glu Gly Arg His Arg Ala Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Thr Ala Ile Ile Leu Phe Tyr Ala Thr Cys Ile
245          250          255
Tyr Thr Tyr Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Gln Asp Lys
260          265          270
Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
275          280          285
Ile Tyr Ser Leu Arg Ser Lys Glu Val Lys Lys Ala Leu Ala Asn Val
290          295          300
Ile Ser Arg Lys Arg Thr Ser Ser Phe Leu
305          310

```

<210> 1642

<211> 314

<212> PRT

<213> Unknown (H38g559 protein)

<220>

<223> Synthetic construct

<400> 1642

```

Met Thr Arg Lys Asn Tyr Thr Ser Leu Thr Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Ala Asp Thr Leu Glu Leu Gln Ile Ile Leu Phe Leu Leu Phe Leu
 20          25          30
Val Ile Tyr Thr Leu Thr Val Leu Gly Asn Ile Gly Met Ile Leu Leu
 35          40          45
Ile Arg Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Val
 50          55          60
Asn Leu Ser Phe Val Asp Ile Cys Tyr Ser Thr Thr Ile Thr Pro Lys

```



```

65              70              75              80
Met Leu Ala Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly
              85              90              95
Cys Phe Leu Gln Met Tyr Phe Phe Ile Ala Leu Ala Thr Thr Glu Cys
              100             105             110
Ile Leu Phe Gly Leu Met Ala Tyr Asp Arg Tyr Val Thr Ile Cys Arg
              115             120             125
Pro Leu Leu Tyr Ser Leu Ile Met Ser Arg Thr Val Cys Leu Lys Met
              130             135             140
Ala Ala Gly Ala Phe Ala Ala Gly Leu Leu Asn Ser Met Val Asn Thr
145              150             155             160
Ser Tyr Val Ser Ser Leu Ser Phe Cys Gly Ser Asn Val Ile His His
              165             170             175
Phe Phe Cys Asn Ser Pro Pro Leu Phe Lys Leu Ser Cys Ser Asp Thr
              180             185             190
His Leu Lys Glu Ser Ile Phe Ser Thr Phe Ala Gly Val Asn Lys Val
              195             200             205
Gly Ala Leu Leu Val Ile Leu Ser Ser Tyr Ser Tyr Val Leu Phe Ser
              210             215             220
Ile Phe Ser Met His Ser Gly Glu Gly Arg His Arg Ala Phe Ser Thr
225              230             235             240
Cys Ala Ser His Leu Thr Ala Ile Ile Leu Phe Tyr Thr Thr Ser Ile
              245             250             255
Tyr Thr Tyr Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Gln Asp Lys
              260             265             270
Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Ile Leu Asn Pro Leu
              275             280             285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Ala Asn Val
              290             295             300
Ile Ser Arg Lys Arg Ile Pro Ser Phe Leu
305              310

```

<210> 1643

<211> 314

<212> PRT

<213> Unknown (H38g560 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1643

```

Met Ser Gly Glu Asn Val Thr Lys Val Ser Thr Phe Ile Leu Val Gly
1              5              10              15
Leu Pro Thr Ala Pro Gly Leu Gln Tyr Leu Leu Phe Leu Leu Phe Leu
              20              25              30
Leu Thr Tyr Leu Phe Val Leu Val Glu Asn Leu Ala Ile Ile Leu Ile
              35              40              45
Val Trp Ser Ser Thr Ser Leu His Arg Pro Met Tyr Tyr Phe Leu Ser
              50              55              60
Ser Met Ser Phe Leu Glu Ile Trp Tyr Val Ser Asp Ile Thr Pro Lys
65              70              75              80
Met Leu Glu Gly Phe Leu Leu Gln Gln Lys Arg Ile Ser Phe Val Gly
              85              90              95
Cys Met Thr Gln Leu Tyr Phe Phe Ser Ser Leu Val Cys Thr Glu Cys
              100             105             110
Val Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
              115             120             125

```

Pro Leu Arg Tyr His Val Leu Val Thr Ala Gly Leu Cys Val Gln Leu
 130 135 140
 Val Gly Phe Ser Phe Val Ser Gly Phe Ser Ile Ser Met Ile Lys Val
 145 150 155 160
 Cys Phe Ile Ser Ser Val Thr Phe Cys Gly Ser Asn Val Leu Asn His
 165 170 175
 Phe Phe Cys Asp Ile Ser Pro Ile Leu Lys Leu Ala Cys Thr Asp Phe
 180 185 190
 Ser Thr Ala Glu Leu Val Asp Phe Ile Leu Ala Phe Ile Ile Leu Val
 195 200 205
 Phe Pro Leu Leu Ala Thr Ile Leu Ser Tyr Trp His Ile Thr Leu Ala
 210 215 220
 Val Leu Arg Ile Pro Ser Ala Thr Gly Cys Trp Arg Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Thr Val Phe Tyr Thr Ala Leu Leu
 245 250 255
 Phe Met Tyr Val Arg Pro Gln Ala Ile Asp Ser Gln Ser Ser Asn Lys
 260 265 270
 Leu Ile Ser Ala Val Tyr Thr Val Val Thr Pro Ile Ile Asn Pro Leu
 275 280 285
 Ile Tyr Cys Leu Arg Asn Lys Glu Phe Lys Asp Ala Leu Lys Lys Ala
 290 295 300
 Leu Gly Leu Gly Gln Thr Ser His Xaa Asp
 305 310

<210> 1644

<211> 214

<212> PRT

<213> Unknown (H38g561 protein)

<220>

<223> Synthetic construct

<400> 1644

Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu Val
 1 5 10 15
 His Leu Leu Ser Arg Lys Lys Val Ile Val Phe Thr Leu Cys Ala Ala
 20 25 30
 Arg Leu Leu Phe Leu Leu Ile Gly Gly Cys Thr Gln Cys Ala Leu Leu
 35 40 45
 Gly Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
 50 55 60
 Tyr Pro Asn Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr Ala
 65 70 75 80
 Pro Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe Thr
 85 90 95
 Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Trp Cys
 100 105 110
 Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala Ser
 115 120 125
 Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro Val
 130 135 140
 Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val Lys
 145 150 155 160
 Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr Tyr
 180 185 190
 Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val Ser Val Phe
 195 200 205
 Tyr Pro Ile Val Thr Pro

210

<210> 1645

<211> 316

<212> PRT

<213> Unknown (H38g562 protein)

<220>

<223> Synthetic construct

<400> 1645

```

Met Leu Glu Ser Asn Tyr Thr Met Pro Thr Glu Phe Leu Phe Val Gly
 1           5           10           15
Phe Thr Asp Tyr Leu Pro Leu Arg Val Thr Leu Phe Leu Val Phe Leu
      20           25           30
Leu Val Tyr Thr Leu Thr Met Val Gly Asn Ile Leu Leu Ile Ile Leu
      35           40           45
Val Asn Ile Asn Ser Ser Leu Gln Ile Pro Met Tyr Tyr Phe Leu Ser
      50           55           60
Asn Leu Ser Phe Leu Asp Ile Ser Cys Ser Thr Ala Ile Thr Pro Lys
      65           70           75           80
Met Leu Ala Asn Phe Leu Ala Ser Arg Lys Ser Ile Ser Pro Tyr Gly
      85           90           95
Cys Ala Leu Gln Met Phe Phe Phe Ala Ser Phe Ala Asp Ala Glu Cys
      100          105          110
Leu Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn
      115          120          125
Pro Leu Leu Tyr Thr Thr Leu Met Ser Arg Arg Val Cys Val Cys Phe
      130          135          140
Ile Val Leu Ala Tyr Phe Ser Gly Ser Thr Thr Ser Leu Val His Val
      145          150          155          160
Cys Leu Thr Phe Arg Leu Ser Phe Cys Gly Ser Asn Ile Val Asn His
      165          170          175
Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Thr Asp Thr
      180          185          190
Gln Ile Asn Gln Leu Leu Leu Phe Ala Leu Cys Ser Phe Ile Gln Thr
      195          200          205
Ser Thr Phe Val Val Ile Phe Ile Ser Tyr Phe Cys Ile Leu Ile Thr
      210          215          220
Val Leu Ser Ile Lys Ser Ser Gly Gly Arg Ser Lys Thr Phe Ser Thr
      225          230          235          240
Cys Ala Ser His Leu Ile Ala Val Thr Leu Phe Tyr Gly Ala Leu Leu
      245          250          255
Phe Met Tyr Leu Gln Pro Thr Thr Ser Tyr Ser Leu Asp Thr Asp Lys
      260          265          270
Val Val Ala Val Phe Tyr Thr Val Val Phe Pro Met Phe Asn Pro Ile
      275          280          285
Ile Tyr Ser Phe Arg Asn Lys Asp Val Lys Asn Ala Leu Lys Lys Leu
      290          295          300
Leu Glu Arg Ile Gly Tyr Ser Asn Glu Trp Tyr Leu
      305          310          315

```

<210> 1646

<211> 314

<212> PRT

<213> Unknown (H38g563 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1646

```

Met Ser Thr His Arg Met Glu Ile Ser Gln Cys Val Pro Leu Trp Glu
 1              5              10              15
Ser Met Leu Lys Gly Leu Glu Gly Gly Leu Glu Asn Gln Ala Leu Leu
      20              25              30
Phe Ala Val Phe Pro Gly Leu Tyr Met Val Thr Ile Pro Gly Asn Leu
      35              40              45
Thr Met Thr Met Val Ile Ile Leu Asp Thr His Leu His Phe Pro Val
      50              55              60
Asn Phe Phe Leu Gly Ala Ser Pro Phe Leu Asp Leu Gly His Ala Ser
65              70              75              80
Ile Ile Pro Asn Ala Leu Val Asn Phe Ser Ser Ser Ser Lys Val Val
      85              90              95
Thr Phe Ala Gly Cys Ala Ala Arg Phe Phe Phe Ser Leu Leu Ser Thr
      100             105             110
Thr Glu Thr Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Phe Val Ala
      115             120             125
Ile Cys Ser Leu Val Trp Cys Pro Val Thr Thr Cys Leu Ser Ile Cys
      130             135             140
Ile Ile Leu Gly Pro Gly Thr Tyr Cys Arg Val Cys Leu Ser Ser Ile
145             150             155             160
Val Gln Thr Gly Leu Met Phe Gln Leu Pro Ser Ala Gly Thr Asn His
      165             170             175
Ile Asp His Tyr Cys Asp Met Pro Gln Leu Leu Arg Leu Ala Cys Ala
      180             185             190
Cys Leu Ala Leu Asn Glu Leu Thr Lys Phe Ser Leu Cys Gly Leu Met
      195             200             205
Met Val Asn Ala Thr Leu Val Val Leu Val Ser Phe Gly Cys Val Thr
      210             215             220
Val Thr Ile Leu Arg Thr Pro Ser Gly Ser Gln Xaa His Lys Val Phe
225             230             235             240
Thr Cys Ser Ser His Val Met Thr Val Ser Leu Phe Asp Gly Thr Val
      245             250             255
Phe Val Thr Tyr Ala Gln Pro Gly Thr Met Glu Ser Met Glu Gln Gly
      260             265             270
Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Gly Pro
      275             280             285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Arg Arg
      290             295             300
Leu Gly Gln Arg Gln Ala Leu Met Gly Arg
305              310

```

<210> 1647

<211> 252

<212> PRT

<213> Unknown (H38g564 protein)

<220>

<223> Synthetic construct

<400> 1647

```

Met Tyr Phe Phe Leu Gly Asn Leu Ser Phe Cys Asp Ile Cys Tyr Ser
 1              5              10              15
Thr Val Phe Ala Pro Lys Met Leu Val Asn Phe Leu Ser Lys His Lys
      20              25              30
Ser Ser Thr Phe Ser Gly Cys Val Leu Gln Ser Phe Pro Phe Ala Val
      35              40              45
Tyr Val Thr Thr Lys Asp Ile Leu Leu Ser Met Met Ala Tyr Asp His

```

50	55	60
Tyr Val Ala Ile Ala Asn Pro Leu Leu Tyr Thr Val Ile Met Ala Gln		
65	70	75
Lys Val Cys Ile Gln Met Val Leu Ala Ser Tyr Leu Gly Gly Leu Ile		80
	85	90
Asn Ser Leu Thr His Thr Ile Gly Leu Leu Lys Leu Asp Phe Cys Gly		95
	100	105
Pro Asn Ile Val Asn His Tyr Phe Cys Asp Val Pro Pro Leu Leu Arg		110
	115	120
Leu Ser Cys Ser Asp Ala His Ile Asn Glu Met Leu Pro Leu Val Phe		125
	130	135
Ser Gly Leu Ile Ala Met Phe Thr Phe Ile Val Ile Met Val Ser Tyr		140
145	150	155
Ile Cys Ile Ile Ile Ala Ile Gln Arg Ile His Ala Ala Glu Gly Arg		160
	165	170
Tyr Lys Ala Phe Ser Thr Cys Val Ser His Leu Thr Thr Val Thr Leu		175
	180	185
Phe Tyr Gly Ser Val Ser Phe Ser Tyr Ile Gln Pro Ser Ser Gln Tyr		190
	195	200
Ser Leu Glu Gln Glu Lys Val Leu Ala Val Phe Tyr Thr Leu Val Ile		205
	210	215
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys		220
225	230	235
Asp Ala Ala Lys Arg Leu Ile Trp Trp Gly Glu Lys		240
	245	250

<210> 1648

<211> 319

<212> PRT

<213> Unknown (H38g565 protein)

<220>

<223> Synthetic construct

<400> 1648

Met Ser Gly Glu Asn Val Thr Arg Val Gly Thr Phe Ile Leu Val Gly		
1	5	10
Phe Pro Thr Ala Pro Gly Leu Gln Tyr Leu Leu Phe Leu Leu Phe Leu		15
	20	25
Leu Thr Tyr Leu Phe Val Leu Val Glu Asn Leu Ala Ile Ile Leu Thr		30
	35	40
Val Trp Ser Ser Thr Ser Leu His Arg Pro Met Tyr Tyr Phe Leu Ser		45
	50	55
Ser Met Ser Phe Leu Glu Ile Trp Tyr Val Ser Asp Ile Thr Pro Lys		60
65	70	75
Met Leu Glu Gly Phe Leu Leu Gln Gln Lys Arg Ile Ser Phe Val Gly		80
	85	90
Cys Met Thr Gln Leu Tyr Phe Phe Ser Ser Leu Val Cys Thr Glu Cys		95
	100	105
Val Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His		110
	115	120
Pro Leu Arg Tyr His Val Leu Val Thr Pro Gly Cys Ala Ser Arg Leu		125
	130	135
Val Gly Phe Ser Phe Val Ser Gly Phe Thr Ile Ser Met Ile Lys Val		140
145	150	155
Cys Phe Ile Ser Ser Val Thr Phe Cys Gly Ser Asn Val Leu Asn His		160
	165	170
Phe Phe Cys Asp Ile Ser Pro Ile Leu Lys Leu Ala Cys Thr Asp Phe		175
	180	185
Ser Thr Ala Glu Leu Val Asp Phe Ile Leu Ala Phe Ile Ile Leu Val		190
	195	200
		205

Phe Pro Leu Leu Ala Thr Met Leu Ser Tyr Ala His Ile Thr Leu Ala
 210 215 220
 Val Leu Arg Ile Pro Ser Pro Arg Gly Cys Trp Arg Ala Phe Phe Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Thr Val Phe Tyr Thr Ala Leu Leu
 245 250 255
 Phe Met Tyr Val Arg Pro Arg Pro Leu Tyr Ser Arg Ser Ser Asn Lys
 260 265 270
 Leu Ile Ser Val Leu Tyr Thr Val Ile Thr Pro Ile Leu Asn Pro Leu
 275 280 285
 Ile Tyr Cys Leu Arg Asn Lys Glu Phe Lys Asn Ala Leu Lys Asn Ser
 290 295 300
 Arg Leu Asp Asp Cys Ala Val Glu Gly Arg Leu Ser Ser Leu Leu
 305 310 315

<210> 1649

<211> 320

<212> PRT

<213> Unknown (H38g566 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1649

Met Ala Asp Val Asn Phe Thr Leu Val Thr Glu Phe Ile Leu Leu Glu
 1 5 10 15
 Leu Thr Asp Arg Ala Glu Leu Lys Met Val Leu Phe Val Leu Phe Leu
 20 25 30
 Leu Ile Tyr Thr Ile Ser Leu Val Gly Asn Ile Gly Met Leu Phe Leu
 35 40 45
 Ile Tyr Val Thr Pro Lys Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Cys Leu Ser Phe Val Asp Ala Cys Tyr Ser Ser Val Phe Ala Pro Arg
 65 70 75 80
 Met Leu Leu Asn Phe Phe Val Glu Arg Glu Thr Ile Leu Phe Ser Ala
 85 90 95
 Cys Ile Val Gln Tyr Phe Leu Phe Val Ser Leu Leu Thr Thr Glu Gly
 100 105 110
 Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Met Ala Ile Val Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Ala Met Thr Lys Ile Val Cys Ile Val Leu
 130 135 140
 Ala Phe Gly Ser Cys Met Gly Gly Leu Ile Asn Ser Leu Thr His Thr
 145 150 155 160
 Ile Gly Leu Val Lys Leu Ser Phe Cys Gly Pro Asn Val Ile Ser His
 165 170 175
 Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Ser Glu Thr
 180 185 190
 Ser Met Asn Glu Leu Leu Leu Leu Ile Phe Ser Gly Ile Ile Ala Thr
 195 200 205
 Leu Thr Phe Leu Thr Val Val Ile Ser Tyr Ile Phe Ile Val Ala Ala
 210 215 220
 Ile Leu Arg Ile Arg Xaa Ala Ala Gly Arg Arg Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Thr Ser His Leu Ile Thr Val Thr Leu Phe Tyr Gly Ser Ile Ser
 245 250 255
 Phe Ser Tyr Ile Gln Pro Asn Ser Gln Tyr Ser Leu Glu Gln Glu Lys

				260				265				270			
Val	Val	Ser	Val	Phe	Tyr	Thr	Leu	Val	Val	Pro	Met	Leu	Asn	Pro	Leu
				275				280				285			
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Glu	Ala	Val	Lys	Arg	Ala
				290				295				300			
Ile	Glu	Met	Lys	His	Phe	Pro	Cys	Xaa	Phe	His	Ile	Ser	Ile	Ser	Lys
				305				310				315			
												320			

<210> 1650

<211> 313

<212> PRT

<213> Unknown (H38g567 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1) ... (313)

<223> Xaa = Any Amino Acid

<400> 1650

[illegible]

<210> 1651
 <211> 314
 <212> PRT
 <213> Unknown (H38g568 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(314)
 <223> Xaa = Any Amino Acid

<400> 1651
 Ile Xaa Met Ala Asp Arg Asn Val Thr Val Ile Thr Glu Phe Ile Leu
 1 5 10 15
 Leu Gly Leu Thr Asp Asn Pro Glu Met Asn Val Val Leu Ser Val Leu
 20 25 30
 Phe Leu Leu Ile Tyr Leu Ile Thr Val Leu Gly Asn Phe Trp Ile Ile
 35 40 45
 Ile Ile Ile Leu Ala Ser Ala Gln Leu His Ser Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Gln Leu Ala Phe Leu Asp Phe Cys Tyr Ser Ser Val Leu Ile
 65 70 75 80
 Pro Lys Met Leu Val Asn Tyr Ile Ala Gly Gln Lys Val Ile Ser Tyr
 85 90 95
 His Gly Cys Leu Leu Gln Tyr Ser Phe Val Ser Leu Phe Leu Thr Thr
 100 105 110
 Glu Cys Phe Leu Leu Ala Ala Met Ala Cys Asp Arg Tyr Leu Ala Val
 115 120 125
 Cys His Pro Leu His Tyr Lys Gly Leu Met Thr Pro Thr Phe Xaa Ile
 130 135 140
 Tyr Leu Val Thr Val Ser Tyr Leu Leu Gly Ser Val Asn Ser Leu Thr
 145 150 155 160
 His Leu Ser Ser Leu Ser Leu Ser Phe Cys Gly Ser Asn Val Ile
 165 170 175
 Asn Arg Tyr Phe Cys Asp Ile Pro Leu Leu Phe Gln Leu Ser Cys Ser
 180 185 190
 Asn Thr Gln His Ser Lys Ile Leu Phe Thr Val Leu Ser Gly Ala Thr
 195 200 205
 Ser Val Thr Thr Phe Leu Ile Val Val Ser Ser Tyr Leu Val Ile Leu
 210 215 220
 Leu Ile Val Leu Lys Ile His Ser Thr Arg Gly Arg Asn Lys Ala Ile
 225 230 235 240
 Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu Phe Tyr Arg Thr
 245 250 255
 Val Ile Phe Thr Tyr Leu Gly Ala Asn Pro Gly Tyr Ser Gln Asp Arg
 260 265 270
 Pro Lys Ile Leu Pro Val Glu Cys Thr Leu Leu Leu Ser Ile Leu Asn
 275 280 285
 Leu Leu Ile Tyr Ser Val Arg Asn Arg Glu Val Lys Glu Ala Ile Lys
 290 295 300
 Ile Ile Ile Lys Arg Lys Ile Leu Pro Gln
 305 310

<210> 1652
 <211> 314
 <212> PRT
 <213> Unknown (H38g569 protein)

<220>

<223> Synthetic construct

<400> 1652

```

Met Leu Met Asn Tyr Ser Ser Ala Thr Glu Phe Tyr Leu Leu Gly Phe
 1           5           10           15
Pro Gly Ser Glu Leu His His Ile Leu Phe Ala Ile Phe Phe Phe
          20           25           30
Phe Tyr Leu Val Thr Leu Met Gly Asn Thr Val Ile Ile Met Ile Val
          35           40           45
Cys Val Asp Lys Arg Leu Gln Ser Pro Met Tyr Phe Phe Leu Gly His
          50           55           60
Leu Ser Ala Leu Glu Ile Leu Val Thr Thr Ile Ile Val Pro Val Met
65           70           75           80
Leu Trp Gly Leu Leu Leu Pro Gly Met Gln Thr Ile Tyr Leu Ser Ala
          85           90           95
Cys Val Val Gln Leu Phe Leu Tyr Leu Ala Val Gly Thr Thr Glu Phe
          100          105          110
Ala Leu Leu Gly Ala Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn
          115          120          125
Pro Leu Arg Tyr Asn Ile Ile Met Asn Arg His Thr Cys Asn Phe Val
          130          135          140
Val Leu Val Ser Trp Val Phe Gly Phe Leu Phe Gln Ile Trp Pro Val
          145          150          155          160
Tyr Val Met Phe Gln Leu Thr Tyr Cys Lys Ser Asn Val Val Asn Asn
          165          170          175
Phe Phe Cys Asp Arg Gly Gln Leu Leu Lys Leu Ser Cys Asn Asn Thr
          180          185          190
Leu Phe Thr Glu Phe Ile Leu Phe Leu Met Ala Val Phe Val Leu Phe
          195          200          205
Gly Ser Leu Ile Pro Thr Ile Val Ser Asn Ala Tyr Ile Ile Ser Thr
          210          215          220
Ile Leu Lys Ile Pro Ser Ser Ser Gly Arg Arg Lys Ser Phe Ser Thr
          225          230          235          240
Cys Ala Ser His Phe Thr Cys Val Val Ile Gly Tyr Gly Ser Cys Leu
          245          250          255
Phe Leu Tyr Val Lys Pro Lys Gln Thr Gln Ala Ala Asp Tyr Asn Trp
          260          265          270
Val Val Ser Leu Met Val Ser Val Val Thr Pro Phe Leu Asn Pro Phe
          275          280          285
Ile Phe Thr Leu Arg Asn Asp Lys Val Ile Glu Ala Leu Arg Asp Gly
          290          295          300
Val Lys Arg Cys Cys Gln Leu Phe Arg Asn
          305          310

```

<210> 1653

<211> 312

<212> PRT

<213> Unknown (H38g570 protein)

<220>

<223> Synthetic construct

<400> 1653

```

Met Met Gly Arg Arg Asn Asp Thr Asn Val Ala Asp Phe Ile Leu Thr
 1           5           10           15
Gly Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Met Leu Phe
          20           25           30
Leu Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Leu Leu
          35           40           45
Ile Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60

```

```

Thr His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Val Thr Pro
65          70          75          80
Lys Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Thr Gly
          85          90          95
Cys Phe Ala Gln Met Phe Cys Phe Val Phe Leu Gly Thr Ala Glu Cys
          100         105         110
Tyr Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Ser
          115         120         125
Pro Leu His Tyr Thr Val Ile Met Pro Lys Arg Leu Cys Leu Ala Leu
          130         135         140
Ile Thr Gly Pro Tyr Val Ile Gly Phe Met Asp Ser Phe Val Asn Val
145          150         155         160
Val Ser Met Ser Arg Leu His Phe Cys Asp Ser Asn Ile Ile His His
          165         170         175
Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Thr Asp Thr
          180         185         190
Asp Asn Thr Glu Met Leu Ile Phe Ile Ile Ala Gly Ser Thr Leu Met
          195         200         205
Val Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr
          210         215         220
Ile Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Phe Ser Thr
225          230         235         240
Cys Val Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile
          245         250         255
Phe Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln
          260         265         270
Val Ala Pro Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu
          275         280         285
Ile Tyr Ser Leu Arg Asn Arg Glu Val Lys Asn Ala Leu Ile Arg Val
          290         295         300
Met Gln Arg Arg Gln Asp Ser Arg
305          310

```

<210> 1654

<211> 245

<212> PRT

<213> Unknown (H38g571 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(245)

<223> Xaa = Any Amino Acid

<400> 1654

```

Met Ser Xaa Xaa Ile Phe Cys Leu Pro Lys Ile Ile Ile Thr Leu Leu
1          5          10          15
Gln Xaa Glu Trp Asp Ala Leu Asn Leu Glu Thr Arg Val Phe Leu Glu
          20          25          30
Glu Asp Phe Pro Cys Gly Phe Ser Leu Trp Ile Val Arg Gln Leu Ser
          35          40          45
Phe Phe Leu Glu Ile Asn Xaa Phe Ala His Leu Lys Lys Xaa Cys Arg
          50          55          60
Lys His Thr Ser Thr Phe Ser Leu Ser Asn Leu Ala Phe Xaa Asp Phe
65          70          75          80
Cys Tyr Ala Ser Val Ile Thr Ser Lys Met Phe Gly Ser Phe Leu Tyr
          85          90          95
Lys Gln Lys Lys Leu Thr Phe Asn Ala Leu Gly Cys Ser Leu Thr Phe
          100         105         110
Met Thr Thr Glu Cys Leu Leu Leu Ala Phe Met Ala Cys Asp Gln Tyr

```

```

      115              120              125
Leu Val Ile Cys Asn Pro Pro Leu Tyr Met Val Thr Met Ser Pro Pro
 130              135              140
Gln Gly Val Cys Ile Gln Leu Met Pro Ala Ser Tyr Ser Tyr Ser Phe
145              150              155              160
Leu Met Thr Leu Ser His Tyr Leu Ser Ala Phe Arg Leu Pro Tyr Cys
      165              170              175
Pro Ser Val Ser Leu Met Phe Asn Gly Ser Leu Phe Leu Tyr Cys Thr
      180              185              190
Xaa Cys Ser Glu Asn Ser Leu Asp Thr Asp Arg Met Ala Ser Val Phe
 195              200              205
Tyr Thr Val Val Ile Pro Met Leu Ser Pro Leu Ile Trp Ser Leu Arg
 210              215              220
Asn Lys Asp Val Lys Asp Ala Leu Arg Lys Val Ile Val Asn Arg Asn
225              230              235              240
Gln Ala Leu Phe Cys
      245

```

<210> 1655

<211> 312

<212> PRT

<213> Unknown (H38g572 protein)

<220>

<223> Synthetic construct

<400> 1655

```

Met Ala Pro Glu Asn Phe Thr Arg Val Thr Glu Phe Ile Leu Thr Gly
 1              5              10              15
Val Ser Ser Cys Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu
      20              25              30
Val Leu Tyr Val Leu Thr Met Ala Gly Asn Leu Gly Ile Ile Thr Leu
      35              40              45
Thr Ser Val Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg
      50              55              60
His Leu Ala Ile Ile Asn Leu Gly Asn Ser Thr Val Ile Ala Pro Lys
      65              70              75              80
Met Leu Met Asn Phe Leu Val Lys Lys Lys Thr Thr Ser Phe Tyr Glu
      85              90              95
Cys Ala Thr Gln Leu Gly Gly Phe Leu Phe Phe Ile Val Ser Glu Val
      100              105              110
Met Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn,
      115              120              125
Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg Leu Cys Leu Leu Leu
      130              135              140
Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr Ala Ile Val Val Ser
      145              150              155              160
Pro Cys Ile Phe Ser Val Ser Tyr Cys Ser Ser Asn Ile Ile Asn His
      165              170              175
Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
      180              185              190
Tyr Ile Pro Glu Thr Ile Val Phe Ile Ser Ala Ala Thr Asn Leu Phe
      195              200              205
Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe Asn Ile Val Leu Ser
      210              215              220
Ile Leu Arg Ile Arg Ser Pro Glu Gly Arg Lys Lys Ala Phe Ser Thr
      225              230              235              240
Cys Ala Ser His Met Ile Ala Val Thr Val Phe Tyr Gly Thr Met Leu
      245              250              255
Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser Leu Asp Thr Asp Lys
      260              265              270

```

Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Asn Asp Val Asn Val Ala Leu Lys Lys Phe
 290 295 300
 Met Glu Asn Pro Cys Tyr Ser Phe
 305 310

<210> 1656
 <211> 161
 <212> PRT
 <213> Unknown (H38g573 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(161)
 <223> Xaa = Any Amino Acid

<400> 1656
 Ile Cys Gly Ser His Ser Gly Val Thr Glu Phe Cys Leu Leu Gly Phe
 1 5 10 15
 Pro Gly Ser Gln Xaa Val Cys His Leu Leu Pro Ser Ser Phe Val Ser
 20 25 30
 Ile Val Ile Arg Asn Tyr Val Ile Ile Val Cys Val Glu Lys Cys
 35 40 45
 Leu Leu Phe Leu Leu Tyr Leu Phe Tyr Gly Asp Leu Ser Val Met Glu
 50 55 60
 Ile Leu Ile Thr Tyr Thr Ala Val Pro Leu Met Leu Arg Gly Cys Tyr
 65 70 75 80
 Phe Pro Xaa Phe Lys Gln Tyr Leu Xaa Xaa His Val Ser Val Gln Leu
 85 90 95
 Tyr Met Asn Phe Phe Gly Gly Thr Gln Glu Phe Ala Leu Leu Gly Val
 100 105 110
 Met Thr Val Asn His Tyr Val Ala Leu Cys Asn Ser Leu Lys Xaa Asn
 115 120 125
 Ile Ile Met Ser Ser Thr His Cys Ile Trp Leu Val Ile Val Leu Leu
 130 135 140
 Ile Gly Phe Leu Ser Glu Ile Trp Ser Val Tyr Ala Thr Phe Gln Leu
 145 150 155 160
 Pro

<210> 1657
 <211> 324
 <212> PRT
 <213> Unknown (H38g574 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 1657
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser

```

      35              40              45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
  50              55              60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met
  65              70              75              80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85              90              95
His Glu Gly Cys Leu Thr Gln Met Phe Phe Leu Val Leu Phe Ala Cys
      100              105              110
Ile Glu Gly Met Ile Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115              120              125
Ile Cys Arg Pro Leu Asn Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130              135              140
Val Phe Phe Ile Leu Met Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
  145              150              155              160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
      165              170              175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
      180              185              190
Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser Thr Met
      195              200              205
Phe Ala Phe Leu Pro Ile Ser Ala Ile Leu Leu Ser Tyr Tyr Lys Ile
      210              215              220
Val Thr Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
  225              230              235              240
Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
      245              250              255
Thr Asp Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
      260              265              270
Asn Gly Val Val Ala Ser Met Met Tyr Ala Val Val Thr Pro Met Leu
      275              280              285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
  290              295              300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
  305              310              315              320
Phe Phe Leu Cys

```

<210> 1658

<211> 320

<212> PRT

<213> Unknown (H38g575 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1658

```

His Thr Lys Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser
      20              25              30
Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
      35              40              45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu
      50              55              60
Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
  65              70              75              80

```

Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Glu
 85 90 95
 Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Thr Glu
 100 105 110
 Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe
 130 135 140
 Phe Ile Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Ser Xaa Val Val Leu Gln Phe Thr Phe Phe Asn Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Val Cys Glu Pro Ser Gln Leu Val Asn Leu Ala Ser Ser Asp
 180 185 190
 Ser Val Val Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly
 195 200 205
 Phe Leu Pro Ile Leu Gly Val Leu Leu Ser His Tyr Lys Ile Val Pro
 210 215 220
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Val Phe Ala
 225 230 235 240
 Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr Gly
 245 250 255
 Ile Asp Met Tyr Leu Thr Ser Ala Val Ser Pro Pro His Arg Asn Gly
 260 265 270
 Val Val Ala Ser Val Met Tyr Ala Val Phe Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg
 290 295 300
 Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser
 305 310 315 320

<210> 1659

<211> 270

<212> PRT

<213> Unknown (H38g576 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(270)

<223> Xaa = Any Amino Acid

<400> 1659

Val Ser Leu Ile Thr Tyr Leu Ile Thr Val Met Ser Asn Leu Gly Met
 1 5 10 15
 Asn Ile Leu Thr Lys Leu Asp Ser His Leu Tyr Thr Pro Val Val Tyr
 20 25 30
 Phe Leu Ile Lys His Ile Phe Phe Ile Asp Phe Tyr Asn Cys Ile Val
 35 40 45
 Ile Tyr Thr Asn Lys Met Leu Asn Phe Val Val Asp Gln Asn Asn Ile
 50 55 60
 Ser Tyr Tyr Ala Cys Ala Thr His Met Thr Phe Phe Met Phe Ile Ile
 65 70 75 80
 Thr Glu Leu Leu Ile Leu Val Ser Met Ala Tyr Asp Cys Tyr Val Val
 85 90 95
 Asn Ser Asn Pro Leu Phe Tyr Ile Val Ile Met Cys Leu Xaa Leu Xaa
 100 105 110
 His Val Leu Met Ser Ile Pro Tyr Leu Cys Asn Thr Phe Gln Ser Leu
 115 120 125
 Ile Ile Thr Ile Asp Leu Phe Leu Thr Phe Cys Ser Phe Ile Ile Ser

130	135	140
His Phe Tyr Cys Tyr Asp Val Leu Phe Phe His Met Leu Cys Ser Asn		
145	150	155
Ala Gln Glu Arg Glu Leu Leu Ile Thr Leu Leu Thr Ala Phe Asn Leu		160
	165	170
Ile Pro Ser Leu Leu Val Leu Leu Val Leu Asn Ile Leu Ile Leu Leu		175
	180	185
Ala Ile Cys Xaa Met His Ser Ala Leu Gly Arg Lys Lys Ala Phe Ser		190
	195	200
Met Cys Gly Ser His Leu Thr Met Val Val Met Phe Tyr Gly Ser Leu		205
	210	215
Leu Phe Asp Met Asp Lys Val Ala Ser Leu Phe Tyr Thr Leu Met Ile		220
225	230	235
Leu Arg Phe Asn Leu Ile Tyr Ser Phe Ser Asn Leu Gly Val Lys		240
	245	250
Asn Val Phe Tyr Arg Val Phe Lys Asn Xaa Cys Lys Leu Cys		255
	260	265
		270

<210> 1660
 <211> 128
 <212> PRT
 <213> Unknown (H38g577 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(128)
 <223> Xaa = Any Amino Acid

<400> 1660
Met Gly Gly Lys Gln Pro Trp Val Thr Glu Phe Ile Leu Val Gly Phe
1 5 10 15
Gln Leu Cys Ala Glu Met Glu Ile Phe Leu Ser Cys Ile Phe Ser Arg
20 25 30
Phe Tyr Ala Phe Ser Leu Leu Arg Asn Gly Met Asn Met Gly Leu Thr
35 40 45
Tyr Leu Asp Asp Arg Asp Asp Arg Leu His Thr Leu Ile Tyr Ile Phe
50 55 60
Leu Ser His Leu Ala Ile Asn Asp Met Tyr Tyr Ala Ser Asn Asn Val
65 70 75 80
Pro Lys Arg Gln Val Asn Gln Met Asn Gln Lys Lys Lys Asn Phe Val
85 90 95
Leu Trp Ile Lys Gln Ile Phe Leu Tyr Leu Ala Phe Ala His Thr Glu
100 105 110
Cys Leu Ile Xaa Ala Met Met Ser Cys Asn Arg Tyr Val Ala Ile Cys
115 120 125

<210> 1661
 <211> 307
 <212> PRT
 <213> Unknown (H38g578 protein)

<220>
 <223> Synthetic construct

<400> 1661
Met Gly Gln His Asn Leu Thr Val Leu Thr Glu Phe Ile Leu Met Glu
1 5 10 15
Leu Thr Arg Arg Pro Glu Leu Gln Ile Pro Leu Phe Gly Val Phe Leu
20 25 30

Val Ile Tyr Leu Ile Thr Val Val Gly Asn Leu Thr Met Ile Ile Leu
 35 40 45
 Thr Lys Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Ser Ile Arg
 50 55 60
 His Leu Ala Ser Val Asp Leu Gly Asn Ser Thr Val Ile Cys Pro Lys
 65 70 75 80
 Val Leu Ala Asn Phe Val Val Asp Arg Asn Thr Ile Ser Tyr Tyr Ala
 85 90 95
 Cys Ala Ala Gln Leu Ala Phe Phe Leu Met Phe Ile Ile Ser Glu Phe
 100 105 110
 Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Tyr Val Ile Met Ser Gln Arg Leu Cys His Val Leu
 130 135 140
 Val Gly Ile Gln Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Phe Thr
 145 150 155 160
 Ile Lys Ile Phe Thr Leu Thr Phe Cys Gly Ser Asn Val Ile Ser His
 165 170 175
 Phe Tyr Cys Asp Asp Val Pro Leu Leu Pro Met Leu Cys Ser Asn Ala
 180 185 190
 Gln Glu Ile Glu Leu Leu Ser Ile Leu Phe Ser Val Phe Asn Leu Ile
 195 200 205
 Ser Ser Phe Leu Ile Val Leu Val Ser Tyr Met Leu Ile Leu Leu Ala
 210 215 220
 Ile Cys Gln Met His Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Val Val Phe Tyr Gly Ser Leu Leu
 245 250 255
 Phe Met Tyr Met Gln Pro Asn Ser Thr His Phe Phe Asp Thr Asp Lys
 260 265 270
 Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Glu Glu Val Lys Asn Ala Phe Tyr Lys Leu
 290 295 300
 Phe Glu Asn
 305

<210> 1662

<211> 218

<212> PRT

<213> Unknown (H38g579 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(218)

<223> Xaa = Any Amino Acid

<400> 1662

Leu Pro Asp Ile Ser Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Val Ile Phe Gly Gly Met Glu Glu Ser Met Leu
 35 40 45
 Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 65 70 75 80
 Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ala Gln Leu His Asn Leu


```

      85          90          95
Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe
      100          105          110
Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe
      115          120          125
Thr Ile Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu
      130          135          140
Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Ile
      145          150          155
Leu Arg Val Ser Ser Ser Gly Gly Arg Tyr Lys Ala Leu Ser Thr Cys
      165          170          175
Gly Ser His Val Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val Gly
      180          185          190
Gly Tyr Leu Ser Ser Asp Val Ser Phe Ser Pro Arg Lys Gly Ala Val
      195          200          205
Ala Ser Val Met Tyr Ala Val Val Thr Pro
      210          215

```

<210> 1663

<211> 227

<212> PRT

<213> Unknown (H38g580 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(227)

<223> Xaa = Any Amino Acid

<400> 1663

```

Met Tyr Phe Phe Phe Ser Asn Leu Ser Leu Pro Asp Asp Gly Phe Thr
  1          5          10          15
Ser Thr Thr Val Pro Lys Met Ile Val Asp Ile Gln Ser His Ser Arg
  20          25          30
Val Thr Ser Tyr Ala Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile
  35          40          45
Phe Gly Gly Met Glu Glu Ser Met Leu Leu Ser Val Met Ala Tyr Asp
  50          55          60
Arg Phe Val Ala Ile Cys His Pro Leu Cys His Ser Ala Ile Thr Asn
  65          70          75          80
Pro Cys Phe Cys Gly Phe Leu Val Leu Leu Ser Phe Phe Phe Leu Ser
  85          90          95
Leu Leu Asp Ala Gln Leu His Asn Leu Ile Ala Leu Gln Arg Thr Cys
  100          105          110
Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln Phe
  115          120          125
Pro Arg Leu Ala Cys Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr
  130          135          140
Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe
  145          150          155          160
Ser Tyr Asp Lys Ile Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly
  165          170          175
Gly Lys His Lys Ala Phe Ser Thr Arg Gly Ser His Leu Ser Val Val
  180          185          190
Cys Xaa Phe Tyr Gly Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val
  195          200          205
Ser Ser Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val
  210          215          220
Ala Ile Pro
  225

```

<210> 1664
 <211> 194
 <212> PRT
 <213> Unknown (H38g581 protein)

<220>
 <223> Synthetic construct

<400> 1664
 Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ile
 1 5 10 15
 Ser Cys Val Pro Gly Met Leu Val Asn Leu Trp Glu Pro Lys Lys Thr
 20 25 30
 Ile Ile Leu Leu Gly Cys Ser Val Gln Phe Phe Ile Phe Leu Ser Leu
 35 40 45
 Gly Thr Thr Glu Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr
 50 55 60
 Met Ala Ile Cys Gln Pro Leu His Tyr Ala Thr Ile Val His Pro Leu
 65 70 75 80
 Leu Cys Trp Gln Leu Ala Ser Val Ala Trp Val Met Ser Leu Val Glu
 85 90 95
 Ser Val Val Gln Thr Pro Ser Thr Leu His Leu Pro Phe Cys Pro Asp
 100 105 110
 Arg Gln Val Asp Asp Phe Val Cys Glu Val Pro Ala Leu Ile Arg Leu
 115 120 125
 Ser Cys Glu Asp Thr Ser Tyr Asn Glu Ile Gln Leu Ala Val Ala Ser
 130 135 140
 Val Phe Ile Leu Ala Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly
 145 150 155 160
 Ala Ile Ala Trp Ala Val Leu Arg Thr Asn Ser Ala Lys Gly Gln Arg
 165 170 175
 Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Phe
 180 185 190
 Tyr Ser

<210> 1665
 <211> 320
 <212> PRT
 <213> Unknown (H38g582 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

<400> 1665
 Met Val Ser Ser Asn Gln Thr Ser Pro Val Leu Gly Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu Ile
 20 25 30
 Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu
 35 40 45
 Val Thr Ile Leu Asp Ser Arg Leu Asp Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Val Leu
 65 70 75 80
 Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser Ala Cys Ala

<210> 1666
<211> 318
<212> PRT
<213> Unknown (H38g583 protein)

<220>
<223> Synthetic construct

910

His Phe Thr Cys Glu Ile Leu Ala Val Gln Lys Leu Ala Cys Ala Asp
 180 185 190
 Ile Ser Val Asn Val Ile Ser Met Gly Val Thr Asn Val Ile Phe Leu
 195 200 205
 Gly Val Pro Val Leu Phe Ile Ser Phe Ser Tyr Val Phe Ile Ile Ala
 210 215 220
 Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ser Ala His Leu Thr Val Val Val Ile Phe Tyr Gly Thr Ile
 245 250 255
 Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp
 260 265 270
 Lys Gln Asp Phe Ala Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val
 275 280 285
 Thr Pro Met Leu Asn Pro Ile Tyr Ser Leu Arg Asn Lys Asp Val
 290 295 300
 Lys Ala Ala Val Arg Asp Leu Ile Phe Gln Lys Cys Phe Ala
 305 310 315

<210> 1667

<211> 321

<212> PRT

<213> Unknown (H38g584 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1667

Met Asn Arg Ser Asn Glu Ala Ser Pro Val Leu Gly Phe Val Leu Leu
 1 5 10 15
 Gly Leu Ser Ala His Pro Xaa Leu Glu Lys Thr Phe Phe Val Phe Ile
 20 25 30
 Leu Leu Val Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu
 35 40 45
 Val Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Val Leu
 65 70 75 80
 Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser Ala Cys Ala
 85 90 95
 Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu Cys Val Leu
 100 105 110
 Leu Ser Met Met Ala Phe Asp His Tyr Leu Asp Met Cys Asn Pro Leu
 115 120 125
 Arg Tyr Pro Val Val Met Ser Lys Ala Ala Tyr Met Pro Met Ala Val
 130 135 140
 Gly Ser Trp Ala Ala Gly Ile Thr Asn Ser Val Val Gln Ile Ser Leu
 145 150 155 160
 Ala Met Xaa Leu Pro Phe Cys Gly Asp Asn Val Ile Asn His Phe Thr
 165 170 175
 Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile Cys Ile
 180 185 190
 Asn Val Ile Ser Met Val Val Thr Asn Met Ile Phe Leu Ala Leu Pro
 195 200 205
 Val Leu Phe Ile Phe Val Ser Tyr Val Phe Ile Ile Ala Thr Ile Leu
 210 215 220
 Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser

```

225          230          235          240
Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Met Ile Leu Phe Met
          245          250          255
Tyr Gly Lys Pro Lys Ser Lys Asp Pro Met Gly Ala Asp Lys Gln Asp
          260          265          270
Leu Ala Asp Lys Leu Ile Ser Ile Phe Tyr Gly Val Val Thr Pro Ile
          275          280          285
Leu Asn Pro Ile Ile Tyr Ser Pro Arg Asn Lys Asp Leu Lys Ala Ala
          290          295          300
Met Arg Asn Leu Val Ala Gln Lys His Leu Thr Glu Xaa Leu Ser Gln
305          310          315          320
Ile

```

<210> 1668
 <211> 125
 <212> PRT
 <213> Unknown (H38g585 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(125)
 <223> Xaa = Any Amino Acid

```

<400> 1668
Arg Leu Asn Val Ile Ser His Leu Pro Phe Tyr Gly Asp Ile Ile Asn
1          5          10          15
His Leu Thr Cys Glu Val Leu Ala Val Leu Lys Leu Ala Cys Ala Asp
          20          25          30
Ile Ser Ile Asn Met Ile Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala
          35          40          45
His Leu Thr Val Val Val Ile Phe Tyr Arg Thr Ile Leu Phe Thr His
          50          55          60
Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp Lys Gln Asp Phe
65          70          75          80
Ala Asp Lys Leu Ile Ser Leu Ser Tyr Gly Val Val Thr Pro Met Leu
          85          90          95
Asn Thr Ile Ile Tyr Ser Leu Arg Lys Lys Gly Val Lys Ala Ala Val
          100          105          110
Lys Asn Leu Val Phe Gln Lys Pro Leu Thr Glu Xaa Gln
          115          120          125

```

<210> 1669
 <211> 216
 <212> PRT
 <213> Unknown (H38g586 protein)

<220>
 <223> Synthetic construct

```

<400> 1669
Phe Val Asp Met Gly Leu Thr Ser Ser Thr Val Thr Lys Met Leu Val
1          5          10          15
Asn Ile Gln Thr Arg His His Thr Ile Thr Tyr Thr Gly Cys Leu Thr
          20          25          30
Gln Met Tyr Phe Phe Leu Met Phe Gly Asp Leu Asp Ser Phe Phe Leu
          35          40          45
Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Cys
50          55          60

```

```

Tyr Ser Thr Val Met Arg Pro Gln Val Cys Ala Leu Met Leu Ala Leu
65          70          75          80
Cys Trp Val Leu Thr Asn Ile Val Ala Leu Thr His Thr Phe Leu Met
      85          90          95
Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe Cys
      100         105         110
Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile Asn
      115         120         125
Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro Phe
      130         135         140
Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu Arg
145          150         155         160
Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser Ser
      165         170         175
His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala Tyr
      180         185         190
Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala Ala
      195         200         205
Ala Met Tyr Thr Ile Val Thr Pro
      210         215

```

<210> 1670

<211> 319

<212> PRT

<213> Unknown (H38g587 protein)

<220>

<223> Synthetic construct

<400> 1670

```

Met Glu Lys Ala Asn Glu Thr Ser Pro Val Met Gly Phe Val Leu Leu
1          5          10          15
Arg Leu Ser Ala His Pro Glu Leu Glu Lys Thr Phe Phe Val Leu Ile
      20         25         30
Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu
      35         40         45
Val Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
      50         55         60
Gly Asn Leu Ser Phe Leu Asp Ile Cys Phe Thr Thr Ser Ser Val Pro
65          70          75          80
Leu Val Leu Asp Ser Phe Leu Thr Pro Gln Glu Thr Ile Ser Phe Ser
      85         90         95
Ala Cys Ala Val Gln Met Ala Leu Ser Phe Ala Met Ala Gly Thr Glu
      100        105        110
Cys Leu Leu Leu Ser Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
      115        120        125
Asn Pro Leu Arg Tyr Ser Val Ile Met Ser Lys Ala Ala Tyr Met Pro
      130        135        140
Met Ala Ala Ser Ser Trp Ala Ile Gly Gly Ala Ala Ser Val Val His
145          150        155        160
Thr Ser Leu Ala Ile Gln Leu Pro Phe Cys Gly Asp Asn Val Ile Asn
      165        170        175
His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp
      180        185        190
Ile Ser Ile Asn Val Ile Ser Met Glu Val Thr Asn Val Ile Phe Leu
      195        200        205
Gly Val Pro Val Leu Phe Ile Ser Phe Ser Tyr Val Phe Ile Ile Thr
      210        215        220
Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Val Phe Ser
225          230        235        240
Thr Cys Ser Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Thr Leu

```

<210> 1671
<211> 218
<212> PRT
<213> Unknown (H38g588 protein)

```
<221> VARIANT
<222> (1)...(218)
<223> Xaa = Any Amino Acid
```

<210> 1672
<211> 216
<212> PRT
<213> Unknown (H38g589 protein)

<400> 1672

```

Phe Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala
 1          5          10          15
Asn His Ile Leu Gly Ser Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr
          20          25          30
Gln Leu Tyr Phe Leu Ala Val Cys Gly Asn Met Asp Asn Phe Leu Leu
          35          40          45
Gly Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
          50          55          60
Tyr Thr Thr Lys Met Thr Arg Gln Leu Cys Val Leu Leu Val Val Gly
          65          70          75          80
Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His Ile Leu Leu Met
          85          90          95
Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His Phe Phe Cys
          100          105          110
Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
          115          120          125
Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val Thr Pro Phe
          130          135          140
Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala Val Leu Arg
          145          150          155          160
Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr Cys Gly Ser
          165          170          175
His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Ala Val Tyr
          180          185          190
Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met Ala Ala Ala
          195          200          205
Val Met Tyr Pro Val Val Thr Pro
          210          215

```

<210> 1673

<211> 329

<212> PRT

<213> Unknown (H38g590 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1673

```

Met Ala Glu Glu Asn Lys Ile Leu Val Thr His Phe Val Leu Thr Gly
 1          5          10          15
Leu Thr Asp His Pro Gly Leu Gln Ala Pro Leu Phe Leu Val Phe Leu
          20          25          30
Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Leu Met Ala Leu
          35          40          45
Ile Trp Lys Asp Pro His Leu His Thr Pro Ile Tyr Leu Phe Leu Gly
          50          55          60
Ser Leu Ala Phe Ala Asp Ala Cys Thr Ser Ser Ser Val Thr Ser Lys
          65          70          75          80
Met Leu Ile Asn Phe Leu Ser Lys Asn His Met Leu Ser Met Ala Lys
          85          90          95
Cys Ala Thr Gln Phe Tyr Phe Phe Gly Ser Asn Ala Thr Thr Glu Cys
          100          105          110
Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Leu Tyr Pro Val Val Met Ser Asn Ser Leu Cys Thr Gln Phe
          130          135          140
Ile Gly Ile Ser Tyr Phe Ile Gly Phe Leu His Ser Ala Ile His Val

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145          150          155          160
Gly Leu Leu Phe Arg Leu Thr Phe Cys Arg Ser Asn Ile Ile His Tyr
          165          170          175
Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile Ser Cys Thr Asn Pro
          180          185          190
Thr Val Asn Ile Leu Leu Ile Phe Ile Phe Ser Ala Phe Ile Gln Val
          195          200          205
Phe Thr Phe Met Thr Leu Ile Val Ser Tyr Ser Tyr Ile Leu Ser Ala
          210          215          220
Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ala His Leu Leu Ser Val Ser Leu Phe Tyr Gly Thr Leu Phe
          245          250          255
Phe Met Tyr Val Ser Ser Arg Ser Gly Ser Ala Ala Asp Gln Ala Lys
          260          265          270
Met Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Asp Ala Leu Arg Arg Ile
          290          295          300
Met Lys Lys Xaa Ile Val Val Arg Gln His Ser Asn His Phe Phe Phe
305          310          315          320
Ile Phe Cys Xaa Arg Lys Pro Gln Val
          325

```

<210> 1674

<211> 212

<212> PRT

<213> Unknown (H38g591 protein)

<220>

<223> Synthetic construct

<400> 1674

```

Cys His Ser Gln Val Ser Arg Leu Ala Gly Leu Gly Tyr Leu Glu Gly
1      5      10      15
Arg Arg Leu Ser Ser Ser Tyr Asn Ala Cys Ala Ala Gln Met Phe Phe
20     25     30
Phe Val Ala Leu Ala Thr Val Glu Asn Ile Leu Leu Thr Ser Met Ala
35     40     45
Tyr Asp His Tyr Ile Ala Val Cys Lys Pro Leu His Tyr Thr Thr Thr
50     55     60
Thr Ile Ala Ser Val Cys Ala His Leu Val Ile Gly Ser Tyr Val Cys
65     70     75     80
Gly Phe Leu Asn Ala Ser Leu Arg Ile Val Asp Ile Phe Ser Leu Ser
85     90     95
Phe Cys Lys Ser Asn Leu Val His His Leu Phe Cys Asp Val Pro Pro
100    105    110
Val Met Ala Val Ser Cys Ser Gly Lys His Ile Ser Lys Lys Ile Leu
115    120    125
Val Phe Met Ser Ser Phe Asn Val Phe Leu Ala Leu Leu Val Ile Leu
130    135    140
Thr Ser Tyr Leu Phe Ile Phe Ile Thr Ile Leu Lys Met His Ser Ala
145    150    155    160
Gln Gly His Leu Lys Ala Leu Ser Thr Cys Ala Ser His Leu Ile Ala
165    170    175
Val Ser Ile Phe Tyr Gly Thr Thr Ile Phe Met Tyr Leu Gln Pro Ser
180    185    190
Ser Ser His Ser Met Asp Thr Asp Glu Met Ala Ser Leu Phe Tyr Ala
195    200    205
Val Phe Ile Ser
210

```

<210> 1675
 <211> 314
 <212> PRT
 <213> Unknown (H38g592 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(314)
 <223> Xaa = Any Amino Acid

<400> 1675
 Met Gly Asp Asn Gln Ser Arg Val Thr Glu Phe Ile Leu Val Gly Phe
 1 5 10 15
 Gln Leu Ser Val Glu Met Glu Val Leu Leu Phe Trp Ile Phe Ser Leu
 20 25 30
 Leu Tyr Leu Phe Ser Leu Leu Gly Asn Gly Val Ile Phe Gly Leu Ile
 35 40 45
 Cys Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
 50 55 60
 Leu Ala Val Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met
 65 70 75 80
 Leu Ala Asn Leu Val Asn Gln Lys Arg Thr Ile Ser Phe Ile Ser Cys
 85 90 95
 Ile Met Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Val Cys Leu
 100 105 110
 Ile Leu Val Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro
 115 120 125
 Leu His Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Val Leu Ala
 130 135 140
 Val Ala Ser Trp Val Phe Ser Phe Leu Leu Ala Leu Val His Leu Val
 145 150 155 160
 Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Gln Glu Val Asn His Phe
 165 170 175
 Phe Gly Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp
 180 185 190
 Leu Asn Gln Val Val Ile Phe Ala Ala Cys Met Phe Ile Leu Val Gly
 195 200 205
 Xaa Leu Cys Leu Val Leu Val Ser Tyr Leu His Ile Leu Ala Ala Ile
 210 215 220
 Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val
 245 250 255
 Met Tyr Met Ala Pro Lys Ser Ser His Ser Gln Glu Arg Arg Lys Ile
 260 265 270
 Leu Ser Leu Phe Tyr Ser Leu Phe Asn Pro Ile Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Ala Glu Val Lys Gly Ala Leu Lys Arg Val Leu
 290 295 300
 Trp Lys Gln Arg Ser Ile Glu Glu Ser Phe
 305 310

<210> 1676
 <211> 216
 <212> PRT
 <213> Unknown (H38g593 protein)

<220>

<223> Synthetic construct

<400> 1676

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
 1 5 10 15
 Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp Cys Leu Thr
 20 25 30
 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
 35 40 45
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60
 Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu Val Ala Leu
 65 70 75 80
 Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
 85 90 95
 Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys
 100 105 110
 Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr Arg Val Asn
 115 120 125
 Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe
 130 135 140
 Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
 145 150 155 160
 Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr
 180 185 190
 Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala
 195 200 205
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 1677

<211> 312

<212> PRT

<213> Unknown (H38g594 protein)

<220>

<223> Synthetic construct

<400> 1677

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1 5 10 15
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35 40 45
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Val Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
 130 135 140
 Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
 145 150 155 160

Ala Phe Leu Val Asn Leu Ala Phe Cys Gly Pro Asn Val Leu Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
 195 200 205
 Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr
 210 215 220
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Ser Ala His Ser Thr Val Val Leu Leu Phe Phe Gly Pro Pro Met Phe
 245 250 255
 Val Tyr Thr Arg Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
 290 295 300
 Leu Val Ile Tyr Lys Arg Ile Ser
 305 310

<210> 1678

<211> 128

<212> PRT

<213> Unknown (H38g595 protein)

<220>

<223> Synthetic construct

<400> 1678

Met Asn Ser Glu Asn Leu Thr Arg Ala Ala Val Ala Pro Ala Glu Phe
 1 5 10 15
 Val Leu Leu Gly Ile Thr Asn Arg Trp Asp Leu Arg Val Ala Leu Phe
 20 25 30
 Leu Thr Cys Leu Pro Val Tyr Leu Val Ser Leu Leu Gly Asn Met Gly
 35 40 45
 Met Ala Leu Leu Ile Arg Met Asp Ala Arg Leu His Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Ala Asn Leu Ser Leu Leu Asp Ala Cys Tyr Ser Ser Ala
 65 70 75 80
 Ile Gly Pro Lys Met Leu Val Asp Leu Leu Leu Pro Arg Ala Thr Ile
 85 90 95
 Pro Tyr Thr Ala Cys Ala Leu Gln Met Phe Val Phe Ala Gly Leu Ala
 100 105 110
 Asp Thr Glu Cys Ser Met Gln Leu Met Pro Lys Val Asn Gln Asn Val
 115 120 125

<210> 1679

<211> 270

<212> PRT

<213> Unknown (H38g596 protein)

<220>

<223> Synthetic construct

<400> 1679

Met Thr Ile Val Leu Leu Ser Ala Leu Asp Ser Arg Leu His Thr Pro
 1 5 10 15
 Met Tyr Phe Phe Leu Ala Asn Leu Ser Phe Leu Asp Met Cys Phe Thr
 20 25 30
 Thr Gly Ser Ile Pro Gln Met Leu Tyr Asn Leu Trp Gly Pro Asp Lys

```

      35              40              45
Thr Ile Ser Tyr Val Gly Cys Ala Ile Gln Leu Tyr Phe Val Leu Ala
  50              55              60
Leu Gly Gly Val Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp Arg
  65              70              75              80
Tyr Ala Ala Val Cys Lys Pro Leu His Tyr Thr Ile Ile Met His Pro
      85              90              95
Arg Leu Cys Gly Gln Leu Ala Ser Val Ala Trp Leu Ser Gly Phe Gly
      100              105              110
Asn Ser Leu Ile Met Ala Pro Gln Thr Leu Met Leu Pro Arg Cys Gly
      115              120              125
His Arg Arg Val Asp His Phe Leu Cys Glu Met Pro Ala Leu Ile Gly
      130              135              140
Met Ala Cys Val Asp Thr Met Met Leu Glu Ala Leu Ala Phe Ala Leu
      145              150              155              160
Ala Ile Phe Ile Ile Leu Ala Pro Leu Ile Leu Ile Leu Ile Ser Tyr
      165              170              175
Gly Tyr Val Gly Gly Thr Val Leu Arg Ile Lys Ser Ala Ala Gly Arg
      180              185              190
Lys Lys Ala Phe Asn Thr Cys Ser Ser His Leu Ile Val Val Ser Leu
      195              200              205
Phe Tyr Gly Thr Ile Ile Tyr Met Tyr Leu Gln Pro Ala Asn Thr Tyr
      210              215              220
Ser Gln Asp Gln Gly Lys Phe Leu Thr Leu Phe Tyr Thr Ile Val Thr
      225              230              235              240
Pro Ser Val Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys
      245              250              255
Glu Ala Met Lys Lys Val Leu Gly Lys Gly Ser Ala Glu Ile
      260              265              270

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<210> 1680

<211> 114

<212> PRT

<213> Unknown (H38g597 protein)

<220>

<223> Synthetic construct

<400> 1680

```

Ile Cys Phe Pro Leu His Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys
  1              5              10              15
Val Met Met Ile Thr Gly Ser Trp Met Ile Ser Ser Ile Asn Ser Cys
      20              25              30
Ala His Thr Val Tyr Ala Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala
      35              40              45
Ile Asn His Phe Phe Cys Asp Val Pro Ala Met Leu Thr Leu Ala Cys
      50              55              60
Thr Asp Thr Trp Val Tyr Glu Ser Thr Val Phe Leu Ser Ser Thr Ile
      65              70              75              80
Phe Leu Val Leu Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Arg Val
      85              90              95
Leu Leu Ala Val Tyr Arg Met His Ser Ala Glu Gly Arg Lys Lys Ala
      100              105              110
Tyr Ser

```

<210> 1681

<211> 212

<212> PRT

<213> Unknown (H38g598 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1681

```

Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Val
1           5           10           15
Asp Ser Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
          20           25           30
Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Asp Ile Phe Val Leu
          35           40           45
Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg
          50           55           60
Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
65           70           75           80
Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr
          85           90           95
Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys
          100          105          110
Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
          115          120          125
Ser Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
          130          135          140
Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
145          150          155          160
Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
          165          170          175
Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Thr Phe Ile Tyr Arg
          180          185          190
Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
          195          200          205
Thr Ile Thr Pro
          210

```

<210> 1682

<211> 212

<212> PRT

<213> Unknown (H38g599 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1682

```

Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
1           5           10           15
Asn Leu Val Ala Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Thr Met
          20           25           30
Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Cys Met Leu
          35           40           45
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu
          50           55           60
Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
65           70           75           80
Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa Phe Leu

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```

      85              90              95
Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
      100              105              110
Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys Val Ser
      115              120              125
Gln Xaa Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu
      130              135              140
Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Thr
      145              150              155              160
Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu Thr Ala
      165              170              175
Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn
      180              185              190
Ala Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Gly Phe Tyr Thr
      195              200              205
Val Val Met Pro
      210

```

<210> 1683

<211> 215

<212> PRT

<213> Unknown (H38g600 protein)

<220>

<223> Synthetic construct

<400> 1683

```

Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser
 1      5      10      15
Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
      20      25      30
Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser Leu Leu Leu
      35      40      45
Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Leu His
      50      55      60
Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
      65      70      75      80
Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile Glu Ser Leu Met Val
      85      90      95
Leu Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro His Phe Phe Cys
      100      105      110
Glu Leu Asn Gln Ile Ile Arg Ser Ala Cys Ser Asp Thr Phe Leu Asn
      115      120      125
Asp Met Val Met Tyr Leu Ser Ala Val Leu Leu Gly Arg Gly Cys Phe
      130      135      140
Thr Gly Ile Leu Tyr Ser Tyr Phe Lys Thr Val Ser Ser Ile Arg Ala
      145      150      155      160
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
      165      170      175
His Leu Ser Val Val Ser Leu Phe Tyr Cys Met Gly Leu Gly Val Tyr
      180      185      190
Leu Ser Ala Ala Ala Pro Thr Thr His Ser Gln Val Gln Gln Pro Leu
      195      200      205
Met Tyr Thr Val Val Thr Pro
      210      215

```

<210> 1684

<211> 114

<212> PRT

<213> Unknown (H38g601 protein)

<220>

<223> Synthetic construct

<400> 1684

```

Ile Cys Phe Pro Leu His Tyr Pro Ile Arg Met Arg Lys Arg Val Cys
 1             5             10             15
Ala Leu Met Ile Thr Gly Ser Trp Met Ile Gly Ser Ile Asn Ser Cys
      20             25             30
Ala His Thr Val Tyr Ala Leu Arg Ile Pro Tyr Cys Lys Ser Arg Ala
      35             40             45
Ile Asn His Phe Phe Cys Asp Val Pro Ala Met Leu Thr Leu Ala Cys
      50             55             60
Thr Asp Thr Trp Val Tyr Glu Cys Thr Val Phe Leu Ser Thr Thr Ile
65             70             75             80
Phe Leu Val Phe Pro Phe Ile Cys Ile Ala Cys Ser Tyr Gly Arg Ile
      85             90             95
Leu Leu Ala Val Tyr His Met His Ser Ala Glu Gly Arg Lys Lys Ala
      100             105             110
Tyr Ser

```

<210> 1685

<211> 216

<212> PRT

<213> Unknown (H38g602 protein)

<220>

<223> Synthetic construct

<400> 1685

```

Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln Leu Leu Ala
 1             5             10             15
His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser Cys Ala Ala
      20             25             30
Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu
      35             40             45
Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg
      50             55             60
Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu Ala Ile Thr
65             70             75             80
Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr Ala Ile Thr
      85             90             95
Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His Ile Ser Cys
      100             105             110
Glu Leu Leu Ala Val Val Arg Leu Ala Arg Val Asp Thr Ser Ser Asn
      115             120             125
Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe
      130             135             140
Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys
145             150             155             160
Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr Cys Ala Ser
      165             170             175
His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr
      180             185             190
Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Phe Ser
      195             200             205
Val Phe Tyr Ala Ile Leu Thr Pro
      210             215

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<210> 1686

<211> 212

<212> PRT
 <213> Unknown (H38g603 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(212)
 <223> Xaa = Any Amino Acid

<400> 1686
 Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Glu
 1 5 10 15
 Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
 20 25 30
 Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Glu Ile Phe Val Leu
 35 40 45
 Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg
 50 55 60
 Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
 65 70 75 80
 Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Val Leu Thr
 85 90 95
 Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys
 100 105 110
 Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
 115 120 125
 Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
 130 135 140
 Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
 145 150 155 160
 Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
 165 170 175
 Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile Tyr Arg
 180 185 190
 Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
 195 200 205
 Thr Ile Thr Pro
 210

<210> 1687
 <211> 114
 <212> PRT
 <213> Unknown (H38g604 protein)

<220>
 <223> Synthetic construct

<400> 1687
 Ile Cys Lys Pro Leu Leu Tyr Pro Ala Ile Met Thr Asn Gly Leu Cys
 1 5 10 15
 Ile Arg Leu Leu Ile Leu Ser Tyr Val Gly Gly Leu Leu His Ala Leu
 20 25 30
 Ile His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile
 35 40 45
 Val His His Ile Tyr Cys Asp Ile Ile Pro Leu Ser Lys Ile Ser Cys
 50 55 60
 Thr Asp Ser Ser Ile Asn Phe Leu Met Val Phe Ile Phe Ser Gly Ser
 65 70 75 80
 Ile Gln Val Phe Ser Ile Val Thr Ile Leu Val Ser Tyr Thr Phe Val
 85 90 95

Leu Phe Ala Ile Leu Lys Arg Lys Ser Asp Lys Gly Val Arg Lys Ala
 100 105 110
 Phe Ser

<210> 1688
 <211> 111
 <212> PRT
 <213> Unknown (H38g605 protein)

<220>
 <223> Synthetic construct

<400> 1688
 Ile Cys Asn Pro Leu Arg Tyr Pro Ile Ile Met Ser Arg His Val Cys
 1 5 10 15
 Val Gln Met Ala Ala Ile Ser Trp Val Thr Gly Cys Leu Thr Ala Leu
 20 25 30
 Leu Val Thr Ser Cys Ala Leu Gln Ile Pro Leu Cys Gly Asn Val Ile
 35 40 45
 Asp His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Val
 50 55 60
 Ser Ser Leu Leu Val Asp Met Val Met Leu Val Val Ser Ile Leu Leu
 65 70 75 80
 Leu Pro Ile Pro Met Leu Leu Ile Cys Ile Ser Tyr Gly Phe Ile Leu
 85 90 95
 Ser Thr Ile Leu Arg Ile Gly Ser Thr Glu Gly Arg Asn Lys Ala
 100 105 110

<210> 1689
 <211> 223
 <212> PRT
 <213> Unknown (H38g606 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(223)
 <223> Xaa = Any Amino Acid

<400> 1689
 Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Cys Gly Gly Met Glu Glu Ser Met Leu
 35 40 45
 Leu Ser Val Met Ala Tyr Gly Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Asp Leu
 65 70 75 80
 Leu Ser Ser Phe Cys Phe Val Ser Val Phe Leu Ser Leu Leu Asp Ser
 85 90 95
 Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Gly Phe Lys Asp Val
 100 105 110
 Asp Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Leu His Leu Ala
 115 120 125
 Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn Leu Tyr Phe Pro Ala Ala
 130 135 140
 Val Phe Gly Phe Leu Pro Ile Leu Gly Thr Phe Phe Ser Tyr Cys Lys

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145          150          155          160
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
          165          170          175
Ala Phe Ser Thr Cys Gly Ser His Leu Pro Val Val Cys Xaa Phe Cys
          180          185          190
Gly Thr Gly Val Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro
          195          200          205
Arg Lys Ser Ala Val Pro Ser Val Met Tyr Pro Val Val Thr Ser
          210          215          220

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<210> 1690
 <211> 215
 <212> PRT
 <213> Unknown (H38g607 protein)

<220>
 <223> Synthetic construct

```

<400> 1690
Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser
 1          5          10          15
Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Asp Cys Ile Thr
          20          25          30
Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser Leu Leu Leu
          35          40          45
Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Leu His
          50          55          60
Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
          65          70          75          80
Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile Glu Ser Leu Met Val
          85          90          95
Leu Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro His Phe Phe Cys
          100          105          110
Glu Leu Asn Gln Ile Ile Arg Ser Ala Cys Ser Asp Thr Phe Leu Asn
          115          120          125
Asp Met Val Met Tyr Leu Ser Ala Val Leu Leu Gly Arg Gly Cys Phe
          130          135          140
Thr Gly Ile Leu Tyr Ser Tyr Phe Lys Thr Val Ser Ser Ile Arg Ala
          145          150          155          160
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
          165          170          175
His Leu Ser Val Val Ser Leu Phe Tyr Cys Met Ser Leu Gly Val Tyr
          180          185          190
Leu Ser Ala Ala Ala Pro Thr Thr His Ser Gln Val Gln Gln Pro Leu
          195          200          205
Met Tyr Thr Val Val Thr Pro
          210          215

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<210> 1691
 <211> 278
 <212> PRT
 <213> Unknown (H38g608 protein)

<220>
 <223> Synthetic construct

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<400> 1691
Met Ala Ile Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe Phe
 1          5          10          15
Leu Ala Asn Met Ser Phe Leu Glu Ile Trp Tyr Val Thr Val Thr Ile
          20          25          30

```

Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly Gln
 35 40 45
 Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu Gly
 50 55 60
 Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Asn Asp Arg
 65 70 75 80
 Tyr Met Ala Ile Cys Tyr Leu Leu His Asn Pro Val Ile Val Ser Gly
 85 90 95
 Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe Gly
 100 105 110
 Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Asn Gly Gly
 115 120 125
 Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu Asn
 130 135 140
 Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile Leu
 145 150 155 160
 Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser Tyr
 165 170 175
 Val Ala Ile Thr Gly Ala Val Met His Ile Pro Ser Ala Ala Gly Arg
 180 185 190
 Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Phe Asn Val Val Ile Ile
 195 200 205
 Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu Ser
 210 215 220
 Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile Val
 225 230 235 240
 Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val Lys
 245 250 255
 Arg Ala Leu Cys Ile Leu His Leu Tyr Gln His Gln Asp Pro Asp
 260 265 270
 Pro Lys Lys Gly Ser Arg
 275

<210> 1692

<211> 314

<212> PRT

<213> Unknown (H38g609 protein)

<220>

<223> Synthetic construct

<400> 1692

Met Glu Phe Thr Asp Arg Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu
 1 5 10 15
 Leu Gly Phe Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Met
 20 25 30
 Phe Leu Thr Leu Tyr Ala Ile Ile Leu Ile Gly Asn Ile Gly Leu Met
 35 40 45
 Leu Leu Ile Arg Ile Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Ser Phe Val Asp Leu Cys Tyr Phe Ser Asp Ile Val
 65 70 75 80
 Pro Lys Met Leu Val Asn Phe Leu Ser Glu Asn Lys Ser Ile Ser Tyr
 85 90 95
 Tyr Gly Cys Ala Leu Gln Phe Tyr Phe Phe Cys Thr Phe Ala Asp Thr
 100 105 110
 Glu Ser Phe Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Leu Tyr Thr Val Val Met Ser Arg Gly Ile Cys Met
 130 135 140
 Arg Leu Ile Val Leu Ser Tyr Leu Gly Gly Asn Met Ser Ser Leu Val

145 150 155 160
 His Thr Ser Phe Ala Phe Ile Leu Lys Tyr Cys Asp Lys Asn Val Ile
 165 170 175
 Asn His Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Thr
 180 185 190
 Asp Thr Thr Ile Asn Glu Trp Leu Leu Ser Thr Tyr Gly Ser Ser Val
 195 200 205
 Glu Ile Ile Cys Phe Ile Ile Ile Ile Ser Tyr Phe Phe Ile Leu
 210 215 220
 Leu Ser Val Leu Lys Ile Arg Ser Phe Ser Gly Arg Lys Lys Thr Phe
 225 230 235 240
 Ser Thr Cys Ala Ser His Leu Thr Ser Val Thr Ile Tyr Gln Gly Thr
 245 250 255
 Leu Leu Phe Ile Tyr Ser Arg Pro Ser Tyr Leu Tyr Ser Pro Asn Thr
 260 265 270
 Asp Lys Ile Ile Ser Val Phe Tyr Thr Ile Phe Ile Pro Val Leu Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ala Glu
 290 295 300
 Lys Val Leu Arg Ser Lys Val Asp Ser Ser
 305 310

<210> 1693

<211> 316

<212> PRT

<213> Unknown (H38g610 protein)

<220>

<223> Synthetic construct

<400> 1693

Met Asp Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1 5 10 15
 Glu His Pro Gly Leu Gly Arg Thr Leu Phe Val Asp Val Ile Thr Ser
 20 25 30
 Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
 35 40 45
 Leu Asp Thr Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
 65 70 75 80
 Ala Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
 85 90 95
 Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
 100 105 110
 Met Lys Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
 115 120 125
 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
 130 135 140
 Val Ala Trp Val Ile Gly Leu Val Gly Ser Val Val Gln Thr Pro Ser
 145 150 155 160
 Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
 165 170 175
 Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
 180 185 190
 Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
 195 200 205
 Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
 210 215 220
 Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
 225 230 235 240

Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
 245 250 255
 Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
 260 265 270
 Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
 275 280 285
 Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
 290 295 300
 Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
 305 310 315

<210> 1694

<211> 309

<212> PRT

<213> Unknown (H38g611 protein)

<220>

<223> Synthetic construct

<400> 1694

Met Lys Arg Glu Asn Phe Thr Leu Ile Thr Asp Phe Val Phe Gln Gly
 1 5 10 15
 Phe Ser Ser Phe His Glu Gln Gln Ile Thr Leu Phe Gly Val Phe Leu
 20 25 30
 Ala Leu Tyr Ile Leu Thr Leu Ala Gly Asn Ile Ile Ile Val Thr Ile
 35 40 45
 Ile Arg Ile Asp Leu His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Met Leu Ser Thr Ser Glu Thr Val Tyr Thr Leu Val Ile Leu Pro Arg
 65 70 75 80
 Met Leu Ser Ser Leu Val Gly Met Ser Gln Pro Met Ser Leu Ala Gly
 85 90 95
 Cys Ala Thr Gln Met Phe Phe Phe Val Thr Phe Gly Ile Thr Asn Cys
 100 105 110
 Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Met Val Ile Met Asn Lys Arg Leu Arg Ile Gln Leu
 130 135 140
 Val Leu Gly Ala Cys Ser Ile Gly Leu Ile Val Ala Ile Thr Gln Val
 145 150 155 160
 Thr Ser Val Phe Arg Leu Pro Phe Cys Ala Arg Lys Val Pro His Phe
 165 170 175
 Phe Cys Asp Ile Arg Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr
 180 185 190
 Val Asn Glu Ile Leu Thr Leu Ile Ile Ser Val Leu Val Leu Val Val
 195 200 205
 Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Ile
 210 215 220
 Leu Lys Ile Ala Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys
 225 230 235 240
 Ala Ser His Leu Thr Val Val Ile Val His Tyr Ser Cys Ala Ser Ile
 245 250 255
 Ala Tyr Leu Lys Pro Lys Ser Glu Asn Thr Arg Glu His Asp Gln Leu
 260 265 270
 Ile Ser Val Thr Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Val Val
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Ala Val
 290 295 300
 Gly Gly Lys Phe Ser
 305

<210> 1695
 <211> 216
 <212> PRT
 <213> Unknown (H38g612 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(216)
 <223> Xaa = Any Amino Acid

<400> 1695
 Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Ala Pro Lys Met Ile Val
 1 5 10 15
 Asp Met Gln Ser His Arg Arg Ala Ile Ser His Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Phe Leu Phe Leu Cys Ala Cys Val Glu Gly Met Leu Leu
 35 40 45
 Thr Val Met Ala Tyr Asp Cys Phe Val Asp Ile Cys Arg Pro Leu His
 50 55 60
 Tyr Pro Val Ile Gly Asn Pro His Phe Cys Val Phe Phe Val Gly Val
 65 70 75 80
 Ser Phe Leu Leu Ser Leu Trp Asp Ser Gln Leu His Ser Trp Ile Val
 85 90 95
 Leu Gln Ile Thr Ile Phe Lys Asn Val Glu Ile Ser Asn Phe Val Cys
 100 105 110
 Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Gly Val Ile Asn
 115 120 125
 Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu Pro Ile
 130 135 140
 Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg
 145 150 155 160
 Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Gln Ala Val Val Cys Xaa Phe Tyr Arg Thr Gly Ile Gly Met Tyr
 180 185 190
 Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val Ala Ser
 195 200 205
 Leu Ile Tyr Ala Leu Val Thr Pro
 210 215

<210> 1696
 <211> 214
 <212> PRT
 <213> Unknown (H38g613 protein)

<220>
 <223> Synthetic construct

<400> 1696
 Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1 5 10 15
 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly Cys Leu Thr
 20 25 30
 Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Asn Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His
 50 55 60
 Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu Leu Ser Leu
 65 70 75 80

Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile Leu Leu Met
 85 90 95
 Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr Leu Phe Cys
 100 105 110
 Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile His Val Asn
 115 120 125
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Leu
 130 135 140
 Gly Phe Met Ile Thr Ser Asn Ala Arg Ile Val Arg Ala Ile Leu Gln
 145 150 155 160
 Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly Met Val Tyr
 180 185 190
 Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met His Ala Val Val Thr
 210

<210> 1697

<211> 212

<212> PRT

<213> Unknown (H38g614 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1697

Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
 1 5 10 15
 Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Thr Met
 20 25 30
 Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu
 50 55 60
 Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
 65 70 75 80
 Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa Phe Leu
 85 90 95
 Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
 100 105 110
 Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys Val Ser
 115 120 125
 Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Ser Glu Ile Ser Ser Leu
 130 135 140
 Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Thr Pro Ser Thr
 145 150 155 160
 Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu Thr Ala
 165 170 175
 Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn
 180 185 190
 Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr
 195 200 205
 Val Val Ile Pro
 210

<210> 1698
 <211> 212
 <212> PRT
 <213> Unknown (H38g615 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(212)
 <223> Xaa = Any Amino Acid

<400> 1698
 Leu Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Arg
 1 5 10 15
 Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Thr Met
 20 25 30
 Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe Val Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu
 50 55 60
 Tyr Thr Val Ala Met Tyr Gln A Cys Ser Leu Leu Val Ala Thr
 65 70 75 80
 Ser Tyr Cys Trp Gly Ile V Leu Thr Leu Thr Xaa Phe Leu
 85 90 95
 Leu Glu Leu Ser Phe Arg Ile Ile Asn Asn Phe Val Cys
 100 110
 Glu His Ala Ala Ile Cys Ser Asp Pro Cys Val Ser
 115 125
 Gln Glu Ile Thr I Phe Asn Glu Ile Ser Ser Leu
 130 140
 Thr Ser Tyr Ala Val Met Arg Thr Pro Ser Thr
 145 155 160
 Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu Thr Ala
 165 170 175
 Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn
 180 185 190
 Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr
 195 200 205
 Val Val Ile Pro
 210

<210> 1699
 <211> 312
 <212> PRT
 <213> Unknown (H38g616 protein)

<220>
 <223> Synthetic construct

<400> 1699
 Met Ser Ile Ser Asn Ile Thr Val Tyr Met Pro Ser Val Leu Thr Leu
 1 5 10 15
 Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys Trp Ile Gly Ile Pro
 20 25 30
 Phe Cys Ala Ile Tyr Leu Ile Ala Met Ile Gly Asn Ser Leu Leu Leu
 35 40 45
 Ser Ile Ile Lys Ser Glu Arg Ser Leu His Glu Pro Leu Tyr Ile Phe
 50 55 60
 Leu Gly Met Leu Gly Ala Thr Asp Ile Ala Leu Ala Ser Ser Ile Met
 65 70 75 80

Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Val Pro Glu Ile Tyr Phe
 85 90 95
 Asp Ser Cys Leu Leu Gln Met Trp Phe Ile His Thr Leu Gln Gly Ile
 100 105 110
 Glu Ser Gly Ile Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg His Ala Asn Ile Phe Thr His Gln Leu Val Ile
 130 135 140
 Gln Ile Gly Thr Met Val Val Leu Arg Ala Ala Ile Leu Val Ala Pro
 145 150 155 160
 Cys Leu Val Leu Ile Lys Cys Arg Phe Gln Phe Tyr His Thr Thr Val
 165 170 175
 Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala
 180 185 190
 Ala Asn Val Gln Val Asn Lys Ile Tyr Gly Leu Phe Val Ala Phe Thr
 195 200 205
 Val Ala Gly Phe Asp Leu Thr Phe Ile Thr Leu Ser Tyr Ile Gln Ile
 210 215 220
 Phe Ile Thr Val Phe Arg Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala
 225 230 235 240
 Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu
 245 250 255
 Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ser His Ile Pro
 260 265 270
 Pro Tyr Ile His Ile Leu Phe Ser Ser Ile Tyr Leu Leu Val Pro Pro
 275 280 285
 Phe Leu Asn Pro Leu Val Tyr Gly Ala Lys Thr Thr Gln Ile Arg Ile
 290 295 300
 His Val Val Lys Met Phe Cys Ser
 305 310

<210> 1700

<211> 318

<212> PRT

<213> Unknown (H38g617 protein)

<220>

<223> Synthetic construct

<400> 1700

Met Trp Gln Lys Asn Gln Thr Ser Leu Ala Asp Phe Ile Leu Glu Gly
 1 5 10 15
 Leu Phe Asp Asp Ser Leu Thr His Leu Phe Leu Phe Ser Leu Thr Met
 20 25 30
 Val Val Phe Leu Ile Ala Val Ser Gly Asn Thr Leu Thr Ile Leu Leu
 35 40 45
 Ile Cys Ile Asp Pro Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Gln Leu Ser Leu Met Asp Leu Met His Val Ser Thr Ile Ile Leu Lys
 65 70 75 80
 Met Ala Thr Asn Tyr Leu Ser Gly Lys Lys Ser Ile Ser Phe Val Gly
 85 90 95
 Cys Ala Thr Gln His Phe Leu Tyr Leu Cys Leu Gly Gly Ala Glu Cys
 100 105 110
 Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Ala Val Leu Met Asn Lys Lys Val Gly Leu Met Met
 130 135 140
 Ala Val Met Ser Trp Leu Gly Ala Ser Val Asn Ser Leu Ile His Met
 145 150 155 160
 Ala Ile Leu Met His Phe Pro Phe Cys Gly Pro Arg Lys Val Tyr His

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      165      170      175
Phe Tyr Cys Glu Phe Pro Ala Val Val Lys Leu Val Cys Gly Asp Ile
      180      185      190
Thr Val Tyr Glu Thr Thr Val Tyr Ile Ser S r Ile Leu Leu Leu Leu
      195      200      205
Pro Ile Phe Leu Ile Ser Thr Ser Tyr Val Phe Ile Leu Gln Ser Val
      210      215      220
Ile Gln Met Arg Ser Ser Gly Ser Lys Arg Asn Ala Phe Ala Thr Cys
      225      230      235      240
Gly Ser His Leu Thr Val Val Ser Leu Trp Phe Gly Ala Cys Ile Phe
      245      250      255
Ser Tyr Met Arg Pro Arg Ser Gln Cys Thr Leu Leu Gln Asn Lys Val
      260      265      270
Gly Ser Val Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Ser Leu Ile
      275      280      285
Tyr Thr Leu Arg Asn Lys Asp Val Ala Lys Ala Leu Arg Arg Val Leu
      290      295      300
Arg Arg Asp Val Ile Thr Gln Cys Ile Gln Arg Leu Gln Leu
      305      310      315

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<210> 1701

<211> 294

<212> PRT

<213> Unknown (H38g618 protein)

<220>

<223> Synthetic construct

<400> 1701

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Ala Thr Tyr Asn Ser Ser Asn Thr Val Val Thr Glu Phe Val Phe Leu
  1      5      10      15
Ser Phe Pro Glu Leu His His Leu Gln Gly Leu Leu Phe Val Ser Leu
      20      25      30
Leu Ile Ile Tyr Val Val Thr Ile Leu Glu Asp Leu Ala Val Val Gly
      35      40      45
Thr Ile Arg Ala Ser His His Leu His Ile Ser Thr His Leu Phe Leu
      50      55      60
Ala Gln Leu Ser Val Leu Glu Thr Leu Tyr Thr Ser Val Thr Val Pro
      65      70      75      80
Lys Leu Leu Ala Gly Leu Pro Ala Glu Arg Arg Pro Ser Ile Ser Phe
      85      90      95
Ser Gly His Leu Thr Trp Leu Leu Leu Phe Leu Ser Leu Ser Ser
      100      105      110
Glu Cys Val Leu Pro Ala Asn Met Asp Cys Asp Trp His Pro Val Ile
      115      120      125
Cys His Leu Leu His Tyr Leu Ser Pro Ser Trp Thr Pro Cys Ser Trp
      130      135      140
Leu Cys Leu His Leu Ala Ile Ser Ala Gln Leu Ser Ser Phe Pro Ala
      145      150      155      160
Ser Phe Val Ser Thr Ala Leu Asn Ser Ser Leu Arg Leu Arg Ser Pro
      165      170      175
Asp Val Leu Asn His Phe Cys Asp Ile Pro Pro Pro Leu Gly Leu Ser
      180      185      190
Cys Ser Ser Thr Thr Thr Ile Glu Met Arg Thr Gln Ala Ala Gln Val
      195      200      205
Ile Leu Ala Ala Ser Leu Gln Ala Thr Thr Val Ser Tyr Thr His Ile
      210      215      220
Leu Ala Arg Ser Leu Arg Ile Pro Glu Arg Pro Ser Lys Leu Lys Ala
      225      230      235      240
Phe Pro Thr Tyr Ala Ser His Leu Gly Cys Gly Ser Ser Asn Leu Ile
      245      250      255

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Lys Leu Val Ser Gly Val Tyr Leu Val Gly Ile Pro Leu Leu Lys Pro
 260 265 270
 Ile Ile Tyr Cys Leu Arg Asn Cys Asn Ile Arg Glu Ala Leu Ala Lys
 275 280 285
 Leu Leu Gln Ala Leu Pro
 290

<210> 1702
 <211> 295
 <212> PRT
 <213> Unknown (H38g619 protein)

<220>
 <223> Synthetic construct

<400> 1702
 Ala Thr Tyr Asn Ser Ser Asn Thr Val Val Thr Glu Phe Val Phe Leu
 1 5 10 15
 Ser Phe Pro Glu Leu Arg His Leu Gln Gly Leu Leu Phe Gly Leu Leu
 20 25 30
 Leu Ile Ile Tyr Val Val Thr Ile Leu Glu Asp Leu Ala Val Val Gly
 35 40 45
 Thr Ile Arg Ala Ser His His Leu His Ile Ser Thr His Leu Phe Leu
 50 55 60
 Ala Lys Leu Ser Val Leu Glu Thr Leu Tyr Thr Ser Val Thr Val Pro
 65 70 75 80
 Lys Leu Leu Ala Gly Leu Pro Gly Thr Ser Asp Asp His Leu Ile Ser
 85 90 95
 Phe Ser Gly His Leu Thr Trp Leu Leu Phe Leu Ser Leu Ser Ser
 100 105 110
 Ser Glu Cys Ile Leu Pro Ala Asn Met Asp Cys Asp Trp His Pro Val
 115 120 125
 Ile Cys His Leu Leu His Tyr Pro Ala His His Gly Leu His Ala Ala
 130 135 140
 Arg Leu Cys Leu His Leu Ala Ile Ser Ala Gln Leu Ser Ser Phe Pro
 145 150 155 160
 Ala Ser Phe Val Ser Thr Ala Leu Asn Ser Ser Leu Arg Leu Arg Ser
 165 170 175
 Pro Asp Val Leu Asn His Phe Cys Asp Ile Pro Pro Pro Leu Gly Leu
 180 185 190
 Ser Cys Ser Ser Thr Thr Thr Ile Glu Met Arg Thr Gln Ala Ala Gln
 195 200 205
 Val Ile Leu Ala Ala Ser Leu Gln Ala Thr Thr Val Ser Tyr Thr His
 210 215 220
 Ile Leu Ala Arg Ser Leu Arg Ile Pro Ala Lys Ala Gln Gln Leu Lys
 225 230 235 240
 Ala Phe Pro Thr Tyr Ala Ser His Leu Gly Trp Arg Pro Ser Asn Leu
 245 250 255
 Ile Lys Leu Val Ser Gly Val Tyr Leu Val Gly Ile Pro Leu Leu Lys
 260 265 270
 Pro Ile Ile Tyr Cys Leu Arg Asn Cys Asn Ile Arg Glu Ala Leu Ala
 275 280 285
 Lys Leu Leu Gln Ala Leu Pro
 290 295

<210> 1703
 <211> 175
 <212> PRT
 <213> Unknown (H38g620 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(175)

<223> Xaa = Any Amino Acid

<400> 1703

Leu	Leu	Met	Ala	Ala	Asp	Asn	His	Thr	Arg	Val	Glu	Ala	Phe	Val	Leu
1				5					10					15	
Gln	Gly	Phe	Ser	Glu	Asp	Leu	Pro	Leu	Gln	Gly	Cys	Cys	Phe	Ala	Phe
			20					25					30		
Phe	Leu	Leu	Tyr	Leu	Met	Ala	Leu	Val	Gly	Asn	Ile	Leu	Met	Val	Met
		35					40					45			
Ala	Ile	Ser	Leu	Asn	Pro	Gly	Leu	His	Thr	Pro	Val	Tyr	Phe	Phe	Leu
	50					55					60				
Thr	Asn	Leu	Ala	Leu	Leu	Asp	Ile	Val	Cys	Thr	Ser	Met	Asp	Asn	Ser
65					70				75					80	
Arg	Val	Val	Ala	Val	Leu	Tyr	Thr	Val	Val	Ser	Pro	Thr	Leu	Asn	Pro
			85					90					95		
Ser	Pro	Thr	Pro	Cys	Gly	Thr	Arg	Thr	Tyr	Gln	Xaa	His	Xaa	Gly	Glu
			100					105					110		
Cys	Phe	Leu	Ala	Ser	Gly	Lys	Arg	Lys	Gly	Ser	Phe	Xaa	Cys	Glu	Met
		115				120						125			
Phe	Gln	Val	Leu	Thr	Asn	Xaa	Phe	Gln	His	Met	Thr	Leu	Arg	Ile	Ser
	130					135					140				
Cys	Lys	Gln	Gln	Gly	Thr	Arg	Lys	Xaa	Leu	Met	Pro	His	Ile	Tyr	Lys
145					150				155					160	
Xaa	Cys	Ala	Pro	Ala	Arg	Gly	Cys	His	His	Ser	Met	Trp	Asn	Ser	
			165					170					175		

<210> 1704

<211> 317

<212> PRT

<213> Unknown (H38g621 protein)

<220>

<223> Synthetic construct

<400> 1704

Met	Glu	Arg	Thr	Asn	Asp	Ser	Thr	Ser	Thr	Glu	Phe	Phe	Leu	Val	Gly
1				5					10					15	
Leu	Ser	Ala	His	Pro	Lys	Leu	Gln	Thr	Val	Phe	Phe	Val	Leu	Ile	Leu
			20					25					30		
Trp	Met	Tyr	Leu	Met	Ile	Leu	Leu	Gly	Asn	Gly	Val	Leu	Ile	Ser	Val
		35				40						45			
Ile	Ile	Phe	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Cys
	50					55					60				
Asn	Leu	Ser	Phe	Leu	Asp	Val	Cys	Tyr	Thr	Ser	Ser	Ser	Val	Pro	Leu
65					70				75					80	
Ile	Leu	Ala	Ser	Phe	Leu	Ala	Val	Lys	Lys	Lys	Val	Ser	Phe	Ser	Gly
			85					90					95		
Cys	Met	Val	Gln	Met	Phe	Ile	Ser	Phe	Ala	Met	Gly	Ala	Thr	Glu	Cys
			100					105					110		
Met	Ile	Leu	Gly	Thr	Met	Ala	Leu	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Tyr
		115				120						125			
Pro	Leu	Arg	Tyr	Pro	Val	Ile	Met	Ser	Lys	Gly	Ala	Tyr	Val	Ala	Met
	130					135					140				
Ala	Ala	Gly	Ser	Trp	Val	Thr	Gly	Leu	Val	Asp	Ser	Val	Val	Gln	Thr
145					150				155					160	
Ala	Phe	Ala	Met	Gln	Leu	Pro	Phe	Cys	Ala	Asn	Asn	Val	Ile	Lys	His
			165					170					175		

Phe Val Cys Glu Ile Leu Ala Ile Leu Lys Leu Ala Cys Ala Asp Ile
 180 185 190
 Ser Ile Asn Val Ile Ser Met Thr Gly Ser Asn Leu Ile Val Leu Val
 195 200 205
 Ile Pro Leu Leu Val Ile Ser Ile Ser Tyr Ile Phe Ile Val Ala Thr
 210 215 220
 Ile Leu Arg Ile Pro Ser Thr Glu Gly Lys His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe
 245 250 255
 Phe Met Tyr Ala Lys Pro Glu Ser Lys Ala Ser Val Asp Ser Gly Asn
 260 265 270
 Glu Asp Ile Ile Glu Ala Leu Ile Ser Leu Phe Tyr Gly Val Met Thr
 275 280 285
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300
 Ala Ala Val Lys Asn Ile Leu Cys Arg Lys Asn Phe Ser
 305 310 315

<210> 1705

<211> 318

<212> PRT

<213> Unknown (H38g622 protein)

<220>

<223> Synthetic construct

<400> 1705

Met Glu Trp Glu Asn Gln Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1 5 10 15
 His Ser Val His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
 20 25 30
 Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
 35 40 45
 Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
 65 70 75 80
 Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys
 100 105 110
 Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asn Ala Tyr Val Pro Met
 130 135 140
 Ala Val Gly Ser Trp Phe Ala Gly Ile Val Asn Ser Ala Val Gln Thr
 145 150 155 160
 Thr Phe Val Val Gln Leu Pro Phe Cys Arg Lys Asn Val Ile Asn His
 165 170 175
 Phe Ser Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile
 180 185 190
 Ser Gly Asn Glu Phe Leu Met Leu Val Ala Thr Ile Leu Phe Thr Leu
 195 200 205
 Met Pro Leu Leu Leu Ile Val Ile Ser Tyr Ser Leu Ile Ile Ser Ser
 210 215 220
 Ile Leu Lys Ile His Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
 245 250 255
 Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp

```

                260                265                270
Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
      275                280                285
Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290                295                300
Glu Ala Val Lys His Leu Pro Asn Arg Arg Phe Phe Ser Lys
305                310                315

```

<210> 1706
 <211> 124
 <212> PRT
 <213> Unknown (H38g623 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(124)
 <223> Xaa = Any Amino Acid

```

<400> 1706
Phe Leu Leu Xaa Ala Asn Tyr Ser Ala Glu Glu Arg Phe Leu Leu Leu
 1                5                10                15
Gly Phe Ser Asp Trp Pro Ser Leu Gln Pro Val Leu Phe Ala Leu Val
      20                25                30
Leu Leu Cys Tyr Leu Leu Thr Leu Thr Gly Asn Ser Ala Leu Val Leu
      35                40                45
Leu Ala Val Asp Pro Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Cys
      50                55                60
His Leu Ala Leu Val Asp Ala Gly Phe Thr Thr Ser Val Val Pro Pro
      65                70                75                80
Leu Leu Ala Asn Leu Arg Gly Pro Ala Leu Tyr Val Pro Arg Ser His
      85                90                95
Cys Thr Ala Gln Leu Cys Ala Ser Leu Ala Leu Gly Ser Ala Glu Cys
      100                105                110
Val His Leu Ala Val Met Ala Leu Gly Arg Ala Val
      115                120

```

<210> 1707
 <211> 315
 <212> PRT
 <213> Unknown (H38g624 protein)

<220>
 <223> Synthetic construct

```

<400> 1707
Met Arg Gln Asn Asn Asn Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
 1                5                10                15
Gln Asp Pro Gly Val Gln Lys Ala Leu Phe Val Met Phe Leu Leu Thr
      20                25                30
Tyr Leu Val Thr Val Val Gly Asn Leu Leu Ile Val Val Asp Ile Ile
      35                40                45
Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys Leu
      50                55                60
Ser Phe Ile Asp Ala Ala Tyr Ser Thr Thr Ile Ser Pro Lys Leu Ile
      65                70                75                80
Val Gly Leu Phe Cys Asp Lys Lys Thr Ile Ser Phe Gln Gly Cys Met
      85                90                95
Gly Gln Leu Phe Ile Asp His Phe Phe Gly Gly Ala Glu Val Phe Leu
      100                105                110

```

Leu Val Val Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Leu Thr Ile Met Asn Arg Gln Val Cys Phe Leu Leu Leu Val
 130 135 140
 Val Ala Met Ile Gly Gly Phe Val His Ser Ala Phe Gln Ile Val Val
 145 150 155 160
 Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Val His Phe Ser Cys
 165 170 175
 Asp Met His Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr Tyr Phe Ile
 180 185 190
 Gly Leu Thr Val Val Val Asn Ser Gly Ala Ile Cys Met Val Ile Phe
 195 200 205
 Asn Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Ser Ser Leu Lys Thr
 210 215 220
 Tyr Ser Gln Glu Lys Arg Gly Lys Ala Leu Ser Thr Cys Ser Ser Gly
 225 230 235 240
 Ser Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Ile Tyr Val
 245 250 255
 Arg Pro Val Ser Asn Phe Pro Thr Asp Lys Phe Met Thr Val Phe Tyr
 260 265 270
 Thr Ile Ile Thr His Met Leu Ser Pro Leu Ile Tyr Thr Leu Arg Asn
 275 280 285
 Ser Glu Met Arg Asn Ala Ile Glu Lys Leu Leu Gly Lys Lys Leu Thr
 290 295 300
 Ile Phe Ile Ile Gly Gly Val Ser Val Leu Met
 305 310 315

<210> 1708

<211> 117

<212> PRT

<213> Unknown (H38g625 protein)

<220>

<223> Synthetic construct

<400> 1708

Arg Cys Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala
 1 5 10 15
 Leu Leu Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln
 20 25 30
 Met Phe Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile
 35 40 45
 Leu Ala Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe
 50 55 60
 Ser Gly Gly Arg Gln Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr
 65 70 75 80
 Ala Val Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro
 85 90 95
 Ala Gln Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr
 100 105 110
 Thr Val Val Thr Pro
 115

<210> 1709

<211> 313

<212> PRT

<213> Unknown (H38g626 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1709

Gly Leu Ser Asn Asn Val Thr Glu Phe Val Leu Leu Gly Asn Thr Gln
 1 5 10 15
 Cys Pro Asp Val Gln Asn Ala Leu Phe Val Met Val Leu Leu Thr Tyr
 20 25 30
 Val Val Ser Met Ala Gly Asn Leu Leu Ala Val Val Ala Ile Ile Ser
 35 40 45
 Ser Pro Ser Phe Gly Ser Pro Met Tyr Phe Phe Leu Thr Cys Leu Leu
 50 55 60
 Phe Ile Tyr Ala Ala Tyr Ser Asn Thr Ile Ser Pro Lys Leu Ile Ile
 65 70 75 80
 Gly Leu Leu His Asp Lys Lys Thr Ile Phe Phe Thr Ala Cys Met Gly
 85 90 95
 Gln Leu Phe Ile Asp His Leu Phe Gly Gly Ala Glu Val Phe Leu Leu
 100 105 110
 Val Gly Met Ser Tyr Asp Phe Tyr Val Ala Ile Ser Lys Pro Leu His
 115 120 125
 Tyr Leu Thr Ile Met Asn Gln Gln Val Cys Ile Leu Leu Val Val
 130 135 140
 Ala Val Thr Gly Gly Phe Val Ser Cys Val Phe Gln Ile Val Val Val
 145 150 155 160
 Tyr Thr Leu Ser Phe Cys Gly Pro Asn Val Thr Asp His Phe Val Cys
 165 170 175
 Asp Met Tyr Pro Leu Leu Glu Leu Val Cys Thr Asp Thr Tyr Phe Ile
 180 185 190
 Gly Leu Thr Val Val Ala Asn Gly Leu Ala Ile Cys Met Val Val Phe
 195 200 205
 Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Asn Phe Lys Thr
 210 215 220
 Tyr Ser Gln Glu Gly Arg Leu Lys Ala Leu Ser Ala Cys Ile Ser Tyr
 225 230 235 240
 Ile Thr Val Thr Val Leu Phe Leu Val Pro Cys Ile Phe Leu Phe Val
 245 250 255
 Arg Pro Val Ser Asn Phe Pro Ile Asp Lys Phe Met Thr Val Phe Tyr
 260 265 270
 Thr Val Ile Ile His Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
 275 280 285
 Leu Glu Met Arg Ile Ala Val Lys Ser Asn Val Lys Lys Leu Trp His
 290 295 300
 Xaa Lys Leu Asn Tyr Ser Xaa Asn Glu
 305 310

<210> 1710

<211> 323

<212> PRT

<213> Unknown (H38g627 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1710

Met Arg Leu Ser Ser Asp Val Thr Ala Phe Val Leu Leu Gly Leu Thr
 1 5 10 15

Gln Asp Pro Asp Val Xaa Asn Ala Leu Phe Val Val His Leu Leu Thr
 20 25 30
 Tyr Ile Met Thr Met Val Gly Asn Leu Pro Ile Val Val Thr Ile Ile
 35 40 45
 Ala Thr Pro Thr Leu Gly Ser Pro Val Tyr Phe Phe Ile Val Cys Leu
 50 55 60
 Ser Phe Ile Asp Val Val Tyr Ser Thr Thr Ile Pro Pro Lys Leu Ile
 65 70 75 80
 Val Ser Tyr Leu His Asp Lys Lys Thr Ile Ser Phe Arg Ala Cys Met
 85 90 95
 Gly Gln Pro Phe Ile Asp His Leu Val Gly Gly Ala Glu Ala Phe Ile
 100 105 110
 Leu Leu Val Met Ala Tyr Asn Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Phe Thr Ile Met Asn Xaa Gln Val Cys Ile Leu Leu Leu Val
 130 135 140
 Val Ala Val Thr Ala Gly Phe Val His Ser Val Phe Gln Ile Leu Val
 145 150 155 160
 Ala Tyr Ser Leu Leu Phe Cys Gly Pro Asn Ile Ile Asp His Phe Phe
 165 170 175
 Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala His Thr Asp Thr Tyr Phe
 180 185 190
 Ile Gly Leu Thr Val Val Ala Asn Gly Gly Gly Ile Cys Met Val Leu
 195 200 205
 Phe Ile Leu Leu Leu Ile Ser Cys Gly Val Ile Leu Ile Ser Leu Lys
 210 215 220
 Thr Tyr Ser Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser
 225 230 235 240
 His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
 245 250 255
 Val Arg Pro Val Ser Asn Phe Pro Ile Asn Lys Phe Ile Thr Val Phe
 260 265 270
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Xaa Glu Met Lys Asn Ala Ile Gly Asn Leu Trp Cys Lys Tyr Xaa
 290 295 300
 Leu Xaa Ile Glu Xaa Glu Gly Thr Phe Ser Cys Arg Tyr Arg Val Met
 305 310 315 320
 Gln Val Lys

<210> 1711

<211> 235

<212> PRT

<213> Unknown (H38g628 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(235)

<223> Xaa = Any Amino Acid

<400> 1711

Pro Met Tyr Leu Phe Leu Gly Asn Leu Ser Phe Ile Asp Leu Cys Tyr
 1 5 10 15
 Ser Phe Val Phe Thr Pro Lys Met Leu Met Ser Phe Ile Ser Glu Arg
 20 25 30
 Asn Ile Ile Ser Phe Pro Gly Cys Ile Thr Gln Leu Phe Phe Phe Cys
 35 40 45
 Phe Phe Val His Ser Glu Cys Tyr Val Leu Thr Ala Met Ala Tyr Asp

```

      50              55              60
Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Met Val Thr Thr Ser
65              70              75              80
Pro Gln Ile Cys Ser Leu Leu Met Leu Gly Ser Tyr Val Met Gly Phe
      85              90              95
Ala Gly Ala Met Val His Thr Glu Cys Met Met Lys Leu Ile Phe Cys
      100              105              110
Asp Ser Asn Val Ile Asn His Asn Met Cys Asp Ile Phe Pro Leu Leu
      115              120              125
Gln Leu Ser Cys Ser Ser Thr Xaa Ala Asn Glu Leu Val Met Ser Val
      130              135              140
Ile Val Gly Thr Val Val Ile Val Ser Ser Leu Ile Ile Leu Ile Ser
145              150              155              160
Tyr Ala Leu Ile Leu Phe Asn Ile Leu His Met Ser Ser Ala Glu Gly
      165              170              175
Trp Phe Lys Ala Ile Gly Thr Cys Gly Ser His Ile Ile Thr Val Gly
      180              185              190
Leu Phe Tyr Glu Phe Gly Leu Ile Thr His Val Lys Leu Ser Ser Asp
      195              200              205
Trp Tyr Met Gly Gln Gly Lys Phe Leu Ser Val Phe Tyr Thr Asn Val
      210              215              220
Val Pro Met Leu Asn Pro Phe Ile Tyr Cys Leu
225              230              235

```

<210> 1712

<211> 308

<212> PRT

<213> Unknown (H38g629 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 1712

```

Met Arg Gln Asn Asn Asn Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
1      5      10      15
Gln Tyr Pro Asp Val Gln Asn Ala Leu Phe Val Met Phe Leu Leu Ile
      20      25      30
Tyr Ile Val Thr Met Val Gly Asn Leu Leu Ile Val Val Ser Ile Ile
      35      40      45
Ala Ser Pro Phe Leu Gly Ser Pro Val Tyr Phe Phe Leu Ala Cys Leu
      50      55      60
Ser Phe Ile Asp Ala Val Tyr Ser Thr Thr Ile Ser Pro Val Leu Ile
65      70      75      80
Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met
      85      90      95
Gly Gln Leu Phe Ile Glu His Leu Phe Gly Asp Thr Asp Val Phe Leu
      100      105      110
Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys Lys Pro Leu
      115      120      125
Arg Tyr Leu Thr Ile Met Asn Xaa Gln Val Cys Ile Leu Leu Leu Val
      130      135      140
Val Ala Val Thr Gly Gly Phe Leu His Ser Val Phe Gln Ile Leu Val
145      150      155      160
Val Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Tyr His Phe Phe
      165      170      175
Cys Asn Ile Tyr Pro Leu Leu Asp Leu Glu Cys Thr Asp Thr Tyr Phe
      180      185      190

```

Val Gly Leu Ala Val Val Phe Asn Gly Gly Ala Ile Cys Met Val Ile
 195 200 205
 Phe Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Ser Leu Lys
 210 215 220
 Thr Tyr Ser Pro Glu Gly Arg His Lys Ala Pro Phe Ile Cys Ser Ser
 225 230 235 240
 His Phe Ile Met Val Ile Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
 245 250 255
 Val Arg Pro Val Ser Asn Phe Pro Ile Asp Lys Phe Leu Thr Val Phe
 260 265 270
 Tyr Ser Val Ile Thr Pro Lys Leu Asn Pro Phe Ile Tyr Met Leu Arg
 275 280 285
 Asn Ser Glu Met Arg Asn Ala Ile Glu Asn Leu Leu Gly Tyr Gln Ser
 290 295 300
 Gly Lys Thr Gly
 305

<210> 1713

<211> 230

<212> PRT

<213> Unknown (H38g630 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(230)

<223> Xaa = Any Amino Acid

<400> 1713

Pro Met Tyr Leu Phe Leu Ala Asn Leu Ser Leu Pro Asp Ile Gly Phe
 1 5 10 15
 Thr Ser Ser Met Val Pro Lys Met Ile Val Asp Ile Xaa Ser His Ser
 20 25 30
 Arg Leu Ile Ser Xaa Ala Gly Cys Leu Thr Pro Met Ser Leu Phe Ala
 35 40 45
 Ile Phe Gly Gly Met Glu Glu Asn Met Leu Leu Ser Val Ile Ala Tyr
 50 55 60
 Asp Pro Phe Val Ala Ile Cys His Pro Leu Tyr His Ser Ala Ile Met
 65 70 75 80
 Asn Pro Cys Phe Cys Gly Phe Leu Val Leu Leu Ser Phe Phe Ser Gln
 85 90 95
 Ser Leu Leu Asp Ala Gln Val His Asn Leu Ile Ala Leu Gln Met Thr
 100 105 110
 Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln
 115 120 125
 Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met
 130 135 140
 Tyr Ser Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu
 145 150 155 160
 Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Arg Arg Val Ser Ser Ser
 165 170 175
 Gly Gly Lys Tyr Lys Ala Cys Ser Thr Cys Gly Ser His Leu Ser Val
 180 185 190
 Val Cys Xaa Phe Tyr Gly Thr Gly Phe Trp Gly Tyr Leu Ser Ser Asp
 195 200 205
 Val Ser Ser Ser Pro Gly Lys Ala Ala Val Ala Ser Val Met Tyr Thr
 210 215 220
 Val Val Thr Pro Met Leu
 225 230

<210> 1714
 <211> 227
 <212> PRT
 <213> Unknown (H38g632 protein)

<220>
 <223> Synthetic construct

<400> 1714
 Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro Lys Met Leu
 1 5 10 15
 Gly Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe Leu Gly Cys Ala
 20 25 30
 Thr Gln Met Tyr Phe Phe Phe Phe Gly Val Ala Glu Cys Phe Leu
 35 40 45
 Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu
 50 55 60
 His Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Ala
 65 70 75 80
 Ala Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val Gln Thr Thr Trp
 85 90 95
 Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val Asn His Phe Phe
 100 105 110
 Cys Asp Ser Pro Pro Val Leu Lys Leu Val Cys Ala Asp Thr Ala Leu
 115 120 125
 Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Val Met Ile Pro
 130 135 140
 Cys Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ala Ile Leu
 145 150 155 160
 Lys Ile Pro Ser Ala Lys Gly Lys His Lys Ala Phe Ser Thr Cys Ser
 165 170 175
 Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser Leu Ser Leu Thr
 180 185 190
 Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly Lys Lys Leu Leu
 195 200 205
 Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Phe His Leu
 210 215 220
 Leu Ser Trp
 225

<210> 1715
 <211> 192
 <212> PRT
 <213> Unknown (H38g633 protein)

<220>
 <223> Synthetic construct

<400> 1715
 Met Val Thr Glu Phe Leu Leu Leu Gly Phe Leu Leu Gly Pro Arg Ile
 1 5 10 15
 Gln Met Leu Leu Phe Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu
 20 25 30
 Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu
 35 40 45
 His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Val Val Asp Ile
 50 55 60
 Ala Tyr Ala Cys Asn Thr Val Pro Arg Met Leu Val Asn Leu Leu His
 65 70 75 80
 Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu
 85 90 95

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Phe Ser Thr Phe Ala Val Thr Glu Cys Leu Leu Leu Val Val Met Ser
      100      105      110
Tyr Asp Leu Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Phe Ile Ile
      115      120      125
Met Thr Trp Lys Val Cys Ile Thr Leu Ala Ile Thr Ser Trp Thr Cys
      130      135      140
Gly Ser Leu Leu Ala Met Val His Val Ser Leu Ile Leu Arg Leu Pro
      145      150      155
Phe Cys Gly Pro Arg Glu Ile Asn His Phe Leu Cys Glu Ile Leu Ala
      165      170      175
Val Leu Arg Leu Gly Cys Ala Asp Thr Trp Leu Asn Gln Val Val Ile
      180      185      190

```

<210> 1716

<211> 308

<212> PRT

<213> Unknown (H38g634 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 1716

```

Tyr Ala Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
  1      5      10      15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
      20      25      30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
      65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
      100      105      110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile
      115      120      125
Cys His Pro Leu Tyr His Leu Thr Ile Met Asn Pro Cys Phe Cys Ala
      130      135      140
Phe Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln
      145      150      155      160
Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val Glu
      165      170      175
Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys
      180      185      190
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
      195      200      205
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
      210      215      220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
      225      230      235      240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
      245      250      255
Arg Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
      260      265      270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Ser Met Leu

```

275 280 285
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu
 290 295 300
 Arg Arg Pro Gln
 305

<210> 1717
 <211> 238
 <212> PRT
 <213> Unknown (H38g635 protein)

<220>
 <223> Synthetic construct

<400> 1717
 Met Tyr Leu Phe Leu Arg Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr
 1 5 10 15
 Ser Thr Ile Val Pro Lys Met Ile Val Asp Ile Gln Ser His Ser Arg
 20 25 30
 Val Ile Ser Tyr Ala Gly Arg Leu Thr Gln Met Ser Leu Phe Ala Ile
 35 40 45
 Phe Gly Gly Met Glu Asp Asn Met Leu Leu Ser Val Met Ala Tyr Asp
 50 55 60
 Arg Phe Val Ala Ile Cys His Pro Leu Tyr His Ser Ala Ile Met Asn
 65 70 75 80
 Pro Cys Phe Cys Gly Phe Leu Leu Leu Leu Ser Phe Phe Phe Phe Leu
 85 90 95
 Ser Leu Leu Asp Thr Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr
 100 105 110
 Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln
 115 120 125
 Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Val
 130 135 140
 Tyr Phe Pro Ala Val Ile Phe Val Phe Leu Pro Ile Ser Gly Thr Leu
 145 150 155 160
 Phe Ser Leu Lys Leu Phe Val Ser Ser Ile Leu Arg Val Ser Ser Ser
 165 170 175
 Gly Gly Lys Tyr Lys Thr Phe Ser Thr Cys Gly Ser His Leu Ser Val
 180 185 190
 Ile Cys Leu Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp
 195 200 205
 Val Ser Ser Ser Leu Arg Lys Ala Ala Val Ala Ser Val Met Tyr Lys
 210 215 220
 Met Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Thr Leu Arg
 225 230 235

<210> 1718
 <211> 321
 <212> PRT
 <213> Unknown (H38g636 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(321)
 <223> Xaa = Any Amino Acid

<400> 1718
 Phe Lys Arg Ser Ile Thr Phe Thr Pro Thr Thr Phe Thr Leu Val Gly
 1 5 10 15

```

Ile Pro Gly Leu Glu Ala Glu His Tyr Trp Ile Ser Ile Pro Phe Cys
      20      25      30
Leu Ile Tyr Thr Ile Ile Phe Pro Gly Asn Gly Ile Ile Leu His Ile
      35      40      45
Ile Arg Ile Asp Ser Ser Leu His Gln Pro Met Tyr Tyr Phe Leu Ala
      50      55      60
Met Pro Ala Phe Val Glu Leu Gly Val Ser Ala Ser Thr Met Pro Thr
      65      70      75      80
Val Leu Ser Ile Phe Leu Phe Gly Ile Asn Asp Val Ser Phe Gly Gly
      85      90      95
Cys Leu Leu Gln Met Phe Ser Met His Ser Phe Thr Leu Met Glu Ser
      100      105      110
Gly Val Leu Leu Ala Met Ser Val Asp Arg Phe Val Ala Ile Tyr Ser
      115      120      125
Pro Leu Arg Tyr Thr Thr Ile Leu Thr Ile Ala Cys Ile Ser Gly Met
      130      135      140
Gly Ala Ala Ile Ala Leu Arg Ser Val Met Leu Met Leu Pro Leu Leu
      145      150      155      160
Phe Leu Leu Arg Arg Leu Pro Phe Cys Gly His Asn Thr Leu Thr His
      165      170      175
Ser Tyr Cys Leu His Ser Asp Leu Ile Lys Leu Pro Cys Gly Asp Thr
      180      185      190
Arg Pro Asn Ser Ile Leu Ala Leu Phe Val Ile Thr Phe Thr Phe Gly
      195      200      205
Leu Asp Leu Leu Phe Ile Val Val Ser Tyr Val Leu Ile Leu His Thr
      210      215      220
Val Leu Glu Ile Ala Ser Arg Ser Arg Ala Trp Gln Ala Leu Asn Thr
      225      230      235      240
Cys Val Ser His Ile Cys Ala Val Leu Val Tyr Tyr Val Pro Met Ile
      245      250      255
Ser Leu Ser Xaa Val His Arg Phe Gly Arg His Leu Pro Pro Leu Phe
      260      265      270
Gln Thr Val Thr Ala Asn Ala Tyr Leu Phe Phe Pro Pro Val Val Asn
      275      280      285
Pro Ile Val Tyr Ser Ile Lys Ile Lys Glu Ile Arg Asn Ser Val Val
      290      295      300
Leu Thr Leu Ser Arg Lys Arg Gly Glu Phe Xaa Trp Arg Pro Lys Ile
      305      310      315      320
Pro

```

<210> 1719

<211> 291

<212> PRT

<213> Unknown (H38g637 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1) ... (291)

<223> Xaa = Any Amino Acid

<400> 1719

```

Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe Leu
      1      5      10      15
Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      20      25      30
Met Ser Pro Asp Ser His Leu His Thr Ser Met Tyr Phe Phe Leu Ser
      35      40      45
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Gln

```


50	55	60
Met Thr Val Asp Ile	Gln Ser Arg Ser Arg	Val Ile Ser Tyr Ala Gly
65	70	75
Cys Leu Thr Gln Lys	Ser Leu Phe Ala Ile	Phe Gly Gly Thr Glu Glu
85	90	95
Asn Met Leu Leu Ser	Val Met Ala Tyr Asp Arg	Phe Val Ala Ile Cys
100	105	110
His Pro Leu Tyr His	Ser Ala Ile Met Asn Leu Cys	Phe Cys Gly Phe
115	120	125
Leu Val Leu Leu Ser	Phe Phe Phe Leu Ser Leu Leu	Asp Ser Gln Leu
130	135	140
Tyr Asn Leu Ile Ala	Leu Leu Met Thr Cys Phe Lys	Glu Val Asp Ile
145	150	155
Pro Asn Phe Phe Cys	Asp Leu Ser Gln Leu Pro His	Leu Ala Cys Cys
165	170	175
Asp Thr Phe Ile Asn	Asn Ile Ile Met Tyr Phe Pro	Thr Ala Ile Phe
180	185	190
Gly Phe Leu Pro Ile	Ser Gly Thr Leu Phe Ser Tyr	Tyr Lys Ile Val
195	200	205
Ser Ser Ile Leu Arg	Val Ser Ser Ser Gly Gly Lys	Tyr Lys Ala Phe
210	215	220
Ser Thr Cys Gly Ser	His Leu Ser Val Val Cys Xaa	Phe Tyr Gly Arg
225	230	235
Gly Val Gly Gly Tyr	Leu Ser Ser Asp Val Ser Ser	Ser Pro Arg Lys
245	250	255
Gly Ala Val Ala Ala	Val Met Tyr Thr Val Val Thr	Ser Met Leu Asn
260	265	270
Pro Phe Ile Tyr Ser	Leu Gly Asn Arg Asp Ile Lys	Ser Val Leu Arg
275	280	285
Arg Pro Gln		
290		

<210> 1720

<211> 216

<212> PRT

<213> Unknown (H38g638 protein)

<220>

<223> Synthetic construct

<400> 1720

Leu Val Asp Phe Cys Tyr Ser Ser	Ala Val Thr Pro Thr Val Ile Ala
1	5 10 15
Gly Leu Val Ile Gly Asp Lys Val	Ile Ser Tyr Asn Ala Cys Ala Ala
20	25 30
Gln Met Phe Phe Phe Ala Ala Phe	Ala Thr Val Glu Asn Phe Leu Leu
35	40 45
Ala Ser Met Ala Tyr Asp Arg Tyr	Asp Ala Val Cys Lys Pro Leu His
50	55 60
Tyr Thr Thr Thr Met Thr Thr Ser	Val Cys Ala Cys Leu Ala Ile Ile
65	70 75 80
Cys Tyr Val Cys Gly Phe Leu Asn	Ala Ser Ile His Ile Gly Glu Thr
85	90 95
Leu Ser Leu Phe Leu Tyr Gly Pro	Asn Glu Val His Cys Phe Phe Cys
100	105 110
Asp Val Pro Pro Val Met Ala Leu	Ser Cys Cys Asp Arg His Val Asn
115	120 125
Glu Leu Val Leu Ile Tyr Val Ala	Ser Phe Asn Ile Phe Ser Ala Ile
130	135 140
Leu Val Ile Leu Ile Ser Tyr Leu	Phe Ile Phe Ile Thr Ile Leu Lys
145	150 155 160

Met His Ser Ala Ser Gly Tyr Gln Lys Ala Leu Ser Thr Cys Ala Ser
 165 170 175
 His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr
 180 185 190
 Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp Lys Leu Ala Ser
 195 200 205
 Val Phe Tyr Thr Met Ile Ile Pro
 210 215

<210> 1721

<211> 216

<212> PRT

<213> Unknown (H38g639 protein)

<220>

<223> Synthetic construct

<400> 1721

Phe Val Asp Ile Cys Phe Ser Cys Thr Thr Val Pro Lys Met Leu Ala
 1 5 10 15
 Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr
 20 25 30
 Gln Met Tyr Phe Val Phe Met Phe Val Asp Thr Asp Asn Phe Leu Leu
 35 40 45
 Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His
 50 55 60
 Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
 65 70 75 80
 Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
 85 90 95
 Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys
 100 105 110
 Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
 115 120 125
 Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
 130 135 140
 Leu Cys Asn Leu Ala Ser Tyr Met His Ile Thr Cys Thr Gly Leu Lys
 145 150 155 160
 Gly Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ala Val Gly Leu Leu Phe Tyr Ser Thr Ile Thr Ala Val Tyr
 180 185 190
 Phe Asn Pro Leu Ser Ser His Ser Ala Ala Lys Asp Thr Met Ala Thr
 195 200 205
 Val Leu Tyr Thr Val Val Thr Pro
 210 215

<210> 1722

<211> 157

<212> PRT

<213> Unknown (H38g640 protein)

<220>

<223> Synthetic construct

<400> 1722

Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His His Cys
 1 5 10 15
 Phe Trp Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly Ser Thr
 20 25 30
 Ile His Thr Gly Phe Met Leu Arg Leu Phe Leu Cys Lys Thr Asn Val

```

      35      40      45
Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Gly Leu Ser Cys
   50      55      60
Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser Ala Phe
65      70      75      80
Asn Ile Leu Thr Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile Phe Ile
      85      90      95
Ile Ala Ser Ile Leu Arg Ile Arg Ser Thr Glu Gly Arg Ser Lys Ala
      100      105      110
Phe Ser Thr Cys Ser Ser His Ile Leu Ala Val Ala Gly Phe Phe Gly
      115      120      125
Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp
      130      135      140
Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Ile Val Val
145      150      155

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<210> 1723

<211> 325

<212> PRT

<213> Unknown (H38g641 protein)

<220>

<223> Synthetic construct

<400> 1723

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Met Lys Thr Leu Cys Ser Phe Leu Gln Ile Ser Arg Asn Met His Gln
 1      5      10      15
Glu Asn Gln Thr Thr Ile Thr Glu Phe Ile Leu Leu Gly Leu Ser Asn
      20      25      30
Gln Ala Glu His Gln Asn Leu Leu Phe Val Leu Phe Leu Ser Met Tyr
      35      40      45
Val Val Thr Val Val Gly Asn Gly Leu Ile Ile Val Ala Ile Ser Leu
      50      55      60
Asp Ile Tyr Leu His Thr Pro Met Tyr Leu Phe Leu Ala Tyr Leu Ser
65      70      75      80
Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val
      85      90      95
Asn Ile Gln Thr Asn Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr
      100      105      110
Gln Met Tyr Phe Ser Ile Val Phe Val Val Thr Asp Asn Leu Leu Leu
      115      120      125
Gly Thr Met Ala Phe Asp His Phe Val Ala Ile Cys His Pro Leu Asn
      130      135      140
Tyr Thr Thr Phe Met Arg Ala Arg Phe Gly Thr Leu Leu Thr Val Ile
145      150      155      160
Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu
      165      170      175
Ile Gln Leu Leu Phe Cys Asp His Asn Thr Leu Pro His Phe Phe Cys
      180      185      190
Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Met Ile Asn
      195      200      205
Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe
      210      215      220
Val Leu Ile Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Gly
225      230      235      240
Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
      245      250      255
His Leu Thr Ile Ala Leu Leu Phe Tyr Gly Thr Thr Val Gly Val Tyr
      260      265      270
Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala
      275      280      285

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Val Leu Phe Thr Val Val Thr Pro Met Met Asn Pro Phe Ile Tyr Ser
 290 295 300
 Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg Lys Leu Ile Asn Arg
 305 310 315 320
 Lys Ile Ser Ser Leu
 325

<210> 1724

<211> 315

<212> PRT

<213> Unknown (H38g642 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1724

Met Arg Pro Asn Asn Ser Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
 1 5 10 15
 Gln Asp Pro Gly Met Gln Lys Glu Leu Phe Val Met Phe Leu Phe Thr
 20 25 30
 Tyr Val Val Thr Val Leu Gly Asn Gln Leu Ile Val Val Thr Ile Ile
 35 40 45
 Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys Leu
 50 55 60
 Ser Phe Ile Asp Ala Ala Tyr Phe Thr Val Ile Ser Pro Lys Leu Ile
 65 70 75 80
 Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Gln Thr Phe Met
 85 90 95
 Gly Gln Leu Phe Ile Asp His Phe Phe Gly Gly Ala Glu Ala Phe Leu
 100 105 110
 Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Thr Leu
 115 120 125
 His Tyr Leu Thr Ile Met Thr Arg Gln Val Cys Ile Leu Ala Leu Leu
 130 135 140
 Val Ala Ala Thr Gly Gly Phe Val His Ser Val Phe Gln Ile Val Val
 145 150 155 160
 Val Tyr Ser Leu Pro Phe Cys Gly Ala Asn Val Ile Asp His Phe Ser
 165 170 175
 Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala Xaa Thr Asp Thr Tyr Phe
 180 185 190
 Ile Gly Leu Thr Val Val Phe Ser Gly Gly Ala Leu Cys Met Val Ile
 195 200 205
 Phe Thr Leu Leu Ile Ile Ser Tyr Arg Val Ile Leu Asn Ser Leu Lys
 210 215 220
 Thr Tyr Thr Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser
 225 230 235 240
 His Ile Thr Val Ile Val Leu Phe Phe Ile Pro Cys Ile Ser Ile Tyr
 245 250 255
 Val Arg Pro Val Ser Asn Phe Ser Ile Asp Thr Phe Met Thr Val Phe
 260 265 270
 Tyr Thr Val Ile Thr Pro Lys Leu Asn Pro Leu Ile Tyr Thr Phe Arg
 275 280 285
 Asn Ser Glu Met Arg Asn Val Ile Glu Lys Leu Leu Val Lys Lys Val
 290 295 300
 Thr Ile Phe Arg Ile Thr Gly Ser Ile Leu Met
 305 310 315

<210> 1725
 <211> 314
 <212> PRT
 <213> Unknown (H38g643 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(314)
 <223> Xaa = Any Amino Acid

<400> 1725
 Met Arg Gln Asn Lys Asn Asn Thr Glu Phe Val Leu Leu Gly Phe Ser
 1 5 10 15
 Gln Asp Pro Asp Val Gln Asn Ala Leu Phe Val Met Phe Leu Leu Thr
 20 25 30
 Xaa Leu Val Thr Thr Val Gly Asn Leu Leu Ile Val Val Thr Ile Ile
 35 40 45
 Ala Ser Pro Ser Leu Gly Ser Pro Val Tyr Phe Xaa Leu Ala Cys Leu
 50 55 60
 Ser Cys Ile Asp Ala Ala Tyr Ser Thr Thr Ile Ser Pro Lys Leu Ile
 65 70 75 80
 Val Glu Leu Leu Ile Asp Lys Lys Thr Ile Ser Phe Arg Ala Cys Met
 85 90 95
 Gly Gln Leu Phe Ile Glu His Leu Phe Gly Gly Thr Glu Ile Phe Ile
 100 105 110
 Leu Met Met Met Ala Cys Asp Arg Tyr Val Asp Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Leu Thr Ile Met Asn Xaa Gln Val Cys Ile Leu Leu Leu Val
 130 135 140
 Leu Ala Val Thr Gly Gly Phe Val His Ser Met Phe Gln Thr Val Val
 145 150 155 160
 Val Tyr Asn Leu Pro Phe Ser Gly Pro Asn Val Ile Asp Ile Asp His
 165 170 175
 Phe Val Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala Phe Thr Asp Thr
 180 185 190
 Tyr Phe Ile Gly Leu Thr Val Val Val Asn Gly Gly Ala Met Cys Met
 195 200 205
 Val Ile Phe Thr Ile Leu Leu Ile Ser Tyr Gly Ile Ile Leu Asn Ser
 210 215 220
 Leu Lys Thr Tyr Ser Gln Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Ser Pro His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Arg Pro Val Ser Thr Phe Pro Ile Asp Lys Phe Met Thr
 260 265 270
 Val Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr
 275 280 285
 Leu Arg Asn Ser Glu Met Arg Asn Ser Ile Glu Asn Leu Leu Cys Lys
 290 295 300
 Lys Ala Ile Cys Ser Xaa Asn Lys Ser Val
 305 310

<210> 1726
 <211> 315
 <212> PRT
 <213> Unknown (H38g644 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1726

Glu	Xaa	Met	Arg	Gln	Asn	Asn	Ser	Ser	Thr	Glu	Phe	Val	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Gln	Asp	Pro	Asp	Val	Gln	Asn	Ala	Leu	Phe	Val	Met	Phe	Leu
		20						25					30		
Leu	Thr	Tyr	Ile	Val	Thr	Met	Val	Gly	Asn	Leu	Leu	Ile	Val	Val	Thr
	35						40					45			
Ile	Ile	Ala	Ser	Pro	Ser	Leu	Gly	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Ala
	50					55					60				
His	Leu	Ser	Phe	Ile	Asp	Ala	Val	Tyr	Ser	Thr	Thr	Ile	Ser	Pro	Val
65					70					75					80
Leu	Ile	Val	Asp	Leu	Leu	Cys	Asp	Lys	Lys	Thr	Ile	Ser	Phe	Xaa	Ala
			85						90					95	
Cys	Met	Gly	Gln	Leu	Phe	Ile	Asp	His	Leu	Phe	Gly	Gly	Ser	Glu	Val
		100						105					110		
Phe	Leu	Leu	Val	Val	Met	Ala	Cys	Asp	Arg	Cys	Val	Ala	Ile	Cys	Lys
	115						120					125			
Pro	Leu	His	Tyr	Leu	Thr	Ile	Met	Asn	Arg	Gln	Val	Cys	Ile	Leu	Leu
	130					135					140				
Leu	Val	Leu	Ala	Val	Thr	Gly	Gly	Phe	Val	His	Pro	Val	Phe	Gln	Val
145					150					155					160
Val	Val	Val	Tyr	Ser	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Val	Ile	Asp	His
			165						170					175	
Phe	Phe	Cys	Asp	Ile	Tyr	Pro	Leu	Leu	Glu	Leu	Ala	Cys	Thr	Asp	Thr
		180						185					190		
Tyr	Phe	Ile	Gly	Leu	Thr	Val	Val	Phe	Asn	Gly	Gly	Ala	Met	Arg	Met
	195						200					205			
Val	Ile	Leu	Thr	Leu	Leu	Leu	Val	Phe	Tyr	Gly	Val	Ile	Leu	Asn	Ser
	210					215					220				
Leu	Lys	Thr	Tyr	Ser	Gln	Gly	Arg	His	Lys	Ala	Leu	Ser	Thr	Cys	
225					230				235					240	
Ser	Ser	His	Val	Thr	Val	Val	Ile	Leu	Phe	Phe	Ala	Ser	Cys	Ile	Phe
		245							250					255	
Ile	Tyr	Val	Arg	Pro	Val	Ser	Asn	Phe	Pro	Val	Asp	Lys	Phe	Met	Thr
		260						265					270		
Val	Phe	Tyr	Thr	Val	Ile	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Cys	Met
	275						280					285			
Leu	Arg	Asn	Ser	Glu	Met	Arg	Asn	Ala	Ile	Glu	Lys	Leu	Leu	Cys	Lys
	290					295					300				
Met	Asn	Cys	Ser	Xaa	Asn	Lys	Ser	Val	Pro	Ser					
305					310					315					

<210> 1727

<211> 313

<212> PRT

<213> Unknown (H38g645 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1727

Met Gly Leu Ser Asn Asn Val Thr Glu Leu Phe Leu Leu Gly Leu Thr

1	5	10	15
Gln Asp Leu Asp Val Gln Asn Ala Leu Phe Val Met Phe Leu Leu Thr			
20	25	30	
Tyr Ile Val Thr Met Val Gly Asn Leu Leu Ile Val Val Thr Ile Ile			
35	40	45	
Ala Thr Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys Leu			
50	55	60	
Ser Phe Ile Asp Ala Val Tyr Ser Thr Thr Ile Tyr Pro Lys Leu Val			
65	70	75	80
Val Asp Xaa Leu His Asn Xaa Lys Thr Ile Leu Phe Pro Thr Cys Met			
85	90	95	
Gly Gln Pro Leu Thr Asp His Leu Phe Gly Gly Val Glu Val Phe Phe			
100	105	110	
Leu Leu Val Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu			
115	120	125	
His Tyr Phe Thr Ile Met Asn Arg Gln Val Phe Ile Leu Leu Leu Val			
130	135	140	
Val Ala Val Thr Gly Gly Phe Val Arg Ser Val Phe Gln Ile Val Val			
145	150	155	160
Val Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Phe			
165	170	175	
Cys Asn Met Tyr Pro Leu Met Glu Met Ala Xaa Thr Asp Thr Tyr Phe			
180	185	190	
Ile Gly Leu Thr Val Val Phe Lys Val Glu Ala Ile Cys Val Val Ile			
195	200	205	
Phe Thr Leu Leu Leu Ile Ser Ser Gly Val Ile Leu Ile Ser Leu Lys			
210	215	220	
Thr Tyr Ser Gln Glu Gly Arg His Lys Ala Leu Phe Thr Cys Ser Ser			
225	230	235	240
Arg Ile Thr Val Val Leu Phe Phe Val Pro Cys Ile Phe Met Tyr			
245	250	255	
Val Arg Pro Val Phe Asn Phe Pro Ile Asp Lys Phe Ile Ile Val Phe			
260	265	270	
Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Met Leu Arg			
275	280	285	
Asn Ser Xaa Thr Arg Asn Ala Ile Glu Asn Pro Xaa Cys Lys Lys Leu			
290	295	300	
Thr Val Asp Arg Ile Arg Val Tyr Ile			
305	310		

<210> 1728

<211> 315

<212> PRT

<213> Unknown (H38g646 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1728

Met Arg Pro Asn Asn Ser Ile Thr Glu Phe Val Leu Leu Gly Phe Ser		
1	5	10
Gln Asp Pro Asp Met Gln Asn Thr Leu Phe Val Met Phe Leu Leu Thr		
20	25	30
Tyr Ile Val Thr Val Val Gly Asn Leu Leu Val Ala Val Thr Ile Ile		
35	40	45
Val Ser Pro Ser Leu Ser Ser Pro Met Xaa Phe Phe Leu Ala Cys Leu		
50	55	60

```

Ser Leu Ile Asp Ala Val Leu Ser Thr Thr Ile Ser Pro Ile Leu Ile
65          70          75          80
Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met
      85          90          95
Gly Gln Leu Phe Thr Asp His Leu Phe Gly Gly Thr Glu Ile Phe Leu
      100         105         110
Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115         120         125
His Tyr Leu Thr Ile Met Asn Arg Gln Val Ser Ile Leu Leu Leu Val
      130         135         140
Val Ala Met Thr Gly Gly Phe Leu His Ser Val Phe Gln Ile Ala Val
145         150         155         160
Leu Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Phe
      165         170         175
Cys Asp Met Tyr Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr Tyr Ser
      180         185         190
Ile Gly Leu Thr Val Val Phe Ser Gly Gly Ala Met Cys Met Val Ile
      195         200         205
Phe Ala Leu Leu Leu Ile Ser Tyr Gly Val Ser Leu Asn Ser Leu Lys
      210         215         220
Thr Tyr Ser Gln Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys Ser Ser
225         230         235         240
His Ile Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
      245         250         255
Val Arg Pro Val Ser Asn Phe Pro Ile Asp Lys Phe Val Thr Val Phe
      260         265         270
Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Phe Leu Tyr Thr Leu Arg
      275         280         285
Asn Ser Glu Met Ile Asn Ala Ile Lys His Leu Leu Cys Lys Lys Leu
      290         295         300
Thr Ile Val Arg Ile Arg Val Ser Leu Leu Met
305          310          315

```

<210> 1729

<211> 322

<212> PRT

<213> Unknown (H38g647 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1729

```

Met Gly Ser Ser Asn Asn Val Thr Glu Phe Val Leu Leu Ala Leu Thr
1          5          10          15
Gln Ala Pro Asp Val Gln Lys Val Leu Phe Val Met Phe Leu Phe Thr
      20         25         30
Tyr Ile Val Thr Met Val Gly Asn Leu Leu Thr Val Val Thr Ile Phe
      35         40         45
Ala Ser Pro Ser Leu Gly Ser Pro Val Xaa Leu Phe Leu Ala Cys Leu
      50         55         60
Ser Leu Met Asp Ala Val Tyr Ser Thr Ser Phe Ser Pro Lys Leu Met
65          70          75          80
Ile Asp Leu Leu Cys Asp Lys Lys Thr Val Ser Phe Pro Ala Cys Met
      85          90          95
Gly Gln Leu Phe Ala Asp His Leu Phe Gly Gly Val Glu Val Phe Leu
      100         105         110
Phe Val Gly Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu

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      115      120      125
His Tyr Leu Ile Ile Val Asn Arg Leu Val Cys Ile Leu Leu Leu Val
 130      135      140
Val Ala Val Thr Gly Gly Phe Xaa His Ser Met Phe Leu Phe Phe Xaa
145      150      155      160
Ile Tyr Leu Phe Phe Tyr Val Asn Ser Met Phe Gln Ile Val Val Val
      165      170      175
Tyr Ser Leu Pro Phe Cys Gly Ser Asn Val Ile Asp His Ile Val Cys
      180      185      190
Asp Met Tyr Pro Leu Leu Glu Leu Ala Cys Ala Asp Thr Tyr Phe Ile
      195      200      205
Gly Leu Thr Val Ile Ala Asn Gly Gly Ala Ile Cys Met Val Ile Phe
      210      215      220
Cys Leu Leu Leu Thr Ser Tyr Gly Val Ile Leu Asn Phe Leu Lys Thr
225      230      235      240
Tyr Ser Gln Glu Gly Arg His Arg Thr Leu Ser Thr Cys Ser Ser His
      245      250      255
Ile Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Met Tyr Val
      260      265      270
Arg Pro Val Ser Asn Phe Pro Ile Asp Lys Phe Ile Thr Glu Phe Tyr
      275      280      285
Thr Val Ile Thr Pro Lys Leu Asn Pro Leu Ile Gln Pro Leu Arg Asn
      290      295      300
Xaa Glu Met Arg Ile Thr Met Lys Lys Leu Trp Cys Xaa Thr Xaa Thr
305      310      315      320
Ile Val

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<210> 1730

<211> 310

<212> PRT

<213> Unknown (H38g648 protein)

<220>

<223> Synthetic construct

<400> 1730

```

Met Lys Asn Lys Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1      5      10      15
Gln Asn Pro Glu Gly Gln Lys Val Leu Phe Val Thr Phe Leu Leu Ile
      20      25      30
Tyr Met Val Thr Ile Met Gly Asn Leu Leu Ile Ile Val Thr Ile Met
      35      40      45
Ala Ser Gln Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Ser Leu
      50      55      60
Ser Phe Ile Asp Thr Val Tyr Ser Thr Ala Phe Ala Pro Lys Met Ile
      65      70      75      80
Val Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Gln Gly Cys Met
      85      90      95
Ala Gln Leu Phe Met Asp His Leu Phe Ala Gly Ala Glu Val Ile Leu
      100      105      110
Leu Val Val Met Ala Tyr Asp Arg Tyr Met Ala Ile Cys Lys Pro Leu
      115      120      125
His Glu Leu Ile Thr Met Asn Arg Arg Val Cys Val Leu Met Leu Leu
      130      135      140
Ala Ala Trp Ile Gly Gly Phe Leu His Ser Leu Val Gln Phe Leu Phe
145      150      155      160
Ile Tyr Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp Asn Phe Leu
      165      170      175
Cys Asp Leu Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asn Thr Tyr Val
      180      185      190

```

Thr Gly Leu Ser Met Ile Ala Asn Gly Gly Ala Ile Cys Ala Val Thr
 195 200 205
 Phe Phe Thr Ile Leu Leu Ser Tyr Gly Val Ile Leu His Ser Leu Lys
 210 215 220
 Thr Gln Ser Leu Glu Gly Lys Arg Lys Ala Phe Tyr Thr Cys Ala Ser
 225 230 235 240
 His Val Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
 245 250 255
 Ala Arg Pro Asn Ser Thr Phe Pro Ile Asp Lys Ser Met Thr Val Val
 260 265 270
 Leu Thr Phe Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Lys
 275 280 285
 Asn Ala Glu Met Lys Ser Ala Met Arg Lys Leu Trp Ser Lys Lys Val
 290 295 300
 Ser Leu Ala Gly Lys Trp
 305 310

<210> 1731

<211> 275

<212> PRT

<213> Unknown (H38g649 protein)

<220>

<223> Synthetic construct

<400> 1731

Met Val Gly Asn Leu Leu Ile Trp Val Thr Thr Ile Gly Ser Pro Ser
 1 5 10 15
 Leu Gly Ser Leu Met Tyr Phe Phe Leu Ala Tyr Leu Ser Leu Met Asp
 20 25 30
 Ala Ile Tyr Ser Thr Ala Met Ser Pro Lys Leu Met Ile Asp Leu Leu
 35 40 45
 Cys Asp Lys Ile Ala Ile Ser Leu Ser Ala Cys Met Gly Gln Leu Phe
 50 55 60
 Ile Glu His Leu Leu Gly Gly Ala Glu Val Phe Leu Leu Val Val Met
 65 70 75 80
 Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro Leu His Tyr Leu Asn
 85 90 95
 Ile Met Asn Arg Leu Val Cys Ile Leu Leu Leu Val Val Ala Met Ile
 100 105 110
 Gly Gly Phe Val His Ser Val Val Gln Ile Val Phe Leu Tyr Ser Leu
 115 120 125
 Pro Ile Cys Gly Pro Asn Val Ile Asp His Ser Val Cys Asp Met Tyr
 130 135 140
 Pro Leu Leu Glu Leu Leu Cys Leu Asp Thr Tyr Phe Ile Gly Leu Thr
 145 150 155 160
 Val Val Ala Asn Gly Gly Ile Ile Cys Met Val Ile Phe Thr Phe Leu
 165 170 175
 Leu Ile Ser Cys Gly Val Ile Leu Asn Phe Leu Lys Thr Tyr Ser Gln
 180 185 190
 Glu Glu Arg His Lys Ala Leu Pro Thr Cys Ile Ser His Ile Ile Val
 195 200 205
 Val Ala Leu Val Phe Val Pro Cys Ile Phe Met Tyr Val Arg Pro Val
 210 215 220
 Ser Asn Phe Pro Phe Asp Lys Leu Met Thr Val Phe Tyr Ser Ile Ile
 225 230 235 240
 Thr Leu Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Gln Ser Glu Met
 245 250 255
 Lys Asn Ala Met Lys Asn Leu Trp Cys Glu Lys Leu Ser Ile Val Arg
 260 265 270
 Lys Arg Val

275

<210> 1732
 <211> 218
 <212> PRT
 <213> Unknown (H38g650 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(218)
 <223> Xaa = Any Amino Acid

<400> 1732
 Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Leu Ile Ser Xaa Ala Gly Cys Leu Thr
 20 25 30
 Pro Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
 35 40 45
 Leu Ser Val Ile Ala Tyr Asp Pro Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 65 70 75 80
 Leu Ser Phe Phe Ser Gln Ser Leu Leu Asp Ala Gln Val His Asn Leu
 85 90 95
 Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe
 100 105 110
 Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe
 115 120 125
 Thr Asn Asn Ile Ile Met Tyr Ser Pro Ala Ala Ile Phe Gly Phe Leu
 130 135 140
 Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile
 145 150 155 160
 Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Leu Ser Thr Cys
 165 170 175
 Gly Ser Arg Leu Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val Gly
 180 185 190
 Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg Lys Gly Ala Val
 195 200 205
 Ala Ser Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 1733
 <211> 216
 <212> PRT
 <213> Unknown (H38g651 protein)

<220>
 <223> Synthetic construct

<400> 1733
 Ser Met Ala Leu Met Leu Ile Cys Thr Thr Gly Pro Lys Met Ala Phe
 1 5 10 15
 Asn Tyr Leu Ser Gly Ser Lys Ser His Phe Tyr Gly Cys Cys Ala Thr
 20 25 30
 Gln Ile Phe Phe Tyr Thr Ser Leu Leu Gly Ser Glu Cys Phe Leu Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile Cys His Pro Leu Arg
 50 55 60

Tyr Thr Asn Leu Met Ser Pro Lys Ile Cys Gly Leu Met Thr Ala Phe
 65 70 75 80
 Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Val Val Ala Thr
 85 90 95
 Phe Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys
 100 105 110
 Asp Phe Pro Ser Leu Leu Ile Leu Ser Cys Ser Asp Thr Ser Ile Phe
 115 120 125
 Glu Lys Ile Leu Phe Ile Cys Cys Ile Val Met Ile Val Phe Pro Val
 130 135 140
 Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala Val Ile His
 145 150 155 160
 Met Gly Ser Gly Glu Gly Arg Arg Lys Ala Phe Thr Thr Cys Ser Ser
 165 170 175
 His Leu Leu Val Val Gly Met Tyr Tyr Gly Ala Ala Leu Phe Met Tyr
 180 185 190
 Ile Arg Pro Thr Ser Asp Arg Ser Pro Thr Gln Asp Lys Met Val Ser
 195 200 205
 Val Phe Tyr Thr Ile Leu Thr Pro
 210 215

<210> 1734

<211> 212

<212> PRT

<213> Unknown (H38g652 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1734

Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Glu
 1 5 10 15
 Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
 20 25 30
 Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Glu Ile Phe Val Leu
 35 40 45
 Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg
 50 55 60
 Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
 65 70 75 80
 Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr
 85 90 95
 Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Glu His Tyr Phe Cys
 100 105 110
 Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
 115 120 125
 Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
 130 135 140
 Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
 145 150 155 160
 Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
 165 170 175
 Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile Tyr Arg
 180 185 190
 Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
 195 200 205
 Thr Ile Thr Pro

210

<210> 1735
 <211> 223
 <212> PRT
 <213> Unknown (H38g653 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(223)
 <223> Xaa = Any Amino Acid

<400> 1735
 Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Xaa Gly Arg Glu Glu Ser Met Leu
 35 40 45
 Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Pro
 50 55 60
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Val Cys
 65 70 75 80
 Cys Pro Cys Phe Phe Phe Phe Phe Phe Phe Leu Ser Leu Leu Asp Ser
 85 90 95
 Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
 100 105 110
 Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala
 115 120 125
 Cys Cys Asp Ile Phe Thr Arg Asn Ile Asn Leu Tyr Phe Pro Ala Ala
 130 135 140
 Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys
 145 150 155 160
 Ile Val Ser Ser Ile Leu Arg Val Ser Ser Gly Gly Arg Tyr Lys
 165 170 175
 Ala Leu Ser Thr Cys Gly Ser His Val Ser Val Val Cys Xaa Val Tyr
 180 185 190
 Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Phe Ser Pro
 195 200 205
 Arg Lys Gly Ala Val Ala Ser Val Met Tyr Ala Val Val Thr Pro
 210 215 220

<210> 1736
 <211> 216
 <212> PRT
 <213> Unknown (H38g654 protein)

<220>
 <223> Synthetic construct

<400> 1736
 Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val
 1 5 10 15
 Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala
 20 25 30
 Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu
 35 40 45
 Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg Pro Leu His
 50 55 60

Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala
 65 70 75 80
 Ser Arg Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser Thr Leu Thr
 85 90 95
 Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys
 100 105 110
 Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn
 115 120 125
 Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu Ile Pro Leu
 130 135 140
 Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg
 145 150 155 160
 Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser
 165 170 175
 His Leu Ile Val Val Ser Leu Phe Asn Ser Thr Ala Val Ser Val Tyr
 180 185 190
 Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser
 195 200 205
 Leu Phe Tyr Gly Ile Ile Ala Pro
 210 215

<210> 1737

<211> 218

<212> PRT

<213> Unknown (H38g655 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(218)

<223> Xaa = Any Amino Acid

<400> 1737

Leu Pro Asp Ile Gly Phe Thr Ser Thr Ile Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Arg Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Asp Ser Met Leu
 35 40 45
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu
 65 70 75 80
 Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln Leu His Asn Leu
 85 90 95
 Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe
 100 105 110
 Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe
 115 120 125
 Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu
 130 135 140
 Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Ser Ser Ile
 145 150 155 160
 Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Tyr
 165 170 175
 Gly Ser His Leu Ser Asp Val Ser Xaa Phe Tyr Gly Thr Gly Val Gly
 180 185 190
 Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys Thr Ala Val
 195 200 205
 Ala Ser Val Met Tyr Thr Val Val Thr Pro

210

215

<210> 1738
 <211> 221
 <212> PRT
 <213> Unknown (H38g656 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(221)
 <223> Xaa = Any Amino Acid

<400> 1738
 Phe Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Pro Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Gly Asp Thr Glu Glu Asn Met Phe
 35 40 45
 Leu Ser Val Val Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Asp Ser
 65 70 75 80
 Leu Ser Leu Val Phe Phe Phe Phe Phe Ser Leu Leu Asp Ser Gln Leu
 85 90 95
 His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile
 100 105 110
 Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys Cys
 115 120 125
 Asp Ile Phe Thr Arg Asn Ile Asn Leu Tyr Phe Pro Ala Ala Ile Phe
 130 135 140
 Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Cys Tyr Lys Ile Val
 145 150 155 160
 Ser Phe Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe
 165 170 175
 Ser Ala Cys Gly Ser His Leu Ser Val Val Tyr Xaa Phe Tyr Gly Thr
 180 185 190
 Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys
 195 200 205
 Thr Ala Val Ala Ser Val Met Tyr Ala Val Val Thr Pro
 210 215 220

<210> 1739
 <211> 216
 <212> PRT
 <213> Unknown (H38g657 protein)

<220>
 <223> Synthetic construct

<400> 1739
 Val Leu Asp Val Gly Cys Ile Thr Val Thr Val Pro Ala Met Leu Gly
 1 5 10 15
 Arg Leu Leu Ser His Lys Ser Thr Ile Ser Tyr Asp Ala Cys Leu Ser
 20 25 30
 Gln Leu Phe Phe Phe His Leu Leu Ala Gly Met Asp Cys Phe Leu Leu
 35 40 45
 Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala Ile Cys Gln Pro Leu Thr
 50 55 60

Tyr Ser Thr Arg Met Ser Gln Thr Val Gln Arg Met Leu Val Ala Ala
 65 70 75 80
 Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu Thr His Thr Val Ala Met
 85 90 95
 Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu Val Asn His Phe Tyr Cys
 100 105 110
 Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys Ser Ser Thr Gln Leu Asn
 115 120 125
 Glu Leu Leu Phe Val Ala Ala Phe Met Ala Val Ala Pro Leu
 130 135 140
 Val Phe Ile Ser Val Pro Tyr Ala His Val Val Ala Ala Val Leu Gln
 145 150 155 160
 Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Gly Ile Phe Tyr Gly Thr Gly Val Phe Ser Tyr
 180 185 190
 Met Arg Leu Gly Ser Val Glu Ser Ser Asp Lys Asp Lys Gly Val Gly
 195 200 205
 Val Phe Met Thr Val Ile Asn Pro
 210 215

<210> 1740

<211> 212

<212> PRT

<213> Unknown (H38g658 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1740

Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Glu
 1 5 10 15
 Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
 20 25 30
 Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Asp Ile Phe Val Leu
 35 40 45
 Thr Val Met Ala Phe Asp Arg Cys Ala Ala Ile Cys Gln Pro Leu Arg
 50 55 60
 Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
 65 70 75 80
 Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr
 85 90 95
 Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys
 100 105 110
 Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
 115 120 125
 Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
 130 135 140
 Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
 145 150 155 160
 Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
 165 170 175
 Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile Tyr Arg
 180 185 190
 Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
 195 200 205
 Thr Ile Thr Pro

210

<210> 1741
 <211> 216
 <212> PRT
 <213> Unknown (H38g659 protein)

<220>
 <223> Synthetic construct

<400> 1741
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
 1 5 10 15
 Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp Cys Leu Thr
 20 25 30
 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
 35 40 45
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60
 Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu Val Ala Leu
 65 70 75 80
 Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
 85 90 95
 Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys
 100 105 110
 Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr Arg Val Asn
 115 120 125
 Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe
 130 135 140
 Leu Leu Ile Leu Gly Ser Tyr Ala Arg Val Val Ser Ser Ile Leu Lys
 145 150 155 160
 Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr
 180 185 190
 Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala
 195 200 205
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 1742
 <211> 146
 <212> PRT
 <213> Unknown (H38g660 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(146)
 <223> Xaa = Any Amino Acid

<400> 1742
 Thr Leu Gln Asn Ile Thr Ser Thr Ser Ile Ile Phe Leu Leu Thr Gly
 1 5 10 15
 Val Pro Gly Leu Glu Ala Phe His Thr Trp Ile Ser Ile Pro Phe Cys
 20 25 30
 Phe Leu Ser Val Thr Ala Leu Leu Gly Asn Ser Leu Ile Leu Phe Ala
 35 40 45
 Thr Ile Thr Gln Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ser
 50 55 60

Met Leu Ser Ala Thr Asp Leu Gly Leu Ser Ile Ser Thr Leu Val Thr
 65 70 75 80
 Met Leu Ser Ile Phe Trp Phe Asn Val Arg Glu Ile Ser Phe Asn Ala
 85 90 95
 Cys Leu Ser His Met Phe Phe Ile Lys Phe Phe Thr Val Met Glu Ser
 100 105 110
 Ser Val Leu Leu Ala Met Ala Phe Asp Arg Leu Val Pro Ser Leu Ser
 115 120 125
 Pro Xaa Tyr Ala Met Ile Xaa Leu Thr Gln Ile Ala Lys Met Ser Ala
 130 135 140
 Val Tyr
 145

<210> 1743

<211> 334

<212> PRT

<213> Unknown (H38g661 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 1743

Ala Gly Val Glu Asn Asp Asn Thr Ser Ser Phe Glu Gly Phe Ile Leu
 1 5 10 15
 Val Gly Phe Ser Asp Arg Pro His Leu Glu Leu Ile Val Phe Val Val
 20 25 30
 Val Leu Ile Phe Tyr Leu Leu Thr Leu Leu Gly Asn Met Thr Ile Val
 35 40 45
 Leu Leu Ser Ala Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ala Asn Leu Ser Phe Leu Asp Met Cys Phe Thr Thr Gly Ser Ile
 65 70 75 80
 Pro Gln Met Leu Tyr Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr
 85 90 95
 Val Gly Cys Ala Ile Gln Leu Tyr Phe Val Leu Ala Leu Gly Gly Val
 100 105 110
 Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Val
 115 120 125
 Cys Lys Pro Leu His Tyr Thr Ile Ile Met His Pro Arg Leu Cys Gly
 130 135 140
 Gln Leu Ala Ser Val Ala Trp Leu Ser Gly Phe Gly Asn Ser Leu Ile
 145 150 155 160
 Met Ala Pro Gln Thr Leu Met Leu Pro Arg Cys Gly His Arg Arg Val
 165 170 175
 Asp His Phe Leu Cys Glu Met Pro Ala Leu Ile Gly Met Ala Cys Val
 180 185 190
 Asp Thr Met Met Leu Glu Ala Leu Ala Phe Ala Leu Ala Ile Phe Ile
 195 200 205
 Ile Leu Ala Pro Leu Ile Leu Ile Leu Ile Ser Tyr Gly Tyr Val Gly
 210 215 220
 Gly Thr Val Leu Arg Ile Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe
 225 230 235 240
 Asn Thr Cys Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr
 245 250 255
 Ile Ile Tyr Met Tyr Leu Gln Pro Ala Asn Thr Tyr Ser Gln Asp Gln
 260 265 270
 Gly Lys Phe Leu Thr Leu Phe Tyr Thr Ile Val Thr Pro Ser Val Asn

275	280	285
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Glu Ala Met Lys		
290	295	300
Lys Val Leu Gly Lys Gly Ser Ala Glu Ile Xaa Xaa Gly Val Ile Lys		
305	310	315
Leu Trp Asp Cys Ile Leu Thr His Leu Leu Tyr Met Leu Leu		
325	330	

<210> 1744

<211> 275

<212> PRT

<213> Unknown (H38g662 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(275)

<223> Xaa = Any Amino Acid

<400> 1744

Leu Tyr Leu Ile Lys His Asp His Ser Leu His Glu Pro Met Tyr Tyr		
1	5	10
Phe Leu Thr Met Leu Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr		
20	25	30
Met Pro Thr Val Met Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser		
35	40	45
Ser Val Gly Cys Phe Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val		
50	55	60
Val Glu Ser Gly Ser Leu Ala Met Ala Tyr Asp Arg Leu Ile Ala		
65	70	75
Ile Arg Asn Pro Leu Arg Tyr Ala Ser Ile Ser Thr Asn Thr Arg Val		
85	90	95
Ile Ala Leu Gly Val Gly Leu Phe Leu Arg Gly Leu Val Ser Ile Leu		
100	105	110
Pro Val Ile Leu Arg Leu Phe Pro Phe Pro Tyr Gly Lys Ser His Val		
115	120	125
Ile Thr Arg Ala Phe Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys		
130	135	140
Ala Asp Ile Thr Ser Asn Lys Leu Tyr Pro Val Ile Leu Ile Ser Leu		
145	150	155
Thr Ile Ser Leu Asn Ser Leu Ile Thr Pro Ser Ser Tyr Ile Leu Ile		
165	170	175
Leu Asn Thr Val Ile Gly Ile Ala Ser Gly Glu Glu Lys Thr Lys Ala		
180	185	190
Leu Asn Thr Cys Ile Ser His Ile Ser Cys Val Leu Ile Ser Tyr Val		
195	200	205
Thr Val Met Gly Leu Thr Phe Ile Tyr Lys Phe Gly Lys Asn Val Pro		
210	215	220
Lys Val Val His Ile Ile Ile Ser Tyr Ile Tyr Phe Leu Phe Pro Pro		
225	230	235
Leu Met Asn Pro Val Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr		
245	250	255
Gly Ile Ile Arg Leu Leu Ser Lys His Arg Phe Ser Arg Xaa Thr Arg		
260	265	270
Ile Trp Lys		
275		

<210> 1745

<211> 219

<212> PRT

<213> Unknown (H38g663 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(219)

<223> Xaa = Any Amino Acid

<400> 1745

```

Leu Ala Asp Ile Gly Phe Thr Ser Asn Thr Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
          20           25           30
Gln Met Ser Leu Phe Ala Val Phe Gly Gly Met Glu Glu Asn Met Leu
          35           40           45
Leu Ser Val Arg Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
          50           55           60
Tyr Cys Ser Ala Ile Phe Asn Pro Cys Phe Cys Gly Phe Leu Asp Leu
          65           70           75           80
Leu Ser Phe Phe Phe Phe Phe Leu Ser Leu Ser Asp Ser Gln Leu His
          85           90           95
Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro
          100          105          110
Asn Phe Phe Trp Glu Pro Ser Gln Leu Ser His Leu Ala Cys Cys Asp
          115          120          125
Thr Phe Thr Arg Asn Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe
          130          135          140
Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Phe Ser
          145          150          155          160
Ile Leu Arg Val Ser Ser Ser Gly Gly Lys His Lys Ala Phe Ser Thr
          165          170          175
Arg Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Ile
          180          185          190
Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys Ala Ala
          195          200          205
Val Ala Ser Val Met Tyr Thr Val Ala Ile Pro
          210          215

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<210> 1746

<211> 218

<212> PRT

<213> Unknown (H38g664 protein)

<220>

<223> Synthetic construct

<400> 1746

```

Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro Lys Met Val Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
          20           25           30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Thr Leu Leu
          35           40           45
Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys His Pro Leu
          50           55           60
Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu
          65           70           75           80
Leu Ser Phe Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu His Asn Met
          85           90           95
Ile Ala Leu Gln Met Thr Cys Ile Lys Asp Val Glu Ile Pro Asn Phe

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<210> 1747
<211> 216
<212> PRT
<213> Unknown (H38g665 protein)
```

<220>
<223> Synthetic construct

<210> 1748
<211> 216
<212> PRT
<213> Unknown (H38g666 protein)

<220>
<223> Synthetic construct

<221> VARIANT

<222> (1)...(216)

<223> Xaa = Any Amino Acid

<400> 1748

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
          20           25           30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
          35           40           45
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
          50           55           60
Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
          65           70           75           80
Leu Ser Phe Phe Phe Ser Phe Ser Gln Leu His Asn Leu Ile Ala Leu
          85           90           95
Lys Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys Asp
          100          105          110
Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn Lys
          115          120          125
Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser
          130          135          140
Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Ile Leu Arg Val
          145          150          155          160
Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His
          165          170          175
Leu Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val Gly Gly Tyr Leu
          180          185          190
Ser Ser Asp Asp Val Ser Ser Ser Pro Arg Lys Gly Ala Val Ala Ser
          195          200          205
Val Met Tyr Thr Val Val Thr Pro
          210          215

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<210> 1749

<211> 217

<212> PRT

<213> Unknown (H38g667 protein)

<220>

<223> Synthetic construct

<400> 1749

```

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Lys Val Pro Lys Met Leu Thr
 1           5           10           15
Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
          20           25           30
Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
          35           40           45
Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
          50           55           60
Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
          65           70           75           80
Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
          85           90           95
Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
          100          105          110
Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
          115          120          125
Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro

```

130		135		140
Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu				
145		150		155
Gly Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser				160
		165		170
Ser His Leu Cys Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met				175
		180		185
Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu				190
		195		200
Ser Leu Phe Tyr Ser Leu Phe Asn Pro				205
210		215		

<210> 1750

<211> 216

<212> PRT

<213> Unknown (H38g668 protein)

<220>

<223> Synthetic construct

<400> 1750

Leu Val Asp Phe Cys Tyr Ser Ser Ala Val Thr Pro Thr Val Ile Ala				
1		5		10
Gly Leu Val Ile Gly Asp Glu Val Ile Ser Tyr Ser Ala Cys Ala Ala				15
		20		25
Gln Met Phe Phe Phe Ala Ala Phe Ala Thr Val Glu Asn Phe Leu Leu				30
		35		40
Ala Ser Met Ala Tyr Asp Arg Tyr Asp Ala Val Cys Lys Pro Leu His				45
		50		55
Tyr Thr Thr Thr Met Thr Thr Ser Val Cys Ala Cys Leu Ala Ile Ile				60
65		70		75
Cys Tyr Val Cys Gly Phe Leu Asn Ala Ser Ile His Ile Gly Glu Thr				80
		85		90
Leu Ser Leu Phe Leu Asn Gly Pro Asn Glu Val His Cys Ile Phe Cys				95
		100		105
Asp Val Pro Pro Val Met Ala Leu Ser Cys Cys Asp Arg His Val Asn				110
		115		120
Glu Leu Val Leu Ile Tyr Val Ala Ser Phe Asn Ile Phe Ser Ala Ile				125
		130		135
Leu Val Ile Leu Val Ser Tyr Leu Phe Ile Phe Ile Thr Ile Leu Glu				140
145		150		155
Met His Ser Ala Ser Gly Tyr Gln Lys Ala Leu Ser Asn Cys Ala Ser				160
		165		170
His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr				175
		180		185
Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp Lys Leu Ala Ser				190
		195		200
Val Phe Tyr Thr Met Ile Ile Pro				205
210		215		

<210> 1751

<211> 311

<212> PRT

<213> Unknown (H38g669 protein)

<220>

<223> Synthetic construct

<400> 1751

Met Ala Ala Glu Asn Ser Ser Phe Val Thr Gln Phe Ile Leu Ala Gly			
1		5	10
			15

Leu Thr Asp Gln Pro Gly Val Gln Ile Pro Leu Phe Phe Leu Phe Leu
 20 25 30
 Gly Phe Tyr Val Val Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
 35 40 45
 Ile Arg Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Tyr
 50 55 60
 Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Met Ser Phe Val Leu Lys Lys Asn Ser Ile Ser Tyr Ala Gly
 85 90 95
 Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe Val Val Ser Glu Ser
 100 105 110
 Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln Val Cys Phe Leu Leu
 130 135 140
 Leu Leu Gly Val Tyr Gly Met Gly Phe Ala Gly Ala Met Ala His Thr
 145 150 155 160
 Ala Cys Met Met Gly Val Thr Phe Cys Ala Asn Asn Leu Val Asn His
 165 170 175
 Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Cys Ala Cys Thr Ser Thr
 180 185 190
 Tyr Val Asn Glu Leu Val Val Phe Val Val Val Gly Ile Asp Ile Gly
 195 200 205
 Val Pro Thr Val Thr Ile Phe Ile Ser Tyr Ala Leu Ile Leu Ser Ser
 210 215 220
 Ile Phe His Ile Asp Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala
 245 250 255
 Phe Met Tyr Leu Lys Pro Phe Ser Leu Leu Ala Met Asn Gln Gly Lys
 260 265 270
 Val Ser Ser Leu Phe Tyr Thr Thr Val Val Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Lys Lys Ile
 290 295 300
 Leu Asn Lys Asn Ala Phe Ser
 305 310

<210> 1752

<211> 309

<212> PRT

<213> Unknown (H38g670 protein)

<220>

<223> Synthetic construct

<400> 1752

Met Thr Leu Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly
 1 5 10 15
 Leu Ser Glu Gln Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30
 Gly Ile Tyr Val Phe Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu
 35 40 45
 Ile Gly Ile Asn Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Cys Val Phe Thr Pro Lys
 65 70 75 80
 Met Leu Asn Asp Phe Val Ser Glu Ser Ile Ile Ser Tyr Val Gly Cys
 85 90 95
 Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr

100	105	110
Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro		
115	120	125
Leu Leu Tyr Met Val Thr Met Ser Pro Arg Val Cys Phe Leu Leu Met		
130	135	140
Phe Gly Ser Tyr Val Val Gly Phe Ala Gly Ala Met Ala His Thr Gly		
145	150	155
Ser Met Leu Arg Leu Thr Phe Cys Asp Ser Asn Val Ile Asp His Tyr		
165	170	175
Leu Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr His		
180	185	190
Val Ser Glu Leu Val Phe Phe Ile Val Val Gly Val Ile Thr Met Leu		
195	200	205
Ser Ser Ile Ser Ile Val Ile Ser Tyr Ala Leu Ile Leu Ser Asn Ile		
210	215	220
Leu Cys Ile Pro Ser Ala Glu Gly Arg Ser Lys Ala Phe Ser Thr Trp		
225	230	235
Gly Ser His Ile Ile Ala Val Ala Leu Phe Phe Gly Ser Gly Thr Phe		
245	250	255
Thr Tyr Leu Thr Thr Ser Phe Pro Gly Ser Met Asn His Gly Arg Phe		
260	265	270
Ala Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Ser Ile		
275	280	285
Tyr Ser Leu Arg Asn Lys Asp Asp Lys Leu Ala Leu Gly Lys Thr Leu		
290	295	300
Lys Arg Val Leu Phe		
305		

<210> 1753

<211> 297

<212> PRT

<213> Unknown (H38g671 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(297)

<223> Xaa = Any Amino Acid

<400> 1753

Met Lys Xaa Met Ala Val Glu Asn Asn Ser Ser Val Thr Glu Phe Ile	
1	5
Leu Val Arg Leu Thr Asn Ser Arg Cys Pro Ser Val Leu Phe Leu Met	
20	25
Trp Ser Leu Trp Gly Glu Phe Glu His Asn Phe Met Ser Leu Asn Ser	
35	40
His Leu His Thr Pro Thr His Phe Phe Leu Phe Thr Leu Ser Phe Ile	
50	55
Asp Val Cys Tyr Ser Phe Val Cys Thr Thr Lys Ile Pro Met Gly Phe	
65	70
Ile Ser Glu Arg Asn Ile Ile Ser Phe Val Gly Trp Pro Thr Xaa Leu	
85	90
Tyr Phe Phe Cys Ile Phe Val Lys Glu Pro Lys Asn Gly Val Ile Val	
100	105
Gly Ile Met Phe Ser Ala Lys Met Leu Val Cys Arg Glu Ile Met Asp	
115	120
Xaa Ser Leu Met Xaa Asn Xaa Lys Met His Met Ala Leu Glu Arg Ser	
130	135
Asp Phe Arg Met Gly Xaa Thr Gly Ser Ala Thr Lys Lys His Leu Ile	
145	150
	155
	160

Ile Phe Leu Tyr Tyr Ser Asp Tyr Phe Gln Arg Xaa Xaa Gly Cys Arg
165 170 175
Ala Leu Gly Gln Gly Ser Leu Ala Lys Gln Asp Thr Thr Leu Xaa Asn
180 185 190
Cys Thr Cys Thr Leu Lys Ser Leu Leu His Ile Ile Ile Cys Phe Tyr
195 200 205
Ile Trp Lys Gln Lys Lys Ile Ser Tyr Leu Tyr His Lys Ser Xaa Lys
210 215 220
Met Asp Leu Tyr Lys Ile Cys His Val Leu Trp Val Thr His Lys Lys
225 230 235 240
Asn Phe Leu Arg Pro Ser Ser Thr Ser Gln Met Val Gln Gly Lys Met
245 250 255
Leu Leu Lys Gly Tyr Ile Xaa Phe Trp Arg Met Ser Leu Pro Met Cys
260 265 270
Ala Ile Phe Ile Phe Val Arg Arg Tyr Tyr Tyr Leu Leu Lys Lys Leu
275 280 285
Lys Thr Leu Leu Tyr Lys Asn Ser Tyr
290 295

<210> 1754

<211> 313

<212> PRT

<213> Unknown (H38g672 protein)

<220>

<223> Synthetic construct

<400> 1754

Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly
1 5 10 15
Leu Thr Asp Arg Pro Glu Phe Arg Gln Pro Leu Phe Phe Leu Phe Leu
20 25 30
Val Val Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Ile Leu
35 40 45
Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe
50 55 60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
65 70 75 80
Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Tyr Val Gly
85 90 95
Cys Met Thr Gln Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys
100 105 110
Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
115 120 125
Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu
130 135 140
Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr
145 150 155 160
Gly Cys Met Leu Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His
165 170 175
Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
180 185 190
Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Ile Asn Ile Met
195 200 205
Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
210 215 220
Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
225 230 235 240
Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
245 250 255
Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val

<400> 1755																
Met	Asn	Trp	Val	Asn	Lys	Ser	Val	Pro	Gln	Glu	Phe	Ile	Leu	Leu	Val	
1				5					10					15		
Phe	Ser	Asp	Gln	Pro	Trp	Leu	Glu	Ile	Pro	Pro	Phe	Val	Met	Phe	Leu	
			20					25					30			
Phe	Ser	Tyr	Ile	Leu	Thr	Ile	Phe	Gly	Asn	Leu	Thr	Ile	Ile	Leu	Val	
			35				40					45				
Ser	His	Val	Asp	Phe	Lys	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	
	50				55						60					
Asn	Leu	Ser	Leu	Leu	Asp	Leu	Cys	Tyr	Thr	Thr	Ser	Thr	Val	Pro	Gln	
65					70					75				80		
Met	Leu	Val	Asn	Ile	Cys	Asn	Thr	Arg	Lys	Val	Ile	Ser	Tyr	Gly	Gly	
				85					90					95		
Cys	Val	Ala	Gln	Leu	Phe	Ile	Phe	Leu	Ala	Leu	Gly	Ser	Thr	Glu	Cys	
			100					105					110			
Leu	Leu	Leu	Ala	Val	Met	Cys	Phe	Asp	Arg	Phe	Val	Ala	Ile	Cys	Arg	
			115				120					125				
Pro	Leu	His	Tyr	Ser	Ile	Ile	Met	His	Gln	Arg	Leu	Cys	Phe	Gln	Leu	
	130				135						140					
Ala	Ala	Ala	Ser	Trp	Ile	Ser	Gly	Phe	Ser	Asn	Ser	Val	Leu	Gln	Ser	
145					150					155				160		
Thr	Trp	Thr	Leu	Lys	Met	Pro	Leu	Cys	Gly	His	Lys	Glu	Val	Asp	His	
				165					170					175		
Phe	Phe	Cys	Glu	Val	Pro	Ala	Leu	Leu	Lys	Leu	Ser	Cys	Val	Asp	Thr	
			180					185					190			
Thr	Ala	Asn	Glu	Ala	Glu	Leu	Phe	Phe	Ile	Ser	Val	Leu	Phe	Leu	Leu	
			195				200					205				
Ile	Pro	Val	Thr	Leu	Ile	Leu	Ile	Ser	Tyr	Ala	Phe	Ile	Val	Gln	Ala	
	210				215						220					
Val	Leu	Arg	Ile	Gln	Ser	Ala	Glu	Gly	Gln	Arg	Lys	Ala	Phe	Gly	Thr	
225					230					235				240		
Cys	Gly	Ser	His	Leu	Ile	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Ala	Ile	
				245					250					255		
Ser	Met	Tyr	Leu	Gln	Pro	Pro	Ser	Pro	Ser	Ser	Lys	Asp	Arg	Gly	Lys	
			260					265					270			
Met	Val	Ser	Leu	Phe	Cys	Gly	Ile	Ile	Ala	Pro	Met	Leu	Asn	Pro	Leu	
			275				280					285				
Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Lys	Glu	Ala	Phe	Lys	Arg	Leu	
	290				295						300					
Val	Ala	Lys	Ser	Leu	Leu	Asn	Gln	Glu	Ile	Arg	Asn	Met	Gln	Met	Ile	
305					310					315				320		
Ser	Phe	Ala	Lys	Asp	Thr	Val	Leu	Thr	Tyr	Leu	Thr	Asn	Phe	Ser	Ala	
				325					330					335		
Ser	Cys	Pro	Ile	Phe</												

Gln Arg Lys Phe Pro
355

<210> 1756

<211> 331

<212> PRT

<213> Unknown (H38g674 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1756

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Met Ala Pro Gly Asn Gly Phe Phe Met Thr Lys Ile Ile Leu Leu Glu
 1           5           10           15
Leu Thr Asp Gln Pro Asp Leu Gln Leu Pro Leu Phe Phe Leu Phe Leu
      20           25           30
Val Tyr Gly His Cys Val Gly Lys Phe Gly Leu Val Thr Leu Val Val
      35           40           45
Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu
      50           55           60
Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Gln Met Leu
      65           70           75           80
Met Asn Phe Ile Thr Gln Lys Asp Ile Ile Ser His Met Gly Cys Met
      85           90           95
Ser Gln Leu Phe Phe Phe Ala Leu Phe Phe Phe Gly Ile Ser Glu Cys
      100          105          110
Tyr Val Leu Thr Ser Met Ala Tyr Asp Arg Ala Cys His His Asp His
      115          120          125
His Val Ala Ile Cys Asn Pro Leu Leu Tyr Asn Ile Ala Met Ser Pro
      130          135          140
Lys Val Tyr Ser His Leu Met Leu Gly Leu Tyr Leu Leu Ala Phe Ser
      145          150          155          160
Ser Ala Met Ala His Thr Gly Cys Met Leu Arg Leu Thr Phe Cys Asp
      165          170          175
Ala Asn Thr Ile His Pro Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln
      180          185          190
Leu Ser Cys Thr Gly Thr Tyr Ile Asn Glu Leu Val Val Ser Thr Ala
      195          200          205
Ala Val Ile Ile Ser Thr Val Thr Ile Phe Ile Ser Cys Gly Cys Ser
      210          215          220
Ser Tyr Ile Ile Leu His Ile Asn Ser Lys Glu Gly Arg Ser Lys Ala
      225          230          235          240
Leu Asn Thr Cys Ser Ser Asn Leu Ile Ala Val Ser Leu Met Phe Gly
      245          250          255
Ser Cys Ala Phe Met Cys Leu Lys Pro Ser Ser Ala Gly Ser Met Asp
      260          265          270
Glu Gly Lys Ile Ser Ser Val Phe Tyr Thr Asn Thr Ala Pro Leu Met
      275          280          285
Asn Pro Leu Ile Tyr Ser Leu Met Asn Lys Met Phe Asn Phe Leu Xaa
      290          295          300
Glu Lys Asn Pro Ser Arg Lys Lys Phe Xaa Leu Glu Ile Val Ser Phe
      305          310          315          320
Cys Ala Cys Ile Phe Arg Thr Gly Ser Phe Cys
      325          330

```

<210> 1757

<211> 332

<212> PRT
 <213> Unknown (H38g675 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(332)
 <223> Xaa = Any Amino Acid

<400> 1757

Met	Ala	Pro	Gly	Asn	Gly	Ser	Leu	Met	Asn	Glu	Phe	Ile	Leu	Val	Gly
1				5					10					15	
Leu	Thr	Asp	Xaa	Pro	Asp	Leu	Xaa	Leu	Pro	Leu	Phe	Phe	Met	Phe	Leu
			20					25					30		
Val	Met	Tyr	Val	Val	Thr	Val	Ile	Arg	Asn	Phe	Val	Leu	Val	Ile	Leu
		35					40					45			
Thr	Met	Arg	Asn	Ser	Arg	Leu	His	Thr	Pro	Lys	Tyr	Phe	Phe	Leu	Ser
	50					55					60				
Lys	Leu	Phe	Phe	Thr	Asp	Leu	Cys	Tyr	Ser	Ser	Val	Phe	Ile	Leu	Gln
65					70				75					80	
Leu	Pro	Arg	Lys	Cys	Ile	Ser	Glu	Glu	Asn	Val	Ile	Ser	Tyr	Met	Val
			85						90					95	
Cys	Met	Ile	Xaa	Leu	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Xaa
			100					105					110		
Phe	Ile	Ser	Glu	Cys	Tyr	Met	Leu	Thr	Ser	Met	Ala	Tyr	Asp	Cys	Cys
		115					120					125			
Val	Ala	Ile	Cys	Tyr	Pro	Leu	Leu	Tyr	His	Ile	Ala	Met	Ser	Pro	Lys
	130					135					140				
Val	Cys	Phe	Ser	Leu	Met	Leu	Gly	Ser	Tyr	Phe	Leu	Ser	Phe	Ser	Gly
145				150					155					160	
Ala	Met	Ala	His	Thr	Gly	Cys	Met	Leu	Arg	Leu	Thr	Cys	Asp	Ala	Asn
			165					170						175	
Thr	Ile	Asn	His	Tyr	Phe	Arg	Asp	Ile	Leu	Pro	Val	Phe	Gln	Leu	Ser
		180					185						190		
Cys	Thr	Ser	Thr	Tyr	Ile	Asn	Glu	Leu	Val	Val	Phe	Ile	Val	Ala	Gly
	195					200					205				
Ile	Asn	Thr	Ile	Val	Pro	Thr	Val	Thr	Val	Phe	Ile	Ser	Tyr	Gly	Asp
	210					215					220				
Ile	Leu	Ser	Arg	Ile	Leu	His	Ile	Ser	Ser	Asn	Glu	Gly	Arg	Ser	Lys
225				230					235					240	
Ala	Phe	Ser	Thr	Cys	Ser	Ser	His	Ile	Ile	Ala	Val	Ser	Leu	Phe	Phe
			245					250						255	
Gly	Leu	Ser	Ala	Phe	Met	Tyr	Leu	Lys	Pro	Ser	Ser	Ala	Gly	Ser	Met
		260					265					270			
Asp	Glu	Gly	Lys	Phe	Ser	Ser	Val	Phe	Tyr	Met	Asn	Gly	Leu	Pro	Met
	275						280				285				
Met	Ser	Ser	Leu	Ile	Tyr	Ser	Leu	Arg	Arg	Lys	Asp	Val	Lys	Phe	Ala
	290					295				300					
Met	Gly	Lys	Ser	Leu	Ser	Arg	Arg	Met	Phe	Leu	Pro	Xaa	Thr	Thr	Phe
305				310					315					320	
Leu	Cys	Val	Cys	Ser	Tyr	Arg	Met	Gly	Ile	Leu	Cys				
			325					330							

<210> 1758
 <211> 313
 <212> PRT
 <213> Unknown (H38g676 protein)

<220>
 <223> Synthetic construct

<400> 1758

```

Met Asp Ser Leu Asn Gln Thr Arg Val Thr Glu Phe Val Phe Leu Gly
 1          5          10          15
Leu Thr Asp Asn Arg Val Leu Glu Met Leu Phe Phe Met Ala Phe Ser
          20          25          30
Ala Ile Tyr Met Leu Thr Leu Ser Gly Asn Ile Leu Ile Ile Ala
          35          40          45
Thr Val Phe Thr Pro Ser Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Ile Asp Ile Cys His Ser Ser Val Thr Val Pro Lys
65          70          75          80
Met Leu Glu Gly Leu Leu Leu Glu Arg Lys Thr Ile Ser Phe Asp Asn
          85          90          95
Cys Ile Thr Gln Leu Phe Phe Leu His Leu Phe Ala Cys Ala Glu Ile
          100          105          110
Phe Leu Leu Ile Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Thr
          115          120          125
Pro Leu His Tyr Pro Asn Val Met Asn Met Arg Val Cys Ile Gln Leu
          130          135          140
Val Phe Ala Leu Trp Leu Gly Gly Thr Val His Ser Leu Gly Gln Thr
145          150          155          160
Phe Leu Thr Ile Arg Leu Pro Tyr Cys Gly Pro Asn Ile Ile Asp Ser
          165          170          175
Tyr Phe Cys Asp Val Pro Leu Val Ile Lys Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Leu Thr Gly Ile Leu Ile Val Thr Asn Ser Gly Thr Ile Ser Leu
          195          200          205
Ser Cys Phe Leu Ala Val Val Thr Ser Tyr Met Val Ile Leu Val Ser
          210          215          220
Leu Arg Lys His Ser Ala Glu Gly Arg Gln Lys Ala Leu Ser Thr Cys
225          230          235          240
Ser Ala His Phe Met Val Val Ala Leu Phe Phe Gly Pro Cys Ile Phe
          245          250          255
Ile Tyr Thr Arg Pro Asp Thr Ser Phe Ser Ile Asp Lys Val Val Ser
          260          265          270
Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Thr
          275          280          285
Leu Arg Asn Glu Glu Val Lys Ser Ala Met Lys Gln Leu Arg Gln Arg
          290          295          300
Gln Val Phe Phe Thr Lys Ser Tyr Thr
305          310

```

<210> 1759

<211> 331

<212> PRT

<213> Unknown (H38g677 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1759

```

Met Ala Pro Gly Asn Ile Ser Thr Val Ala Glu Leu Ile Leu Val Gly
 1          5          10          15
Leu Lys Asp Gln Thr Asp Leu Gln Pro Pro Leu Phe Phe Leu Phe Leu
          20          25          30
Val Met Gly Val Val Ala Gly Xaa Gly Asn Leu Gly Leu Val Thr Leu

```

```

      35      40      45
Ile Val Phe Ser Ser His Phe His Ala Pro Met Tyr Phe Phe Leu Phe
  50      55      60
Ser Leu Ala Phe Ile Asp His Phe Tyr Ser Ser Val Phe Ile Pro Lys
  65      70      75      80
Met Leu Met Asn Phe Ile Thr Glu Lys Asn Ile Ile Ser Tyr Ala Gly
      85      90      95
Cys Met Ser Ala Phe Phe Ser Phe Phe Phe Cys Phe Phe Val Ile
      100      105      110
Ser Glu Cys Tyr Val Leu Thr Ser Met Val Ser Asp His Tyr Val Ala
      115      120      125
Met Ala Ile Cys Asn Pro Leu Leu Tyr Asn Ile Ala Met Ser Pro Lys
      130      135      140
Val Cys Ser Ser His Met Leu Gly Ser Tyr Phe Trp Pro Phe Ser Gly
  145      150      155      160
Ala Met Ala His Thr Arg Cys Met Leu Lys Leu Thr Ser Cys Glu Ala
      165      170      175
Asn Thr Ile Asn His Tyr Phe Cys Asp Thr Leu His Leu Leu Gln Leu
      180      185      190
Ser Cys Thr Ser Thr Tyr Val Ser Glu Leu Met Val Phe Ile Ala Ala
      195      200      205
Gly Ile Ile Phe Thr Val Pro Ser Ile Thr Ile Phe Ile Ser Tyr Phe
  210      215      220
Phe Thr Ser Pro Leu Ser Tyr His Phe Thr Glu Gly Trp Ser Lys Phe
  225      230      235      240
Phe Ser Thr Cys Ser Phe His Lys Ile Ala Ile Ser Leu Phe Phe Gly
      245      250      255
Leu Gly Ala Ser Leu Cys Leu Lys Leu Ser Ser Thr Gly Thr Ile Asn
      260      265      270
Glu Gly Lys Ile Ser Ser Val Phe His Ile Asp Val Val Pro Met Ile
      275      280      285
Asn Ser Ser Ile Tyr Ser Leu Arg Asn Asn Asp Val Lys Leu Ala Trp
      290      295      300
Arg Lys Ile Leu Ser Trp Arg Lys Phe Pro Phe Glu Thr Ile Ser Leu
  305      310      315      320
His Ala Tyr Ser Tyr Arg Thr Arg Arg Phe Cys
      325      330

```

<210> 1760

<211> 322

<212> PRT

<213> Unknown (H38g678 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1760

```

Met Ser Val Val Glu Ala Asn Asn Ile Ser Gly Pro Val Ser Glu Phe
  1      5      10      15
Ile Leu Leu Gly Phe Pro Cys Arg Cys Arg Glu Thr Lys Ile Leu Leu
      20      25      30
Phe Val Val Phe Ser Leu Ile Tyr Leu Leu Thr Leu Met Gly Asn Thr
      35      40      45
Ser Ile Ile Cys Ala Val Trp Ser Ser Gln Lys Leu His Thr Pro Met
      50      55      60
Tyr Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Cys Cys Ile Ser
  65      70      75      80

```

Ser Asp Val Pro Asn Met Leu Ala Asn Leu Ile Ser His Ile Lys Ser
 85 90 95
 Ile Ser Tyr Ala Gly Cys Leu Leu Gln Phe Phe Tyr Phe Ser Met Cys
 100 105 110
 Ala Ala Glu Gly Tyr Phe Leu Ser Val Met Ser Phe Asp Arg Phe Leu
 115 120 125
 Thr Ile Cys Arg Pro Leu His Tyr Pro Thr Val Met Thr His His Leu
 130 135 140
 Cys Val Xaa Leu Val Ala Phe Cys Arg Ala Gly Gly Phe Leu Ser Ile
 145 150 155 160
 Leu Met Pro Ala Val Leu Met Ser Arg Val Pro Phe Cys Gly Pro Asn
 165 170 175
 Ile Thr Asp His Phe Phe Cys Asn Leu Gly Pro Leu Leu Ala Leu Ser
 180 185 190
 Cys Ala Pro Val Pro Lys Thr Thr Leu Thr Cys Ala Thr Val Ser Ser
 195 200 205
 Leu Ile Ile Phe Ile Thr Phe Leu Tyr Ile Leu Gly Ser His Ile Leu
 210 215 220
 Val Leu Arg Ala Val Leu Trp Val Pro Ala Gly Ser Gly Arg Asn Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Ala Ser His Phe Leu Val Val Ser Phe Phe Tyr
 245 250 255
 Gly Ser Val Met Val Met Tyr Val Ser Pro Gly Ser Arg Ser Arg Pro
 260 265 270
 Gly Thr Gln Lys Phe Val Thr Leu Phe Tyr Cys Thr Ala Thr Pro Phe
 275 280 285
 Phe Asn Pro Leu Thr Tyr Ser Leu Trp Asn Lys Asp Met Thr Asp Ala
 290 295 300
 Leu Lys Lys Val Leu Gly Val Pro Ser Lys Glu Ile Tyr Trp Asn Thr
 305 310 315 320
 Leu Lys

<210> 1761

<211> 335

<212> PRT

<213> Unknown (H38g679 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1761

Met Glu Glu Ala Ile Leu Leu Asn Gln Thr Ser Leu Val Thr Tyr Phe
 1 5 10 15
 Arg Leu Arg Gly Leu Ser Val Asn His Lys Ala Arg Ile Ala Met Phe
 20 25 30
 Ser Met Phe Leu Ile Phe Tyr Val Leu Thr Leu Ile Gly Asn Val Leu
 35 40 45
 Ile Val Ile Thr Ile Ile Tyr Asp His Arg Leu His Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Ser Asn Leu Ser Phe Ile Asp Val Cys His Ser Thr Val
 65 70 75 80
 Thr Val Pro Lys Met Leu Arg Asp Val Trp Ser Glu Glu Lys Leu Ile
 85 90 95
 Ser Ph Asp Ala Cys Val Thr Gln Met Phe Phe Leu His Leu Phe Ala
 100 105 110
 Cys Thr Glu Ile Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val

115	120	125
Ala Ile Cys Lys Pro Leu Gln Tyr Met Ile Val Met Asn Trp Lys Val		
130	135	140
Cys Val Leu Leu Ala Val Ala Leu Trp Thr Gly Gly Thr Ile His Ser		
145	150	155
Ile Ala Leu Thr Ser Leu Thr Ile Lys Leu Pro Tyr Cys Gly Pro Asp		
165	170	175
Glu Ile Asp Asn Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala		
180	185	190
Cys Ile Asp Thr Pro Tyr Val Leu Glu Ile Leu Ile Val Ser Asn Ser		
195	200	205
Gly Leu Ile Ser Val Val Cys Phe Val Val Leu Val Val Ser Tyr Ala		
210	215	220
Val Ile Leu Val Ser Leu Arg Gln Gln Ile Ser Lys Gly Lys Trp Lys		
225	230	235
Ala Leu Ser Thr Cys Ala Ala His Leu Thr Val Val Thr Leu Phe Leu		
245	250	255
Gly His Cys Ile Phe Ile Tyr Ser Arg Pro Ser Thr Ser Leu Pro Glu		
260	265	270
Asp Lys Ala Val Ser Val Phe Phe Thr Ala Val Thr Pro Leu Leu Asn		
275	280	285
Pro Ile Ile Tyr Thr Leu Arg Asn Glu Glu Met Lys Ser Ala Leu Asn		
290	295	300
Lys Leu Val Gly Arg Lys Glu Arg Lys Glu Glu Lys Xaa Lys Cys Pro		
305	310	315
Thr Ser Leu Gly Tyr Val Val Leu Gln Ile Lys Glu Ala Pro Cys		
325	330	335

<210> 1762

<211> 161

<212> PRT

<213> Unknown (H38g680 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(161)

<223> Xaa = Any Amino Acid

<400> 1762

Thr Gly Thr Gly Xaa Trp Leu Cys His Ala Met Ile Leu Thr Pro Leu		
1	5	10
Thr Phe Gln Leu Pro Tyr Cys Gly Leu Thr Arg Trp Asp Tyr Tyr Phe		
20	25	30
Cys Asp Ile Pro Ala Val Leu Pro Leu Ala Cys Lys Asp Thr Ser Leu		
35	40	45
Ala Gln Arg Val Gly Phe Thr Asn Val Gly Leu Leu Ser Leu Ile Cys		
50	55	60
Phe Phe Leu Ile Leu Val Ser Tyr Thr Cys Ile Gly Ile Ser Ile Ser		
65	70	75
Lys Ile Arg Ser Ala Glu Gly Arg Gln Arg Ala Phe Ser Thr Cys Ser		
85	90	95
Ala His Leu Thr Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Val Ile		
100	105	110
Tyr Leu Gln Pro Asn Pro Ser Ala Leu Leu Gly Ser Ile Ile Gln Ile		
115	120	125
Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu		
130	135	140
Arg Asn Lys Asp Val Lys Ser Asp Gln Pro Xaa Gly Met Tyr Phe Pro		
145	150	155
		160

Arg

<210> 1763
 <211> 134
 <212> PRT
 <213> Unknown (H38g681 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(134)
 <223> Xaa = Any Amino Acid

<400> 1763
 Leu Leu Phe Leu Met Phe Phe Ile Thr Ser Leu Gly His Lys Phe His
 1 5 10 15
 Leu Ile Ser Phe Pro Phe Ser Gln Gln Thr Thr Xaa Gln Lys Tyr Phe
 20 25 30
 Ile Ile Phe Glu Val Xaa Leu Cys Xaa Xaa His Thr Leu Thr Ala Leu
 35 40 45
 Ile Tyr Cys Xaa Met Ser Leu Phe Xaa Gly Ile Asp Leu Phe Val Gly
 50 55 60
 Tyr Asn Pro Cys Ser Pro Arg Val Leu Phe Leu Phe Leu Gly Arg Gly
 65 70 75 80
 Pro Ser Gly Phe Ser Leu Glu Ser Leu Ser Phe Tyr Arg Thr Ser Phe
 85 90 95
 Thr Trp Gln His Leu His Leu Lys Phe Tyr Cys Pro Ser Xaa Gly Xaa
 100 105 110
 Leu Leu Lys Ser Phe Leu Ser Ala Ile Trp Leu Leu Phe Ser Thr Tyr
 115 120 125
 Phe Leu Arg Val Leu Ser
 130

<210> 1764
 <211> 311
 <212> PRT
 <213> Unknown (H38g682 protein)

<220>
 <223> Synthetic construct

<400> 1764
 Met Ala Thr Ser Asn His Ser Ser Gly Ala Glu Phe Ile Leu Ala Gly
 1 5 10 15
 Leu Thr Gln Arg Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30
 Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Phe Leu
 35 40 45
 Ile Ala Leu Ser Ser Gln Leu Tyr Pro Pro Val Tyr Tyr Phe Leu Ser
 50 55 60
 His Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Val Pro Glu Glu Asn Ile Ile Ser Phe Leu Glu
 85 90 95
 Cys Ile Thr Gln Leu Tyr Phe Phe Leu Ile Phe Val Ile Ala Glu Gly
 100 105 110
 Tyr Leu Leu Thr Ala Met Glu Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu Leu Tyr Asn Ile Val Met Ser His Arg Val Cys Ser Ile Met

130	135	140
Met Ala Val Val Tyr Ser Leu Gly Phe Leu Trp Ala Thr Val His Thr		
145	150	155
Thr Arg Met Ser Val Leu Ser Phe Cys Arg Ser His Thr Val Ser His		160
	165	170
Tyr Phe Cys Asp Ile Leu Pro Leu Leu Thr Leu Ser Cys Ser Ser Thr		175
	180	185
His Ile Asn Glu Ile Leu Leu Phe Ile Ile Gly Gly Val Asn Thr Leu		190
	195	200
Ala Thr Thr Leu Ala Val Leu Ile Ser Tyr Ala Phe Ile Phe Ser Ser		205
	210	215
Ile Leu Gly Ile His Ser Thr Glu Gly Gln Ser Lys Ala Phe Gly Thr		220
225	230	235
Cys Ser Ser His Leu Leu Ala Val Gly Ile Phe Phe Gly Ser Ile Thr		240
	245	250
Phe Met Tyr Phe Lys Pro Pro Ser Ser Thr Thr Met Glu Lys Glu Lys		255
	260	265
Val Ser Ser Val Phe Tyr Ile Thr Ile Ile Pro Met Leu Asn Pro Leu		270
	275	280
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asn Ala Leu Lys Lys Met		285
	290	295
Thr Arg Gly Arg Gln Ser Ser		300
305	310	

<210> 1765

<211> 316

<212> PRT

<213> Unknown (H38g683 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1765

Met Val Ile Leu Ser Trp Glu Asn Gln Thr Met Arg Val Glu Phe Val	
1	5
Leu Gln Gly Phe Ser Ser Ile Arg Gln Leu Asn Ile Phe Leu Phe Met	10
	20
Ile Ile Leu Val Phe Tyr Ile Leu Thr Val Ser Gly Asn Ile Leu Ile	25
	30
Val Leu Leu Val Leu Val Arg His His Leu His Thr Pro Met Tyr Phe	35
	40
Leu Leu Val Asn Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Asn Ile	45
65	50
Ile Pro Lys Met Leu Leu Ile Ile Ile Ala Glu Xaa Lys Thr Ile Ser	55
	60
Val Ala Gly Trp Leu Ala Gln Phe Tyr Phe Phe Gly Ser Leu Ala Ala	65
	70
Thr Glu Cys Leu Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala	75
	80
Ile Cys Gln Pro Leu Cys Tyr Arg Val Leu Met Thr Gly Pro Leu Cys	85
	90
Ile Arg Leu Ala Ala Gly Ser Trp Phe Cys Cys Phe Leu Leu Thr Ala	95
145	100
Ile Thr Met Val Leu Cys Arg Leu Thr Phe Cys Gly Pro Tyr Glu	105
	110
Thr Asp His Phe Phe Cys Asp Phe Thr Pro Leu Val His Leu Ser Cys	115
	120
	125
	130
	135
	140
	145
	150
	155
	160
	165
	170
	175
	180
	185
	190

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Met Asp Thr Ser Val Thr Glu Thr Ile Ala Phe Ala Thr Ser Ser Ala
    195          200          205
Val Thr Leu Ile Pro Phe Leu Leu Ile Val Ala Ser Tyr Ser Cys Val
    210          215          220
Leu Ser Ala Ile Leu Arg Ile Pro Ser Cys Thr Gly Gln Lys Lys Ala
    225          230          235          240
Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Val Phe Tyr Gly
    245          250          255
Thr Leu Ile Ala Thr Tyr Leu Val Pro Ser Ala Asn Ser Ser Gln Leu
    260          265          270
Leu Cys Lys Gly Ser Ser Leu Leu Tyr Ile Ile Leu Thr Pro Met Phe
    275          280          285
Asn Pro Ile Ile Tyr Ser Leu Arg Asn Arg Asp Ile His Glu Ala Leu
    290          295          300
Lys Lys Cys Leu Arg Lys Lys Ser Gly Val Cys Leu
    305          310          315

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<210> 1766

<211> 315

<212> PRT

<213> Unknown (H38g684 protein)

<220>

<223> Synthetic construct

<400> 1766

```

Pro Val Arg Thr Leu Glu Thr Thr Asn Ile Thr Gly Phe Val Asn Glu
    1          5          10          15
Phe Ile Leu Leu Gly Phe Pro Cys Arg Trp Glu Ile Gln Ile Leu Leu
    20          25          30
Phe Val Val Phe Ser Leu Ile Tyr Leu Leu Thr Leu Leu Gly Asn Thr
    35          40          45
Ser Ile Ile Cys Ala Val Trp Ser Ser Gln Lys Leu His Thr Pro Met
    50          55          60
Tyr Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Cys Cys Val Ser
    65          70          75          80
Ser Asp Val Pro Ile Met Ala Ala Asn Leu Ile Ser Gln Thr Gln Ser
    85          90          95
Ile Ser Cys Ala Gly Cys Leu Leu Arg Phe Tyr Phe Phe Ser Met Cys
    100          105          110
Ala Ala Glu Cys Leu Phe Leu Ser Val Met Ser Phe Asp Arg Phe Pro
    115          120          125
Ala Ile Cys Arg Pro Leu His Tyr Pro Thr Leu Met Thr His His Val
    130          135          140
Cys Ala His Phe Val Ile Phe Cys Trp Val Gly Gly Cys Leu Trp Leu
    145          150          155          160
Leu Thr Pro Leu Thr Leu Ile Ser Gln Val Leu Phe Cys Gly Pro Asn
    165          170          175
Thr Ile Asp His Phe Phe Cys Asp Leu Ala Pro Leu Leu Ala Leu Ser
    180          185          190
Cys Ala Pro Ile Pro Gly Ile Thr Leu Thr Cys Gly Ile Ile Ser Ala
    195          200          205
Leu Ile Ile Phe Leu Thr Phe Leu Tyr Ile Leu Gly Thr Tyr Phe Cys
    210          215          220
Val Leu Ser Thr Val Leu Gln Val Pro Ser Gly Leu Gly Arg His Lys
    225          230          235          240
Ala Phe Ser Thr Cys Gly Cys His Leu Ala Val Val Ser Leu Phe Tyr
    245          250          255
Gly Ser Leu Met Val Met Tyr Val Ser Pro Gly Ser Gly Asp Tyr His
    260          265          270
Gly Ile Lys Lys Phe Ala Thr Leu Phe Tyr Thr Leu Ser Thr Pro Phe

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275	280	285
Phe Asn Pro Leu Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Glu Ala		
290	295	300
Leu Lys Lys Phe Leu Arg Asn Arg His Thr Val		
305	310	315

<210> 1767

<211> 316

<212> PRT

<213> Unknown (H38g685 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1767

Leu Ile Ala Thr Gly Asn Trp Thr Arg Ile Ser Lys Phe Ile Leu Met		
1	5	10
Ser Phe Ser Ser Leu Pro Thr Glu Ile Gln Ser Leu Leu Phe Leu Thr		
20	25	30
Phe Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Cys Leu Ile Ile		
35	40	45
Leu Val Thr Leu Ala Asp Pro Met Leu His Ser Pro Met Tyr Phe Phe		
50	55	60
Leu Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Ala		
65	70	75
Pro Asn Met Leu Trp Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe		
85	90	95
Leu Gly Cys Ala Thr Xaa Met Tyr Phe Val Phe Phe Phe Gly Val Ala		
100	105	110
Glu Cys Leu Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile		
115	120	125
Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg Thr Leu Ala		
130	135	140
Lys Leu Ala Ala Thr Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val		
145	150	155
Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val		
165	170	175
Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu Val Cys Ala		
180	185	190
Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val		
195	200	205
Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr His Ile Ala		
210	215	220
Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe		
225	230	235
Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser		
245	250	255
Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly		
260	265	270
Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn		
275	280	285
Pro Ile Ile Tyr Ser Leu Arg Asn Asn Glu Val Lys Asn Ala Leu Ser		
290	295	300
Arg Thr Val Ser Lys Ala Leu Gly Pro Gln Lys Leu		
305	310	315

<210> 1768

<211> 324
 <212> PRT
 <213> Unknown (H38g686 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 1768
 Met Ala Val Glu Asn Asp Ser Ser Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Gln Pro Glu Ile Xaa Leu Pro Leu Phe Phe Leu Phe Leu
 20 25 30
 Val Asn Tyr Met Thr Thr Met Val Gly Asn Leu Ser Leu Ile Asn Leu
 35 40 45
 Ile Cys Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Phe Val Phe Thr Pro Lys
 65 70 75 80
 Met Leu Met Ser Phe Ile Ser Glu Arg Asn Ile Ile Ser Phe Pro Gly
 85 90 95
 Cys Val Thr Gln Leu Phe Phe Phe Cys Phe Phe Val His Ser Glu Cys
 100 105 110
 Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu Leu Tyr Met Val Thr Thr Ser Pro Gln Ile Cys Ser Leu Leu
 130 135 140
 Met Leu Gly Ser Tyr Val Met Gly Phe Ala Gly Ala Met Val His Thr
 145 150 155 160
 Glu Cys Met Met Lys Leu Ile Phe Cys Asp Ser Asn Val Ile Asn His
 165 170 175
 Tyr Met Cys Asp Ile Phe Pro Leu Leu Gln Leu Ser Cys Ser Ser Thr
 180 185 190
 Xaa Ala Asn Glu Leu Val Met Ser Val Ile Val Gly Thr Val Val Ile
 195 200 205
 Val Ser Ser Leu Ile Ile Leu Ile Ser Tyr Ala Leu Ile Leu Phe Asn
 210 215 220
 Ile Leu His Met Ser Ser Ala Glu Gly Trp Phe Lys Ala Ile Gly Thr
 225 230 235 240
 Cys Gly Ser His Ile Ile Thr Val Gly Leu Phe Tyr Glu Phe Gly Leu
 245 250 255
 Ile Thr His Val Lys Leu Ser Ser Asp Trp Tyr Met Gly Gln Gly Lys
 260 265 270
 Phe Leu Ser Val Phe Tyr Thr Asn Glu Val Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Lys Glu Thr
 290 295 300
 Leu Asn Lys Ile Thr Asn Xaa Val Glu Pro Met Val Leu Pro Xaa Pro
 305 310 315 320
 Leu Ser Asn Cys

<210> 1769
 <211> 331
 <212> PRT
 <213> Unknown (H38g687 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1769

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Met Arg Xaa Ile Asn Gln Thr Gln Val Ile Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Asp Gly Pro His Thr Glu Gln Leu Leu Phe Ile Val Leu Leu
 20           25           30
Gly Val Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Leu Ile Ser Leu
 35           40           45
Val His Val Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50           55           60
Asn Leu Ser Leu Ala Asp Leu Tyr Phe Ser Thr Asn Ile Leu Pro Gln
 65           70           75           80
Ala Leu Val His Leu Leu Ser Ile Asn Asn Leu Ile Ala Phe Thr Leu
 85           90           95
Ser Leu Thr Gln Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys
100          105          110
Ala Leu Ile Ala Val Met Ser Tyr Asn Pro Tyr Val Ala Ile Cys Asn
115          120          125
Pro Leu His Tyr Pro Asn Ile Met Thr Trp Lys Val Cys Val Gln Leu
130          135          140
Ala Thr Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr
145          150          155          160
Thr Phe Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His
165          170          175
Phe Phe Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr
180          185          190
His Ala Ser Glu Met Ala Ile Tyr Leu Thr Gly Val Val Ile Leu Leu
195          200          205
Ile Pro Val Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr
210          215          220
Val Val Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Met Val Val Ile Leu Leu Asn Gly Ser Ala Ile
245          250          255
Leu Thr Cys Met Thr Pro Lys Ser Ser Lys Gln Gln Xaa Lys Ser Val
260          265          270
Ser Val Phe Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Leu Ile Tyr
275          280          285
Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Lys Val Ala Thr
290          295          300
Arg Asn Phe Pro Xaa Arg Leu Gly Ile His Thr Asp Ser Glu Leu Arg
305          310          315          320
Glu Pro Phe Gly Phe Leu Leu Pro Lys Thr Cys
325          330

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<210> 1770

<211> 183

<212> PRT

<213> Unknown (H38g688 protein)

<220>

<223> Synthetic construct

<400> 1770

```

Met Glu Lys Ser Asn Asn Ser Thr Leu Phe Ile Leu Leu Gly Phe Ser
 1           5           10           15

```

Gln Asn Lys Asn Ile Glu Val Leu Cys Phe Val Leu Phe Leu Phe Cys
 20 25 30
 Tyr Ile Ala Ile Trp Met Gly Asn Leu Leu Ile Met Ile Ser Ile Thr
 35 40 45
 Cys Thr Gln Leu Ile His Gln Pro Met Tyr Phe Phe Leu Asn Tyr Leu
 50 55 60
 Ser Leu Ser Asp Leu Cys Tyr Thr Ser Thr Val Thr Pro Lys Leu Met
 65 70 75 80
 Val Asp Leu Leu Ala Glu Arg Lys Thr Ile Ser Tyr Asn Asn Cys Met
 85 90 95
 Ile Gln Leu Phe Thr Thr His Phe Phe Gly Gly Ile Glu Ile Phe Ile
 100 105 110
 Leu Thr Gly Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Ile Ile Met Ser Arg Gln Lys Cys Asn Thr Ile Ile Ile
 130 135 140
 Val Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu Leu
 145 150 155 160
 Thr Ile Ser Val Pro Phe Cys Gly Pro Asn Asp Ile Asp His Tyr Ser
 165 170 175
 Arg Asp Val Tyr Pro Leu Leu
 180

<210> 1771

<211> 224

<212> PRT

<213> Unknown (H38g689 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(224)

<223> Xaa = Any Amino Acid

<400> 1771

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ser Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Arg His Ala
 35 40 45
 Pro Glu Val Met Ala Tyr Asp Leu Phe Val Ala Ile Cys His Leu Leu
 50 55 60
 Tyr Arg Ser Ala Ile Leu Asn Pro Phe Val Arg Gly Phe Leu Asp Leu
 65 70 75 80
 Leu Ser Leu Leu Leu Val Phe Phe Phe Phe Leu Ile Ser Leu Leu Asp
 85 90 95
 Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp
 100 105 110
 Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu
 115 120 125
 Ala Cys Cys Asp Thr Phe Thr Arg Asn Asn Asn Met Tyr Phe Pro Ala
 130 135 140
 Ala Val Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Cys
 145 150 155 160
 Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr
 165 170 175
 Lys Pro Ser Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe
 180 185 190
 Tyr Gly Ala Gly Val Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Phe

195 200 205
 Pro Arg Lys Gly Ala Val Ala Ser Val Thr Tyr Tyr Thr Val Val Thr
 210 215 220

<210> 1772
 <211> 215
 <212> PRT
 <213> Unknown (H38g690 protein)

<220>
 <223> Synthetic construct

<400> 1772
 Met Asp Val Arg Leu Ile Cys Thr Thr Val Pro Lys Met Ala Phe Asn
 1 5 10 15
 Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly Cys Ala Thr Gln
 20 25 30
 Ile Phe Phe Cys Val Ser Leu Leu Gly Ser Glu Cys Phe Leu Leu Ala
 35 40 45
 Val Met Ser Tyr Asp Cys Tyr Ile Ala Ile Cys His Pro Leu Arg Tyr
 50 55 60
 Thr Asn Leu Met Arg Pro Lys Ile Cys Arg Leu Met Thr Ala Phe Ser
 65 70 75 80
 Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Tyr Ala Val Ala Thr Phe
 85 90 95
 Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys Glu
 100 105 110
 Leu Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr Ser Ile Phe Glu
 115 120 125
 Lys Val Ile Phe Ile Cys Ser Ile Val Met Leu Val Phe Pro Val Ala
 130 135 140
 Ile Ile Ile Ala Ser Tyr Ala Gly Val Ile Leu Ala Val Ile His Met
 145 150 155 160
 Gly Ser Gly Glu Gly Arg Arg Lys Ala Phe Thr Thr Cys Ser Ser His
 165 170 175
 Leu Met Val Val Gly Met Phe Tyr Gly Ala Gly Leu Phe Met Tyr Ile
 180 185 190
 Gln Pro Thr Ser Asp Arg Ser Pro Thr Gln Asp Lys Leu Val Ser Val
 195 200 205
 Phe Tyr Thr Ile Leu Thr Pro
 210 215

<210> 1773
 <211> 127
 <212> PRT
 <213> Unknown (H38g691 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(127)
 <223> Xaa = Any Amino Acid

<400> 1773
 Asn Leu Leu Pro Val Trp Thr Pro Gly Ser Arg Val Pro Ser Xaa Ser
 1 5 10 15
 Gln Ile Ser Val Ser Glu Lys Gln Gly Met Ser Phe Pro Lys Lys Leu
 20 25 30
 Phe Gln Asn His Lys Leu Phe Leu Leu Phe Ala Gly Met Asn Val Phe
 35 40 45

```

Leu Gln Thr Val Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro
 50          55          60
Leu His Tyr Arg Val Ile Met Asn Pro Gly Ile Phe Gly Leu Trp Val
65          70          75          80
Leu Val Ser Trp Ser Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Arg
      85          90          95
Met Val Leu Gln Leu Ser Phe Cys Thr Asn Leu Glu Ile Pro His Ile
      100          105          110
Phe Phe Cys Glu Leu Asn Gln Leu Ile Leu Leu Ala Cys Ser Asn
      115          120          125

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<210> 1774

<211> 216

<212> PRT

<213> Unknown (H38g692 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(216)

<223> Xaa = Any Amino Acid

<400> 1774

```

Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
 1          5          10          15
Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys Ile Met
      20          25          30
Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu
      35          40          45
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Leu
      50          55          60
Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
      65          70          75          80
Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa Phe Leu
      85          90          95
Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
      100          105          110
Glu His Ala Ala Val Val Ala Val Ser Trp Ser Asp Pro Cys Val Ser
      115          120          125
Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Gly Leu
      130          135          140
Val Ile Ile Leu Thr Pro Tyr Ala Phe Ile Phe Ile Thr Val Met Lys
      145          150          155          160
Thr Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser
      165          170          175
His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr
      180          185          190
Cys Val Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser
      195          200          205
Val Leu Tyr Thr Val Val Ile Pro
      210          215

```

<210> 1775

<211> 215

<212> PRT

<213> Unknown (H38g693 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(215)

<223> Xaa = Any Amino Acid

<400> 1775

```

Leu Pro Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Ile Val
 1           5           10           15
Asp Met Gln Ser His Ser Arg Ile Ile Ser His Ala Gly Cys Leu Thr
          20           25           30
Gln Ile Pro Phe Phe Val Leu Phe Val Cys Ile Asp Asp Met Leu Leu
          35           40           45
Thr Val Met Ala Tyr Asp Xaa Phe Val Ala Ile Cys His Pro Leu His
          50           55           60
Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu Val Leu Met
65           70           75           80
Ser Ile Phe Leu Ser Leu Leu Asp Ser Xaa Leu His Asn Ser Val Leu
          85           90           95
Leu Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser Asn Phe Phe Cys
          100          105          110
Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Phe Ile Ser Asn
          115          120          125
Ile Phe Ile Arg Leu Asp Ser Thr Ile Phe Gly Phe Leu Pro Ile Ser
          130          135          140
Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg Ile
145          150          155          160
Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His
          165          170          175
Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly Met Tyr Leu
          180          185          190
Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val Val Ala Ser Val
          195          200          205
Leu Tyr Ala Met Val Thr Pro
          210          215

```

<210> 1776

<211> 217

<212> PRT

<213> Unknown (H38g694 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(217)

<223> Xaa = Any Amino Acid

<400> 1776

```

Leu Pro Asp Ile Gly Phe Thr Pro Thr Thr Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly Cys Leu Thr Val
          20           25           30
Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Thr Leu Leu Leu
          35           40           45
Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys His Pro Leu Tyr
          50           55           60
His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu Leu
65           70           75           80
Ser Phe Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu His Asn Met Ile
          85           90           95
Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe
          100          105          110

```

```

Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr
    115                120                125
Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro
    130                135                140
Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Glu Ile Val Ser Ser Ile Leu
    145                150                155                160
Arg Val Ser Ser Xaa Gly Gly Lys Tyr Lys Ala Phe Ala Thr Cys Gly
    165                170                175
Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly Gly
    180                185                190
Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys Thr Ala Val Ala
    195                200                205
Ser Val Met Tyr Ala Val Val Thr Pro
    210                215

```

<210> 1777

<211> 230

<212> PRT

<213> Unknown (H38g695 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(230)

<223> Xaa = Any Amino Acid

<400> 1777

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Ala Lys Met Ile Val
 1          5          10          15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
    20          25          30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Ser Met Leu
    35          40          45
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
    50          55          60
Tyr Arg Ser Ala Ile Leu Ser Arg Asp Ser Val Pro Ser Xaa Ile Cys
    65          70          75          80
Cys Leu Cys Phe Val Leu Phe Cys Phe Val Leu Phe Cys Phe Val Phe
    85          90          95
Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met
    100         105         110
Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Leu Trp Glu Pro Ser
    115         120         125
Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn
    130         135         140
Met Tyr Phe Pro Ala Ala Val Phe Gly Phe Leu Pro Ile Ser Gly Pro
    145         150         155         160
Phe Leu Leu Gln Trp Ser Lys Ile Val Ser Ser Thr Leu Arg Val Ser
    165         170         175
Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu
    180         185         190
Ser Val Val Cys Xaa Phe Cys Gly Thr Gly Val Gly Gly Tyr Leu Gly
    195         200         205
Ser Asp Val Ser Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met
    210         215         220
Tyr Thr Val Val Thr Pro
    225         230

```

<210> 1778

<211> 313

<212> PRT

<213> Unknown (H38g696 protein)

<220>

<223> Synthetic construct

<400> 1778

```

Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly
 1           5           10           15
Leu Thr Asp Arg Pro Glu Phe Arg Gln Pro Leu Phe Phe Leu Phe Leu
      20           25           30
Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Thr Leu
      35           40           45
Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe
 50           55           60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
65           70           75           80
Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Asn Val Gly
      85           90           95
Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys
      100          105          110
Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115          120          125
Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu
      130          135          140
Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr
145           150          155          160
Gly Cys Met Leu Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His
      165          170          175
Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
      180          185          190
Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Thr Asn Ile Thr
      195          200          205
Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
      210          215          220
Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
225           230          235          240
Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
      245          250          255
Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val
      260          265          270
Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu
      290          295          300
Ile Lys Ile Gln Arg Arg Asn Ile Phe
305           310

```

<210> 1779

<211> 308

<212> PRT

<213> Unknown (H38g697 protein)

<220>

<223> Synthetic construct

<400> 1779

```

Met Thr Met Glu Asn Tyr Ser Met Ala Ala Gln Phe Val Leu Asp Gly
 1           5           10           15
Leu Thr Gln Gln Ala Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
      20           25           30

```

Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Gly Met Ile Leu Leu
 35 40 45
 Ile Ala Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Ser Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Leu Gly Lys Lys Asn Thr Ile Leu Tyr Ser Glu
 85 90 95
 Cys Met Val Gln Leu Phe Phe Phe Val Val Phe Val Val Ala Glu Gly
 100 105 110
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser
 115 120 125
 Pro Leu Leu Tyr Asn Ala Ile Met Ser Ser Trp Val Cys Ser Leu Leu
 130 135 140
 Val Leu Ala Ala Phe Phe Leu Gly Phe Leu Ser Ala Leu Thr His Thr
 145 150 155 160
 Ser Ala Met Met Lys Leu Ser Phe Cys Lys Ser His Ile Ile Asn His
 165 170 175
 Tyr Phe Cys Asp Val Leu Pro Leu Leu Asn Leu Ser Cys Ser Asn Thr
 180 185 190
 His Leu Asn Glu Leu Leu Leu Phe Ile Ile Ala Gly Phe Asn Thr Leu
 195 200 205
 Val Pro Thr Leu Ala Val Ala Val Ser Tyr Ala Phe Ile Leu Tyr Ser
 210 215 220
 Ile Leu His Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Ser Ser His Leu Met Ala Val Val Ile Phe Phe Gly Ser Ile Thr
 245 250 255
 Phe Met Tyr Phe Lys Pro Pro Ser Ser Asn Ser Leu Asp Gln Glu Lys
 260 265 270
 Val Ser Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Arg Lys Val
 290 295 300
 Leu Val Gly Lys
 305

<210> 1780

<211> 328

<212> PRT

<213> Unknown (H38g698 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1780

Met Ala Pro Gly Asn Gly Ser Phe Val Thr Glu Phe Ile Leu Ala Gly
 1 5 10 15
 Leu Thr His Gln Pro Asp Leu Gln Ser Pro Leu Phe Phe Leu Phe Leu
 20 25 30
 Val Ile Tyr Val Val Thr Leu Leu Gly Asn Leu Gly Leu Val Thr Leu
 35 40 45
 Ile Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
 65 70 75 80
 Met Leu Met Asn Phe Ile Ser Glu Lys Asn Ile Ile Ser Phe Lys Gly

<210> 1781
<211> 314
<212> PRT
<213> Unknown (H38a699 protein)

<220>
<223> Synthetic construct

<400>	1781																
Met	Lys	Pro	Gly	Asn	Glu	Thr	Gln	Ile	Ser	Gln	Phe	Leu	Leu	Leu	Gly		
1				5					10					15			
Leu	Ser	Glu	Glu	Pro	Glu	Leu	Gln	Pro	Phe	Leu	Phe	Gly	Leu	Phe	Leu		
		20						25					30				
Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala		
		35					40					45					
Thr	Ile	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser		
	50					55					60						
Asn	Leu	Ser	Phe	Ala	Asp	Ile	Cys	Phe	Val	Ser	Thr	Thr	Val	Pro	Lys		
65					70					75					80		
Met	Leu	Val	Asn	Ile	Gln	Thr	Gln	Ser	Arg	Val	Ile	Thr	Tyr	Ala	Asp		
			85						90					95			
Cys	Ile	Thr	Gln	Met	Cys	Phe	Phe	Ile	Leu	Phe	Val	Val	Leu	Asp	Ser		
			100					105					110				
Leu	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His		
		115					120					125					
Pro	Leu	His	Tyr	Thr	Val	Ile	Met	Asn	Ser	Trp	Leu	Cys	Gly	Leu	Leu		
		130				135					140						
Val	Leu	Val	Ser	Trp	Ile	Val	Ser	Ile	Leu	Tyr	Ser	Leu	Leu	Gln	Ser		
145					150					155					160		

Ile Met Ala Leu Gln Leu Ser Phe Cys Thr Glu Leu Lys Ile Pro His
 165 170 175
 Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr
 180 185 190
 Phe Ile Asn Asp Met Met Met Asn Phe Thr Ser Val Leu Leu Gly Gly
 195 200 205
 Gly Cys Leu Ala Gly Ile Leu Tyr Thr Tyr Phe Lys Ile Leu Cys Cys
 210 215 220
 Ile Cys Ser Ile Ser Ser Ala Gln Gly Met Asn Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Val
 245 250 255
 Gly Val Tyr Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Asn Ala
 260 265 270
 Ala Ala Ser Val Met Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Ile Asn Arg Ala Leu Asn Arg Phe
 290 295 300
 Phe Arg Glu Gln Lys Gln Glu Gly His Phe
 305 310

<210> 1782

<211> 324

<212> PRT

<213> Unknown (H38g700 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1782

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Ser Val Leu Ala Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Leu Asn Leu Val Thr Val Leu Arg Asn Leu Leu Ser
 35 40 45
 Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Leu Thr Ser Ala Thr
 65 70 75 80
 Val Pro Lys Val Ile Leu Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Val Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
 100 105 110
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Gly Cys Phe Val Ala
 115 120 125
 Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130 135 140
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Asn Leu Leu Asp Ser Gln
 145 150 155 160
 Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
 165 170 175
 Ile Ser Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys
 180 185 190
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile

210	215	220
Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala		
225	230	235
Phe Ser Thr Tyr Gly Ser His Leu Gly Val Val Cys Trp Phe Tyr Gly		240
	245	250
Thr Val Ile Gly Met Tyr Leu Ala Ser Ala Val Ser Pro Pro Pro Arg		255
	260	265
Asn Gly Val Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu		270
	275	280
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu		285
	290	295
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser		300
305	310	315
Phe Phe Leu Cys		320

<210> 1783

<211> 339

<212> PRT

<213> Unknown (H38g701 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400> 1783

Pro Ile Glu Gln Gly Asn Tyr Thr Arg Val Lys Glu Phe Phe Phe Gln		
1	5	10
Gly Leu Thr Gln Ser Gln Glu Leu Ser Leu Val Leu Phe Leu Phe Leu		15
	20	25
Phe Phe Val Tyr Ser Ala Thr Val Leu Gly Asn Leu Leu Ile Met Val		30
	35	40
Val Val Thr Cys Glu Ser Arg Leu His Thr Pro Thr Tyr Phe Leu Leu		45
	50	55
Cys Asn Leu Ser Val Leu Val Ile Cys Phe Ser Ser Ile Thr Ala Arg		60
65	70	75
Lys Val Leu Ile Asp Leu Ser Ser Arg Lys Thr Ile Ser Phe Asn Gly		80
	85	90
Cys Met Thr Gln Met Phe Phe Phe His Leu Leu Gly Gly Thr Asp Val		95
	100	105
Phe Ser Leu Phe Val Met Ala Phe Asp Gln Tyr Met Ala Ile Phe Lys		110
	115	120
Pro Leu His Cys Val Thr Ile Val Ser Arg Gly Gln Cys Ile Pro Tyr		125
	130	135
Ile Val Ser Arg Gly Arg Glu Xaa Gly Ala Gly Leu Ile Met Ala Ser		140
145	150	155
Trp Val Gly Gly Phe Val His Ser Ile Val Gln Val Phe Leu Leu Leu		160
	165	170
Pro Leu Pro Phe Cys Gly His His Met Ile Asp Gly Phe Tyr Cys Asp		175
	180	185
Val Pro Gln Val Leu Lys Leu Ala Cys Thr His Thr Phe Ala Leu Glu		190
	195	200
Val Leu Met Ile Ser Asn Asn Gly Leu Ile Ser Met Leu Trp Phe Ile		205
	210	215
Phe Leu Leu Ile Ser Tyr Thr Val Ile Leu Met Met Leu Arg Ser His		220
225	230	235
Thr Glu Glu Gly Arg Arg Lys Ala Ile Ala Thr Cys Thr Ser His Ile		240
	245	250
		255

Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr Val His Ala Gln
 260 265 270
 Pro Phe Thr Ala Leu Pro Thr Asp Arg Ala Val Ser Ile Thr Phe Thr
 275 280 285
 Val Ile Ile Pro Val Leu Asn Pro Met Ile Tyr Thr Leu Arg Asn Gln
 290 295 300
 Glu Met Lys Ser Ala Leu Arg Arg Arg Lys Lys Arg Pro Ser Gly Lys
 305 310 315 320
 Gly Xaa Met Leu Arg Ser Pro Asp Trp Lys Ile Arg Thr Glu Lys Tyr
 325 330 335
 Phe Phe Ile

<210> 1784

<211> 335

<212> PRT

<213> Unknown (H38g702 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1784

Ser Thr Tyr Pro Gln Asn Leu Thr Asp Val Ser Leu Phe Leu Leu Leu
 1 5 10 15
 Gly Ser Ser Glu Asp Pro Glu Gln Gln Pro Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Ser Met Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Ile Xaa Ser His Ser Arg Leu Ile Ser Xaa Ala
 85 90 95
 Gly Cys Leu Thr Pro Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100 105 110
 Glu Asn Met Leu Leu Ser Val Ile Ala Tyr Asp Pro Phe Val Ala Ile
 115 120 125
 Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
 130 135 140
 Phe Leu Val Leu Leu Ser Phe Phe Ser Gln Ser Leu Leu Asp Ala Gln
 145 150 155 160
 Val His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
 165 170 175
 Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys
 180 185 190
 Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Ser Pro Ala Ala Ile
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
 210 215 220
 Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
 225 230 235 240
 Cys Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
 245 250 255
 Thr Gly Phe Trp Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Gly
 260 265 270
 Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Pro

275	280	285
Asn Pro Phe Ile Tyr Ser	Leu Arg Asn Arg Asp Ile	Lys Ser Val Leu
290	295	300
Arg Arg Pro His Gly Ser Thr Val	Xaa Cys Gln Tyr Leu Leu Ile	Cys
305	310	315
Ser Met Pro Phe Val Val Trp Val	Lys Lys Gly Ser Lys Val	Lys
325	330	335

<210> 1785

<211> 315

<212> PRT

<213> Unknown (H38g703 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1785

Met Lys Asn Cys Thr Arg Val Lys Glu Phe Ile Phe Leu Gly Leu Thr	
1 5 10 15	
Gln Asn Gly Asp Thr Arg Leu Val Leu Phe Leu Phe Leu Leu Val	
20 25 30	
Tyr Met Thr Thr Leu Leu Gly Asn Leu Leu Ile Met Val Thr Val Thr	
35 40 45	
Cys Glu Ser Cys Leu His Met Pro Met Tyr Phe Leu Leu His Asn Leu	
50 55 60	
Ser Ile Ala Asp Ile Cys Phe Tyr Ser Ile Thr Glu Pro Lys Val Leu	
65 70 75 80	
Val Asp Leu Leu Ser Glu Arg Lys Thr Ile Ser Phe Asn Gly Cys Phe	
85 90 95	
Thr Gln Met Phe Leu Phe His Leu Ile Gly Gly Val Asp Ala Phe Ser	
100 105 110	
Leu Ser Val Met Ala Leu Asp Gln Tyr Val Ala Ile Ser Lys Ser Leu	
115 120 125	
His Tyr Ala Thr Ile Met Ser Arg Asp Arg Cys Ile Gly Leu Thr Val	
130 135 140	
Ala Ala Trp Leu Gly Gly Phe Val His Ser Ile Val Gln Ile Thr Leu	
145 150 155 160	
Leu Leu Pro Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Thr Phe Tyr	
165 170 175	
Cys Asp Val Pro Gln Val Leu Lys Leu Ala His Thr Asp Ile Phe Ile	
180 185 190	
Leu Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Leu Thr Thr Leu Trp	
195 200 205	
Phe Phe Leu Leu Leu Val Ser Tyr Met Val Ile Leu Ser Leu Leu Lys	
210 215 220	
Ser Gln Ala Gly Xaa Gly Arg Arg Lys Val Ile Ser Thr Cys Thr Ser	
225 230 235 240	
His Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr Val Tyr	
245 250 255	
Ala Arg Pro Phe Thr Ala Leu Pro Thr Asp Lys Ala Ile Ser Val Thr	
260 265 270	
Phe Thr Val Ile Ser Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg	
275 280 285	
Asn His Glu Met Lys Ser Thr Met Lys Arg Arg Arg Leu Xaa Pro Ser	
290 295 300	
Asp Arg Lys Xaa Thr Ser Ala Ser Leu Leu Leu	
305 310 315	

<210> 1786
 <211> 321
 <212> PRT
 <213> Unknown (H38g704 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(321)
 <223> Xaa = Any Amino Acid

<400> 1786
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Lys Val Leu Leu Gly
 1 5 10 15
 Ser Leu Xaa Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Val Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Ser Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
 65 70 75 80
 Lys Met Thr Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Val
 85 90 95
 Ser Cys Leu Thr Gln Ile Ser Phe Leu Val Leu Phe Ala Cys Met Glu
 100 105 110
 Asp Met Leu Thr Val Met Ala Tyr Asp Arg Val Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Arg Val Phe Leu
 130 135 140
 Val Leu Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser
 145 150 155 160
 Trp Ile Val Leu Gln Phe Thr Leu Phe Lys Asn Val Glu Asn Ser Ser
 165 170 175
 Phe Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180 185 190
 Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser
 210 215 220
 Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Tyr Gly Ser Gln Leu Ala Ala Leu Cys Xaa Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Met Tyr Leu Thr Ser Ala Val Ala Leu Pro Pro Arg Asn Gly Val
 260 265 270
 Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu Asn Phe Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu
 290 295 300
 Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu
 305 310 315 320
 Cys

<210> 1787
 <211> 318
 <212> PRT
 <213> Unknown (H38g705 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1787

```

Lys Gln Gln Glu Asn Gly Thr Cys Leu Val Thr Glu Phe Leu Met Met
 1          5          10          15
Gly Phe Ser Asn Leu Pro His Leu Arg Asn Thr Leu Phe Thr Leu Phe
          20          25          30
Phe Leu Thr Tyr Leu Val Thr Leu Gly Gly Asn Val Thr Ile Ile Thr
          35          40          45
Ile Thr His Ala Asp Arg Ser Arg His Thr Pro Met Tyr His Phe Leu
          50          55          60
Val Val Leu Ser Leu Ser Glu Thr Val Leu Tyr Thr Leu Val Thr Ile
65          70          75          80
Pro Ser Met Leu Ala His Leu Leu Met Glu Thr Arg Pro Ile Ser Ile
          85          90          95
Pro Gly Cys Gln Ala Gln Met Phe Phe Phe Leu Gly Leu Gly Cys Ser
          100          105          110
His Cys Phe Leu Leu Thr Leu Met Gly Tyr Asp Arg Tyr Val Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ser Met Val Met Arg Pro Thr Val Cys Leu
          130          135          140
Cys Leu Gly Ala Leu Val Phe Cys Ser Gly Phe Ser Val Ala Leu Ile
          145          150          155          160
Glu Thr Ser Met Ile Phe Ser Ser Pro Phe Cys Gly Gly Asp His Val
          165          170          175
Glu His Phe Phe Cys Asp Ile Ala Pro Val Leu Lys Leu Ser Cys Ala
          180          185          190
Lys Ser Ala Ser Lys Ala Leu Gly Ile Phe Phe Leu Ser Val Leu Val
          195          200          205
Val Leu Met Ser Phe Val Pro Ile Leu Phe Ser Tyr Ala Phe Ile Val
          210          215          220
Ala Ala Ile Val Arg Ile Ser Leu Ala Ala Gly Arg Arg Lys Ala Phe
          225          230          235          240
Ser Thr Cys Val Ala His Val Thr Val Val Val His Phe Asp Cys
          245          250          255
Ala Ser Ile Ile Tyr Leu Arg Pro Glu Ser Gly Ala Asn Pro Asp Gln
          260          265          270
Asp Arg Leu Val Ala Val Phe Tyr Thr Val Val Met Pro Leu Leu Asn
          275          280          285
Pro Val Val Cys Thr Leu Trp Asn Lys Glu Val Arg Val Ala Leu Arg
          290          295          300
Arg Thr Leu Ala Trp Ser Arg Gly Val Phe Lys Xaa Glu Ser
          305          310          315

```

<210> 1788

<211> 112

<212> PRT

<213> Unknown (H38g706 protein)

<220>

<223> Synthetic construct

<400> 1788

```

Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala Leu Leu Lys Leu Ala
 1          5          10          15

```

Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln Met Phe Ala Ala Arg
 20 25 30
 Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala Ser Tyr Gly
 35 40 45
 Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly Gly Arg Arg
 50 55 60
 Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val Cys Leu Phe
 65 70 75 80
 Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln Arg Tyr Asn
 85 90 95
 Gln His Gly Asn Arg Phe Val Ser Leu Phe Tyr Thr Val Val Thr Pro
 100 105 110

<210> 1789

<211> 313

<212> PRT

<213> Unknown (H38g707 protein)

<220>

<223> Synthetic construct

<400> 1789

Met Asp Gln Arg Asn Tyr Thr Arg Val Lys Glu Phe Thr Phe Leu Gly
 1 5 10 15
 Ile Thr Gln Ser Arg Glu Leu Ser Gln Val Leu Phe Thr Phe Leu Phe
 20 25 30
 Leu Val Tyr Met Thr Thr Leu Met Gly Asn Phe Leu Ile Met Val Thr
 35 40 45
 Val Thr Cys Glu Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50 55 60
 Asn Leu Ser Ile Leu Asp Ile Cys Phe Ser Ser Ile Thr Ala Pro Lys
 65 70 75 80
 Val Leu Ile Asp Leu Leu Ser Glu Thr Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Val Thr Gln Met Phe Phe Phe His Leu Leu Gly Gly Ala Asp Val
 100 105 110
 Phe Ser Leu Ser Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Ser Lys
 115 120 125
 Pro Leu His Tyr Met Thr Ile Met Ser Arg Gly Arg Cys Thr Gly Leu
 130 135 140
 Ile Val Gly Phe Leu Gly Gly Gly Leu Val His Ser Ile Ala Gln Ile
 145 150 155 160
 Ser Leu Leu Leu Pro Leu Pro Val Cys Gly Pro Asn Val Leu Asp Thr
 165 170 175
 Phe Tyr Cys Asp Val Pro Gln Val Leu Lys Leu Ala Cys Thr Asp Thr
 180 185 190
 Phe Thr Leu Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Val Ser Trp
 195 200 205
 Phe Val Phe Phe Phe Leu Leu Ile Ser Tyr Thr Val Ile Leu Met Met
 210 215 220
 Leu Arg Ser His Thr Gly Glu Gly Arg Arg Lys Ala Ile Ser Thr Cys
 225 230 235 240
 Thr Ser His Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr
 245 250 255
 Val Tyr Ala Arg Pro Phe Thr Ala Leu Pro Thr Asp Thr Ala Ile Ser
 260 265 270
 Val Thr Phe Thr Val Ile Ser Pro Leu Leu Asn Pro Ile Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Glu Met Lys Leu Ala Met Arg Lys Leu Lys Arg Arg
 290 295 300
 Leu Gly Gln Ser Glu Arg Ile Leu Ile

305

310

<210> 1790

<211> 162

<212> PRT

<213> Unknown (H38g708 protein)

<220>

<223> Synthetic construct

<400> 1790

```

Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
 1           5           10           15
Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
 20           25           30
Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
 35           40           45
Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
 50           55           60
Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Ile Phe Ile Phe Gly
 65           70           75           80
Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Thr
 85           90           95
Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
 100          105          110
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
 115          120          125
Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
 130          135          140
Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
 145          150          155          160
Leu Leu

```

<210> 1791

<211> 258

<212> PRT

<213> Unknown (H38g709 protein)

<220>

<223> Synthetic construct

<400> 1791

```

Met Tyr Tyr Phe Leu Cys His Leu Ala Leu Val Asp Ala Gly Phe Thr
 1           5           10           15
Thr Ser Val Val Pro Pro Leu Leu Ala Asn Leu Arg Gly Pro Ala Leu
 20           25           30
Trp Leu Pro Arg Ser His Cys Thr Ala Gln Leu Cys Ala Ser Leu Ala
 35           40           45
Leu Gly Ser Ala Glu Cys Val Leu Leu Ala Val Met Ala Leu Asp Arg
 50           55           60
Ala Ala Ala Val Cys Arg Pro Leu Arg Tyr Ala Gly Leu Val Ser Pro
 65           70           75           80
Arg Leu Cys Arg Thr Leu Ala Ser Ala Ser Trp Leu Ser Gly Leu Thr
 85           90           95
Asn Ser Val Ala Gln Thr Ala Leu Leu Ala Glu Arg Pro Leu Cys Ala
 100          105          110
Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala Leu Leu Lys
 115          120          125
Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln Met Phe Ala
 130          135          140

```

Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala Ser
 145 150 155 160
 Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly Gly
 165 170 175
 Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val Cys
 180 185 190
 Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln Arg
 195 200 205
 Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr Thr Val Val
 210 215 220
 Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Lys Val
 225 230 235 240
 Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser Leu Gly Arg Gly Gln Ala
 245 250 255
 Gly Gln

<210> 1792

<211> 316

<212> PRT

<213> Unknown (H38g710 protein)

<220>

<223> Synthetic construct

<400> 1792

Met Gln Arg Ala Asn His Ser Thr Val Thr Gln Phe Ile Leu Val Gly
 1 5 10 15
 Phe Ser Val Phe Pro His Leu Gln Leu Met Leu Phe Leu Leu Phe Leu
 20 25 30
 Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala Thr
 35 40 45
 Val Trp Ser Glu Arg Ser Leu His Thr Pro Met Tyr Leu Phe Leu Cys
 50 55 60
 Ala Leu Ser Val Ser Glu Ile Leu Tyr Thr Val Ala Ile Ile Pro Arg
 65 70 75 80
 Met Leu Ala Asp Leu Leu Ser Thr Gln Arg Ser Ile Ala Phe Leu Ala
 85 90 95
 Cys Ala Ser Gln Met Phe Phe Ser Phe Ser Phe Gly Phe Thr His Ser
 100 105 110
 Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Gly Cys Ala Cys Leu
 130 135 140
 Val Gly Cys Ser Trp Ala Gly Gly Leu Val Met Gly Met Val Val Thr
 145 150 155 160
 Ser Ala Ile Phe His Leu Ala Phe Cys Gly His Lys Glu Ile His His
 165 170 175
 Phe Ala Cys His Val Pro Pro Leu Leu Lys Leu Ala Cys Gly Asp Asp
 180 185 190
 Val Leu Val Val Ala Lys Gly Val Gly Leu Val Cys Ile Thr Ala Leu
 195 200 205
 Leu Gly Cys Phe Leu Leu Ile Leu Leu Ser Tyr Ala Phe Ile Val Ala
 210 215 220
 Ala Ile Leu Lys Ile Pro Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Val Val Val His Tyr Gly Phe Ala
 245 250 255
 Ser Val Ile Tyr Leu Lys Pro Lys Ser Pro Gln Ser Leu Glu Gly Asp
 260 265 270
 Thr Leu Met Gly Ile Thr Tyr Thr Val Leu Thr Pro Phe Leu Ser Pro

	275		280		285
Ile	Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Val Ala Met Lys Lys				
	290		295		300
Thr	Phe Phe Ser Lys Leu Tyr Pro Glu Lys Asn Val				
305		310		315	

<210> 1793
 <211> 225
 <212> PRT
 <213> Unknown (H38g711 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(225)
 <223> Xaa = Any Amino Acid

<400> 1793

Leu	Pro	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro	Lys	Met	Ile	Val
1				5					10					15	
Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Leu	Ser	Tyr	Ala	Gly	Cys	Leu	Ile
		20						25					30		
Arg	Cys	Leu	Ser	Leu	Pro	Leu	Leu	Glu	Ala	Trp	Lys	Arg	Gly	Met	Leu
		35					40					45			
Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His	Pro	Leu
	50					55				60					
Tyr	Arg	Ser	Ala	Ile	Leu	Asn	Pro	Xaa	Phe	Cys	Gly	Phe	Leu	Asp	Leu
65					70					75				80	
Leu	Ser	Phe	Phe	Phe	Leu	Phe	Val	Cys	Phe	Val	Phe	Leu	Ser	Leu	Leu
			85						90					95	
Asp	Ser	Gln	Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Ser	Lys
		100						105					110		
Asp	Val	Glu	Ile	Pro	Asn	Phe	Phe	Trp	Glu	Pro	Ser	Gln	Leu	Pro	His
		115					120					125			
Leu	Ala	Cys	Cys	Asp	Thr	Phe	Thr	Arg	Asn	Ile	Asn	Met	Tyr	Phe	Pro
	130					135					140				
Ala	Ala	Val	Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Phe	Tyr	Ser	Tyr
145					150					155				160	
Cys	Lys	Ile	Leu	Ser	Ser	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly	Lys
			165						170					175	
Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Cys	Xaa
		180					185						190		
Phe	Tyr	Gly	Thr	Gly	Val	Gly	Gly	Tyr	Leu	Gly	Ser	Asp	Val	Ser	Ser
		195				200						205			
Ser	Pro	Arg	Lys	Ser	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr
	210					215						220			

Pro
 225

<210> 1794
 <211> 218
 <212> PRT
 <213> Unknown (H38g712 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(218)
 <223> Xaa = Any Amino Acid

<400> 1794

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro Lys Met Ile Val
 1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Arg Leu Thr
          20           25           30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Ser Met Leu
          35           40           45
Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
          50           55           60
Cys His Ser Ala Ile Thr Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
65           70           75           80
Leu Ser Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln Leu His Asn Leu
          85           90           95
Ile Ala Leu Gln Arg Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe
          100          105          110
Phe Cys Asp Pro Ser Gln Phe Pro Arg Leu Ala Cys Cys Gly Thr Phe
          115          120          125
Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu
          130          135          140
Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Phe Ser Ile
          145          150          155          160
Leu Arg Val Ser Ser Ser Gly Gly Lys His Lys Ala Phe Ser Thr Arg
          165          170          175
Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly
          180          185          190
Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg Lys Gly Ala Val
          195          200          205
Ala Ser Val Met Tyr Thr Val Val Thr Pro
          210          215

```

<210> 1795

<211> 216

<212> PRT

<213> Unknown (H38g713 protein)

<220>

<223> Synthetic construct

<400> 1795

```

Leu Val Asp Phe Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Met Ala
 1           5           10           15
Gly Phe Leu Ile Glu Asp Lys Val Ile Ser Tyr Asn Ala Cys Ala Ala
          20           25           30
Gln Met Tyr Ile Phe Val Ala Phe Ala Thr Val Glu Asn Tyr Leu Leu
          35           40           45
Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu His
          50           55           60
Tyr Thr Thr Thr Met Thr Thr Thr Val Cys Ala Arg Leu Ala Ile Gly
65           70           75           80
Ser Tyr Leu Cys Gly Phe Leu Asn Ala Ser Ile His Thr Gly Asp Thr
          85           90           95
Phe Ser Leu Ser Phe Cys Lys Ser Asn Glu Val His His Phe Phe Cys
          100          105          110
Asp Ile Pro Ala Val Met Val Leu Ser Cys Ser Asp Arg His Ile Ser
          115          120          125
Glu Leu Val Leu Ile Tyr Val Val Ser Phe Asn Ile Phe Ile Ala Leu
          130          135          140
Leu Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Ile Thr Ile Leu Lys
          145          150          155          160
Met His Ser Ala Ser Val Tyr Gln Lys Pro Leu Ser Thr Cys Ala Ser

```

165 170 175
 His Phe Ile Ala Val Gly Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr
 180 185 190
 Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Met Ala Pro
 195 200 205
 Val Phe Tyr Thr Met Val Ile Pro
 210 215

<210> 1796

<211> 215

<212> PRT

<213> Unknown (H38g714 protein)

<220>

<223> Synthetic construct

<400> 1796

Ile Val Asp Ile Ser Tyr Ala Ser Asn Tyr Val Pro Lys Met Leu Thr
 1 5 10 15
 Asn Leu Met Asn Gln Glu Ser Thr Ile Ser Phe Phe Pro Cys Ile Met
 20 25 30
 Gln Thr Phe Leu Tyr Leu Ala Phe Ala His Val Glu Cys Leu Ile Leu
 35 40 45
 Val Val Met Ser Tyr Asp Arg Tyr Ala Asp Ile Cys His Pro Leu Arg
 50 55 60
 Tyr Asn Ile Leu Met Ser Trp Arg Val Cys Thr Val Leu Ala Val Ala
 65 70 75 80
 Ser Trp Val Phe Ser Phe Leu Leu Ala Leu Val Pro Leu Val Leu Ile
 85 90 95
 Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Cys Glu
 100 105 110
 Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln
 115 120 125
 Val Val Ile Phe Ala Ala Cys Val Phe Ile Leu Val Gly Pro Leu Cys
 130 135 140
 Leu Val Leu Val Ser Tyr Leu Arg Ile Leu Ala Ala Ile Leu Arg Ile
 145 150 155 160
 Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser Ser His
 165 170 175
 Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met
 180 185 190
 Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Ser Leu
 195 200 205
 Phe Tyr Ser Leu Phe Asn Pro
 210 215

<210> 1797

<211> 162

<212> PRT

<213> Unknown (H38g715 protein)

<220>

<223> Synthetic construct

<400> 1797

Val Ala Ile Cys Lys Pro Leu His Tyr Val Val Ile Met Asn Asn Arg
 1 5 10 15
 Val Cys Thr Leu Leu Val Leu Cys Cys Trp Val Ala Gly Leu Met Ile
 20 25 30
 Ile Val Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Asp Ser
 35 40 45

```

Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
 50          55          60
Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala
65          70          75          80
Val Phe Ala Leu Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu
          85          90          95
Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys
          100          105          110
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
          115          120          125
Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu
          130          135          140
Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
145          150          155          160
Leu Leu

```

<210> 1798

<211> 224

<212> PRT

<213> Unknown (H38g716 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(224)

<223> Xaa = Any Amino Acid

<400> 1798

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1          5          10          15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
          20          25          30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
          35          40          45
Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Pro
          50          55          60
Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Gln Asp Leu
65          70          75          80
Leu Ser Leu Tyr Phe Phe Leu Phe Phe Ser Phe Phe Leu Arg Leu Leu
          85          90          95
Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys
          100          105          110
Asp Val Glu Ile Ser Asn Val Phe Trp Glu Pro Ser Gln Leu Ser His
          115          120          125
Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Met Tyr Phe Pro Ala
          130          135          140
Ala Ile Phe Gly Phe Leu Pro Ile Leu Gly Thr Leu Phe Ser Tyr Cys
145          150          155          160
Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr
          165          170          175
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe
          180          185          190
Tyr Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser
          195          200          205
Leu Arg Lys Ala Ala Val Ala Ser Val Met Tyr Lys Met Val Thr Pro
210          215          220

```

<210> 1799

<211> 218

<212> PRT
 <213> Unknown (H38g717 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(218)
 <223> Xaa = Any Amino Acid

<400> 1799
 Leu Ala Asp Ile Gly Phe Thr Ser Asn Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Val Phe Gly Gly Met Glu Glu Ser Met Leu
 35 40 45
 Leu Ser Val Arg Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr Tyr Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 65 70 75 80
 Cys Phe Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu
 85 90 95
 Ile Ala Leu Gln Met Thr Cys Ile Lys Asp Val Glu Ile Pro Asn Phe
 100 105 110
 Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe
 115 120 125
 Thr Ile Asn Ile Val Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu
 130 135 140
 Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Ile
 145 150 155 160
 Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys
 165 170 175
 Gly Ser His Leu Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val Gly
 180 185 190
 Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala Val
 195 200 205
 Ala Ser Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 1800
 <211> 295
 <212> PRT
 <213> Unknown (H38g718 protein)

<220>
 <223> Synthetic construct

<400> 1800
 Leu Ile Phe Phe Leu Ile Tyr Pro Leu Ile Leu Val Gly Asn Asp Gln
 1 5 10 15
 Ile Leu Val Val Val Met Ala Glu Ala Ser Leu His Lys Pro Val Tyr
 20 25 30
 Phe Phe Leu Ile Asn Leu Ser Ala Leu Asp Ile Leu Ser Thr Thr Val
 35 40 45
 Thr Val Pro Lys Thr Leu Pro Leu Phe Leu Leu Gly Asp His Phe Leu
 50 55 60
 Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Leu Phe His Ser Phe Ser
 65 70 75 80
 Cys Ser Glu Ala Phe Ile Leu Val Val Met Ala Tyr Asp Arg Tyr Val
 85 90 95

```

Ala Ile Cys His Pro Leu Gln Tyr Pro Val Leu Met Asn Pro Gln Thr
      100      105      110
Asn Ala Val Leu Ala Thr Gly Ala Trp Leu Thr Ala Leu Leu Pro
      115      120      125
Ile Pro Ala Val Val Gln Thr Ser Gln Met Ala Phe Asp Ser Ile Ala
      130      135      140
Asp Ile Tyr His Cys Phe Cys Asp His Leu Ala Val Val Gln Ala Ser
      145      150      155      160
Cys Ser Asp Thr Ser Pro Gln Thr Phe Met Gly Phe Cys Ile Ala Met
      165      170      175
Val Val Ser Phe Leu Pro Leu Leu Leu Val Leu Leu Ser Tyr Ala His
      180      185      190
Ile Leu Thr Ser Val Leu Arg Ile Asn Ser Gln Glu Gly Arg Ser Lys
      195      200      205
Ala Phe Ser Thr Cys Ser Ser His Leu Pro Val Val Gly Thr Tyr Tyr
      210      215      220
Ser Ser Ile Ala Ile Ala Tyr Val Ala Tyr Ser Ala Asp Leu Pro Leu
      225      230      235      240
Asp Phe His Val Met Gly Asn Val Val His Ala Leu Leu Leu Pro Leu
      245      250      255
Leu Leu Leu Leu Pro Leu Pro Leu Leu Pro Leu Pro Leu Arg Leu Pro
      260      265      270
Leu Leu Leu Leu Leu Arg Ser Pro Ser Ser Ser Ser Ser Pro Ser
      275      280      285
Pro Ser Ser Ser Phe Phe Phe
      290      295

```

<210> 1801

<211> 311

<212> PRT

<213> Unknown (H38g719 protein)

<220>

<223> Synthetic construct

<400> 1801

```

Met Glu Met Glu Asn Cys Thr Arg Val Lys Glu Phe Ile Phe Leu Gly
  1      5      10      15
Leu Thr Gln Asn Arg Glu Val Ser Leu Val Leu Phe Leu Phe Leu Leu
      20      25      30
Leu Val Tyr Val Thr Thr Leu Leu Gly Asn Leu Leu Ile Met Val Thr
      35      40      45
Val Thr Cys Glu Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu His
      50      55      60
Asn Leu Ser Ile Ala Asp Ile Cys Phe Ser Ser Ile Thr Val Pro Lys
      65      70      75      80
Val Leu Val Asp Leu Leu Ser Glu Arg Lys Thr Ile Ser Phe Asn His
      85      90      95
Cys Phe Thr Gln Met Phe Leu Phe His Leu Ile Gly Gly Val Asp Val
      100      105      110
Phe Ser Leu Ser Val Met Ala Leu Asp Arg Tyr Val Ala Ile Ser Lys
      115      120      125
Pro Leu His Tyr Ala Thr Ile Met Ser Arg Asp Gln Cys Ile Gly Leu
      130      135      140
Thr Val Ala Ala Trp Leu Gly Gly Phe Val His Ser Ile Val Gln Ile
      145      150      155      160
Ser Leu Leu Leu Pro Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Thr
      165      170      175
Phe Tyr Cys Asp Val His Arg Val Leu Lys Leu Ala His Thr Asp Ile
      180      185      190
Phe Ile Leu Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Leu Thr Thr

```

```

      195              200              205
Leu Trp Phe Phe Leu Leu Leu Val Ser Tyr Ile Val Ile Leu Ser Leu
  210              215              220
Pro Lys Ser Gln Ala Gly Glu Gly Arg Arg Lys Ala Ile Ser Thr Cys
  225              230              235              240
Thr Ser His Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr
      245              250              255
Val Tyr Ala Arg Pro Phe Thr Ala Leu Pro Met Asp Lys Ala Ile Ser
      260              265              270
Val Thr Phe Thr Val Ile Ser Pro Leu Leu Asn Pro Leu Ile Tyr Thr
      275              280              285
Leu Arg Asn His Glu Met Lys Ser Ala Met Arg Arg Leu Lys Arg Arg
  290              295              300
Leu Val Pro Ser Asp Arg Lys
  305              310

```

<210> 1802

<211> 299

<212> PRT

<213> Unknown (H38g720 protein)

<220>

<223> Synthetic construct

<400> 1802

```

Thr Met Gln Gln Asn Asn Ser Val Pro Glu Phe Ile Leu Leu Gly Leu
  1              5              10              15
Thr Gln Asp Pro Leu Arg Gln Lys Ile Val Phe Val Ile Phe Leu Ile
      20              25              30
Phe Tyr Met Gly Thr Val Val Gly Asn Met Leu Ile Ile Val Thr Ile
  35              40              45
Lys Ser Ser Arg Thr Leu Gly Ser Pro Met Tyr Phe Phe Leu Phe Tyr
  50              55              60
Leu Ser Phe Ala Asp Ser Cys Phe Ser Thr Ser Thr Ala Pro Arg Leu
  65              70              75              80
Ile Val Asp Ala Leu Ser Glu Lys Lys Ile Ile Thr Tyr Asn Glu Cys
      85              90              95
Met Thr Gln Val Phe Ala Leu His Leu Phe Gly Cys Met Glu Ile Phe
      100              105              110
Val Leu Ile Leu Met Ala Val Asp Arg Tyr Val Ala Ile Cys Lys Pro
  115              120              125
Leu Arg Tyr Pro Thr Ile Met Ser Gln Gln Val Cys Ile Ile Leu Ile
  130              135              140
Val Leu Ala Trp Ile Gly Ser Leu Ile His Ser Thr Ala Gln Ile Ile
  145              150              155              160
Leu Ala Leu Arg Leu Pro Phe Cys Gly Pro Tyr Leu Ile Asp His Tyr
      165              170              175
Cys Cys Asp Leu Gln Pro Leu Leu Lys Leu Ala Cys Met Asp Thr Tyr
      180              185              190
Met Ile Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ser Ser
      195              200              205
Ser Phe Met Ile Leu Ile Ile Ser Tyr Ile Val Ile Leu His Ser Leu
  210              215              220
Arg Asn His Ser Ala Lys Gly Lys Lys Lys Ala Leu Ser Ala Cys Thr
  225              230              235              240
Ser His Ile Ile Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Ile
      245              250              255
Tyr Thr Arg Pro Pro Thr Thr Phe Pro Met Asp Lys Met Val Ala Val
      260              265              270
Phe Tyr Thr Ile Gly Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu
  275              280              285

```

Arg Asn Ala Glu Val Lys Asn Ala Met Arg Lys
290 295

<210> 1803

<211> 314

<212> PRT

<213> Unknown (H38g721 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1803

Met	Glu	Leu	Gly	Asn	Val	Thr	Arg	Val	Lys	Glu	Phe	Ile	Phe	Leu	Gly	1	5	10	15
Leu	Thr	Gln	Ser	Gln	Asp	Gln	Ser	Leu	Val	Leu	Phe	Leu	Phe	Leu	Cys	20	25	30	
Leu	Val	Tyr	Met	Thr	Thr	Leu	Leu	Gly	Asn	Leu	Leu	Ile	Met	Val	Thr	35	40	45	
Val	Thr	Cys	Glu	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Leu	Leu	Arg	50	55	60	
Asn	Leu	Ala	Ile	Leu	Asp	Ile	Cys	Phe	Ser	Ser	Thr	Thr	Ala	Pro	Lys	65	70	75	80
Val	Leu	Leu	Asp	Leu	Leu	Ser	Lys	Lys	Lys	Thr	Ile	Ser	Tyr	Thr	Ser	85	90	95	
Cys	Met	Thr	Gln	Ile	Phe	Leu	Phe	His	Leu	Leu	Gly	Gly	Ala	Asp	Ile	100	105	110	
Phe	Ser	Leu	Ser	Val	Met	Ala	Phe	Asp	Cys	Tyr	Met	Ala	Ile	Ser	Lys	115	120	125	
Pro	Leu	His	Tyr	Val	Thr	Ile	Met	Ser	Arg	Gly	Gln	Cys	Thr	Ala	Leu	130	135	140	
Ile	Ser	Ala	Ser	Trp	Met	Gly	Gly	Phe	Val	His	Ser	Ile	Val	Gln	Ile	145	150	155	160
Ser	Leu	Leu	Leu	Pro	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Val	Leu	Asp	Thr	165	170	175	
Phe	Tyr	Cys	Asp	Val	Pro	Gln	Val	Leu	Lys	Leu	Thr	Cys	Thr	Asp	Thr	180	185	190	
Phe	Ala	Leu	Glu	Phe	Leu	Met	Ile	Ser	Asn	Asn	Gly	Leu	Val	Thr	Thr	195	200	205	
Leu	Trp	Phe	Ile	Phe	Leu	Leu	Val	Ser	Tyr	Thr	Val	Ile	Leu	Met	Thr	210	215	220	
Leu	Arg	Ser	Gln	Ala	Gly	Gly	Gly	Arg	Arg	Lys	Ala	Ile	Ser	Thr	Cys	225	230	235	240
Thr	Ser	His	Ile	Thr	Val	Val	Thr	Leu	His	Phe	Val	Pro	Cys	Ile	Tyr	245	250	255	
Val	Tyr	Ala	Arg	Pro	Phe	Thr	Ala	Leu	Pro	Thr	Glu	Lys	Ala	Ile	Ser	260	265	270	
Val	Thr	Phe	Thr	Val	Ile	Ser	Pro	Leu	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	275	280	285	
Leu	Arg	Asn	Gln	Glu	Met	Lys	Ser	Ala	Met	Arg	Arg	Leu	Lys	Arg	Arg	290	295	300	
Leu	Val	Pro	Ser	Glu	Arg	Glu	Xaa	Lys	Thr							305	310		

<210> 1804

<211> 314

<212> PRT

<213> Unknown (H38g722 protein)

<220>

<223> Synthetic construct

<400> 1804

```

Met Leu Gly Leu Asn His Thr Ser Met Ser Glu Phe Ile Leu Val Gly
 1           5           10           15
Phe Ser Ala Phe Pro His Leu Gln Leu Met Leu Phe Leu Leu Phe Leu
      20           25           30
Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala Thr
      35           40           45
Val Trp Ser Glu Arg Ser Leu His Thr Pro Met Tyr Leu Phe Leu Cys
      50           55           60
Val Leu Ser Val Ser Glu Ile Leu Tyr Thr Val Ala Ile Ile Pro Arg
      65           70           75           80
Met Leu Ala Asp Leu Leu Ser Thr Gln Arg Ser Ile Ala Phe Leu Ala
      85           90           95
Cys Ala Ser Gln Met Phe Phe Ser Phe Ser Phe Gly Phe Thr His Ser
      100          105          110
Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Gly Cys Ala Cys Leu
      130          135          140
Val Gly Cys Ser Trp Ala Gly Gly Ser Val Met Gly Met Val Val Thr
      145          150          155          160
Ser Ala Ile Phe Gln Leu Thr Phe Cys Gly Ser His Glu Ile Gln His
      165          170          175
Phe Leu Cys His Val Pro Pro Leu Leu Lys Leu Ala Cys Gly Asn Asn
      180          185          190
Val Pro Ala Val Ala Leu Gly Val Gly Leu Val Cys Ile Met Ala Leu
      195          200          205
Leu Gly Cys Phe Leu Leu Ile Leu Leu Ser Tyr Ala Phe Ile Val Ala
      210          215          220
Asp Ile Leu Lys Ile Pro Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser
      225          230          235          240
Thr Cys Ala Ser His Leu Ile Val Val Ile Val His Tyr Gly Phe Ala
      245          250          255
Ser Val Ile Tyr Leu Lys Pro Lys Gly Pro His Ser Gln Glu Gly Asp
      260          265          270
Thr Leu Met Ala Thr Thr Tyr Ala Val Leu Thr Pro Phe Leu Ser Pro
      275          280          285
Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Val Ala Met Lys Arg
      290          295          300
Thr Phe Leu Ser Thr Leu Tyr Ser Ser Gly
      305          310

```

<210> 1805

<211> 316

<212> PRT

<213> Unknown (H38g723 protein)

<220>

<223> Synthetic construct

<400> 1805

```

Met Pro Gly Gln Asn Tyr Arg Thr Ile Ser Glu Phe Ile Leu Ser Gly
 1           5           10           15
Phe Ser Ala Phe Pro Gln Gln Leu Leu Pro Val Leu Phe Leu Leu Tyr
      20           25           30
Leu Leu Met Phe Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala
      35           40           45

```

Thr Val Trp Ile Glu Arg Arg Leu His Thr Pro Met Tyr Leu Phe Leu
 50 55 60
 Cys Ala Leu Ser Ile Ser Glu Ile Leu Phe Thr Val Ala Ile Thr Pro
 65 70 75 80
 Arg Met Leu Ala Asp Leu Leu Phe Thr His Arg Ser Ile Thr Phe Val
 85 90 95
 Ala Cys Ala Ile Gln Met Phe Phe Ser Phe Met Phe Gly Phe Thr His
 100 105 110
 Ser Phe Leu Leu Met Val Met Gly Tyr Asp His Tyr Val Thr Ile Cys
 115 120 125
 His Pro Leu His Tyr Asn Met Leu Met Ser Pro Arg Gly Cys Ala His
 130 135 140
 Leu Val Ala Trp Thr Trp Ala Gly Gly Ser Val Met Gly Met Met Val
 145 150 155 160
 Thr Met Met Val Phe His Leu Thr Phe Cys Gly Ser Asn Val Ile His
 165 170 175
 His Phe Leu Cys His Val Leu Ser Leu Leu Lys Leu Ala Cys Gly Ser
 180 185 190
 Lys Thr Ser Ser Val Ile Met Gly Val Met Leu Val Cys Val Thr Ala
 195 200 205
 Leu Ile Gly Cys Leu Phe Leu Ile Ile Leu Ser Phe Val Phe Ile Val
 210 215 220
 Ala Ala Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Thr Phe
 225 230 235 240
 Ser Thr Cys Val Ser His Leu Thr Val Val Val Met His Tyr Ser Phe
 245 250 255
 Ala Ser Leu Ile Tyr Leu Lys Pro Lys Gly Leu His Ser Met Tyr Ser
 260 265 270
 Asp Ala Leu Met Ala Thr Thr Tyr Thr Val Phe Thr Pro Phe Leu Ser
 275 280 285
 Pro Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Asn Ala Ile Asn
 290 295 300
 Lys Asn Phe Cys Arg Arg Phe Cys Pro Leu Ser Ser
 305 310 315

<210> 1806

<211> 161

<212> PRT

<213> Unknown (H38g724 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(161)

<223> Xaa = Any Amino Acid

<400> 1806

Gly Trp Lys Ser Ser Thr Phe Asn Ile Ser Cys Thr Lys Phe Phe Leu
 1 5 10 15
 Val Gly Phe Pro Gly Leu Arg Glu Trp Trp Pro Leu Leu Val Leu Pro
 20 25 30
 Leu Val Phe Leu Phe Val Thr Ile Ile Ser Ala Asn Ala Leu Val Ile
 35 40 45
 His Thr Val Val Ala Arg Gln Asn Leu His Gln Pro Thr Cys Met Leu
 50 55 60
 Ile Thr Val Leu Leu Ala Val Asn Ile Arg Ala Ala Thr Ala Val Met
 65 70 75 80
 Pro Lys Met Leu Glu Gly Phe Val Tyr Tyr Ala Asn Pro Ile Ser Leu
 85 90 95
 His Gly Arg Leu Ala Xaa Val Phe Phe Ile Tyr Phe Thr Leu Leu Leu

```

      100      105      110
Asp Tyr Asn Phe Leu Trp Pro Trp Pro Trp Thr Gly Tyr Phe Ala Ile
      115      120      125
Cys His Pro Leu Cys Phe Ser Asp Leu Met Thr Ser Gln Leu Leu Gly
      130      135      140
Leu Leu Ala Ile Leu Ala Phe Glu Gln Ser Pro Gly Ser Asp Pro Ala
145      150      155      160
Pro

```

<210> 1807
 <211> 198
 <212> PRT
 <213> Unknown (H38g725 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(198)
 <223> Xaa = Any Amino Acid

```

<400> 1807
Val Ala Ile Cys His Pro Leu Cys Phe Gln Thr Glu Xaa Leu Pro Ser
  1          5          10          15
Trp Leu Gly Leu Leu Ala Ile Leu Ala Leu Thr Gln Ser Trp Gly Val
      20      25      30
Thr Val Pro Leu Val Val Leu Thr Ala Lys Ala Asp Phe Cys Arg Thr
      35      40      45
Ala Val Ile Arg His Phe Thr Cys Glu Cys Ile Ala Leu Leu Ser Ile
  50          55          60
Ala Cys Gly Asp Leu Thr Phe Asn Asn Trp Leu Gly Leu Ala Met Cys
65          70          75          80
Leu Val Thr Val Ile Ser Asp Met Ala Leu Leu Gly Thr Ser Tyr Thr
      85          90          95
His Ile Ile Tyr Ala Ala Phe Arg Ile Ser Ser Trp Gly Ala Gln Ala
      100      105      110
Lys Ala Leu His Thr Cys Gly Ser His Leu Leu Val Ile Leu Ser Ile
      115      120      125
Tyr Val Ser Gly Leu Ser Thr Ser Ile Thr Phe Xaa Val Ala Lys Thr
      130      135      140
Val Ser Gln Asn Val Gln Asn Leu Leu Ser Ala Ile Tyr Leu Leu Leu
145          150          155          160
Pro Gly Ala Leu Asn Pro Val Ile Tyr Gly Val Arg Thr Arg Glu Ile
      165      170      175
Gln Gln His Val Glu Lys Met Leu Cys Glu Lys Glu Thr Ala Gln Lys
      180      185      190
Ala Gly Glu Lys Pro Lys
      195

```

<210> 1808
 <211> 315
 <212> PRT
 <213> Unknown (H38g726 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 1808

Phe Ser Gln Asn Leu Leu Ile Ser Gly Ser Gly Ser Phe Val Leu Leu
 1 5 10 15
 Gly Met Pro Gly Leu Glu Ala Leu His Ala Trp Leu Ser Val Pro Val
 20 25 30
 Cys Leu Leu Tyr Met Ala Ala Leu Val Gly Asn Ala Leu Leu Val Gly
 35 40 45
 Leu Val Val Ala Asp Lys Ala Leu Trp Ala Pro Met Tyr Gln Leu Leu
 50 55 60
 Trp Leu Leu Ala Ala Ala Asp Phe Val Leu Ala Thr Ser Thr Val Pro
 65 70 75 80
 Lys Ala Leu Ala Val Leu Trp Gly Leu Ser Ser Glu Ile Ser Phe Gly
 85 90 95
 Gly Cys Leu Ala Gln Leu Phe Val Ala His Ser Val Asn His Cys His
 100 105 110
 Ile Ala Glu Ser Ser Val Leu Leu Ser Thr Ala Val Asp Cys Gln Pro
 115 120 125
 Leu Arg Tyr Gly Ala Leu Leu Ala Gln Phe Val Val Gly Leu Val Ala
 130 135 140
 Leu Thr Thr Met Thr Arg Asp Val Cys Val Met Tyr Thr Leu Xaa Phe
 145 150 155 160
 Leu Phe Lys Lys Leu Pro Tyr Cys Gly Gln Trp Ala Leu Pro His Thr
 165 170 175
 Tyr Cys Glu His Met Gly Val Ala Cys Leu Ala Cys Gly Asp Thr Cys
 180 185 190
 Pro Ile Ile Arg Tyr Gly Leu Ala Thr Thr Leu Leu Ser Pro Ala Leu
 195 200 205
 Asp Leu Gly Leu Ile Gly Ala Ser Tyr Ala Leu Ile Phe Arg Ala Val
 210 215 220
 Cys Arg Leu Pro Ser His Val Ala Cys His Lys Ala Leu Gly Asn Cys
 225 230 235 240
 Gly Thr Tyr Ala Ser Ile Ile Gly Leu Phe Tyr Thr Pro Ala Leu Phe
 245 250 255
 Ser Phe Leu Ala His Cys Phe Gly Cys His Thr Val Pro Asn His Ile
 260 265 270
 His Ile Leu Leu Ala Asn Leu Tyr Ala Val Val Phe Pro Ala Phe Asn
 275 280 285
 Pro Val Val Tyr Gly Val Gln Thr Gln Gln Ser Ser Glu Ala Gln Glu
 290 295 300
 Leu Ala Ser Thr Phe Leu Gly Arg Ser Ser Glu
 305 310 315

<210> 1809

<211> 313

<212> PRT

<213> Unknown (H38g727 protein)

<220>

<223> Synthetic construct

<400> 1809

Met Asn Trp Glu Asn Glu Ser Ser Pro Lys Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Ala Trp Leu Gln Met Pro Leu Phe Val Val Leu Leu
 20 25 30
 Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met Met Val
 35 40 45
 Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Thr Val Pro His

```

65          70          75          80
Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr Ala Gly
          85          90          95
Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr Glu Cys
          100         105         110
Leu Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Arg
          115         120         125
Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu Arg Met
          130         135         140
Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu Gln Ser
145         150         155         160
Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val Asp His
          165         170         175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
          180         185         190
Lys Pro Ile Glu Ala Glu Leu Phe Phe Ser Val Leu Ile Leu Leu
          195         200         205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala Gln Ala
          210         215         220
Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
225         230         235         240
Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
          245         250         255
Tyr Met Tyr Leu Gln Pro Pro Ser Ser Thr Ser Lys Asp Trp Gly Lys
          260         265         270
Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Ser Met Leu Asn Ser Leu
          275         280         285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Phe Lys Arg Leu
          290         295         300
Met Pro Arg Ile Phe Phe Cys Lys Lys
305          310

```

<210> 1810

<211> 323

<212> PRT

<213> Unknown (H38g728 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1810

```

Gly Thr Leu Asn Leu Ser Ser Phe Asn Pro Gly Leu Phe Ile Leu Leu
1          5          10          15
Gly Ile Pro Gly Leu Glu Trp Phe Cys Ile Trp Met Gly Ile Leu Ser
          20          25          30
Phe Thr Ser Tyr Leu Val Ser Leu Ala Gly Asn Val Ile Leu Leu Tyr
          35          40          45
Leu Ile Thr Val Glu His Asn Leu His Lys Pro Met Phe Ser Phe Leu
          50          55          60
Ser Ile Pro Ala Ser Ala Asn Leu Ile Leu Cys Ile Thr Tyr Phe Pro
65         70         75         80
Lys Thr Phe Gly Ile Phe Xaa Leu Lys Ala Gln Lys Ile Ile Phe Pro
          85          90          95
Gly Cys Phe Thr Arg Phe Phe Phe Phe Gly Leu Leu His Phe Ser Phe
          100         105         110
Phe Leu Asp Leu Ala Ile Leu Leu Gly Leu Ala Phe Asp His Tyr Met
          115         120         125

```

```

Thr Ile Gly Phe Leu Leu Arg Tyr Thr Ser Gly Leu Thr Pro Arg Thr
130          135          140
Leu Gly Lys Ile Val Val Ser Ile Asp Xaa Arg Phe Asn Asn Ile Leu
145          150          155          160
Pro Ile Asp Phe Leu Gly Lys His Leu Pro Phe Cys Arg Thr His Ile
165          170          175
Asn Ser Asn Thr Tyr Cys Glu His Ile Gly Val Ala Leu Leu Ser Tyr
180          185          190
Ala Asp Ile Ser Ile Asn Ile Trp Tyr Asp Phe Thr Ile Leu Val Met
195          200          205
Thr Ile Ile Ser Asp Leu Ile Leu Thr Asp Ile Ser Tyr Thr Leu Thr
210          215          220
Leu His Ala Val Phe His Leu Pro Ser Ser Asp Ala Leu Leu Lys Ala
225          230          235          240
Leu Ser Thr Cys Gly Ser His Val Ser Val Ile Leu Met Leu Tyr Thr
245          250          255
Pro Thr Met Leu Ser Ala Leu Thr His His Phe Gly Gln Ser Ile Ser
260          265          270
Cys Thr Phe Tyr Ile Met Phe Val Gly Leu Tyr Arg Ala Ile Pro Pro
275          280          285
Val Leu Asn Ser Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gly Asn
290          295          300
Lys Val Ile Leu Leu Phe Phe Leu Lys Gly Met Gln Xaa Tyr Glu Asp
305          310          315          320
Glu Asn Met

```

<210> 1811

<211> 337

<212> PRT

<213> Unknown (H38g729 protein)

<220>

<223> Synthetic construct

<221> VARIANT.

<222> (1)...(337)

<223> Xaa = Any Amino Acid

<400> 1811

```

Met Lys Lys Asn Ala Ser Phe Glu Asp Phe Phe Ile Leu Leu Gly Phe
1      5      10      15
Ser Asn Trp Pro His Leu Glu Val Val Leu Phe Val Val Ile Leu Ile
20     25     30
Phe Tyr Leu Ile Thr Leu Ile Gly Asn Leu Phe Ile Ile Ile Leu Ser
35     40     45
Tyr Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
50     55     60
Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser Ile Pro Gln Leu
65     70     75     80
Leu Val Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ala Gly Cys
85     90     95
Thr Val Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr Ala Glu Cys Val
100    105    110
Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro
115    120    125
Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys Arg Leu Leu Ala
130    135    140
Ala Ala Ser Trp Val Ser Gly Phe Thr Thr Ser Ala Leu His Ser Ser
145    150    155    160
Phe Thr Phe Trp Ile Pro Leu Cys Arg His Arg Leu Val Asp His Phe

```

[illegible]

<210> 1812
<211> 319
<212> PRT
<213> Unknown (H38g730 protein)

```
<220>  
<223> Synthetic construct  
  
<221> VARIANT  
<222> (1)...(319)  
<223> Xaa = Any Amino Acid
```

<400> 1812															
Met	Ala	Met	Tyr	Asn	Met	Ser	Asp	His	Gly	Thr	Gly	Leu	Phe	Ile	Leu
1				5					10					15	
Leu	Gly	Ile	Pro	Gly	Leu	Glu	Gln	Tyr	His	Val	Trp	Ile	Ser	Ile	Pro
			20					25					30		
Phe	Cys	Leu	Ile	Tyr	Leu	Met	Ala	Val	Val	Ala	Lys	Ser	Ile	Leu	Leu
		35					40						45		
Tyr	Leu	Ile	Val	Val	Glu	His	Ser	Leu	His	Ala	Pro	Met	Phe	Phe	Phe
	50					55					60				
Leu	Ser	Met	Leu	Ala	Ile	Thr	Asp	Leu	Ile	Leu	Ser	Thr	Thr	Cys	Val
65					70					75					80
Pro	Lys	Thr	Leu	Ser	Ile	Phe	Trp	Phe	Gly	Pro	Gln	Ile	Ser	Phe	Pro
				85					90					95	
Gly	Cys	Leu	Thr	Gln	Leu	Phe	Phe	Leu	His	Tyr	Ser	Phe	Val	Leu	Asp
			100					105					110		
Ser	Ala	Ile	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Met	Ala	Ile	Cys
		115					120					125			
Ser	Pro	Leu	Arg	Tyr	Thr	Thr	Ile	Leu	Thr	Pro	Lys	Thr	Ile	Val	Lys
	130					135					140				
Ile	Ala	Val	Gly	Ile	Cys	Phe	Arg	Ser	Phe	Cys	Val	Phe	Val	Pro	Cys
145					150					155					160
Val	Phe	Leu	Val	Asn	Arg	Leu	Pro	Phe	Cys	Arg	Thr	His	Ile	Ile	Ser
				165					170					175	
His	Thr	Tyr	Cys	Glu	His	Ile	Gly	Val	Ala	Gln	Leu	Ala	Cys	Ala	Asp
			180					185					190		

```

Ile Ser Ile Asn Ile Trp Cys Gly Phe Cys Val Pro Ile Met Thr Val
    195                200                205
Met Thr Asp Val Ile Leu Ile Ala Val Ser Tyr Thr Leu Met Leu Cys
    210                215                220
Gly Val Phe Cys Leu Pro Ser Gln Asp Ala Arg Gln Lys Ala Leu Cys
    225                230                235                240
Ser Cys Gly Ser His Val Cys Val Ile Leu Ile Phe Tyr Thr Pro Ala
    245                250                255
Phe Phe Ser Ile Leu Ala His Arg Phe Gly His Asn Val Pro His Thr
    260                265                270
Phe His Ile Met Phe Ala Asn Leu Tyr Val Ile Ile Pro Pro Ala Leu
    275                280                285
Asn Pro Ile Val Tyr Arg Ile Lys Thr Lys Gln Ile Gln Asn Arg Ile
    290                295                300
Leu Leu Leu Phe Pro Lys Gly Ser Gln Xaa Xaa Val Pro Glu Leu
    305                310                315

```

<210> 1813

<211> 311

<212> PRT

<213> Unknown (H38g731 protein)

<220>

<223> Synthetic construct

<400> 1813

```

Met Asn Asp Asp Gly Lys Val Asn Ala Ser Ser Glu Gly Tyr Phe Ile
  1      5      10      15
Leu Val Gly Phe Ser Asn Trp Pro His Leu Glu Val Val Ile Phe Val
    20      25      30
Val Val Leu Ile Phe Tyr Leu Met Thr Leu Ile Gly Asn Leu Phe Ile
    35      40      45
Ile Ile Leu Ser Tyr Leu Asp Ser His Leu His Thr Pro Met Tyr Phe
    50      55      60
Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser
    65      70      75      80
Ile Pro Gln Leu Leu Val Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser
    85      90      95
Tyr Ala Gly Cys Met Ile Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr
    100     105     110
Thr Glu Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala
    115     120     125
Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys
    130     135     140
His Leu Leu Ala Val Ala Ser Trp Val Ser Gly Phe Thr Asn Ser Ala
    145     150     155     160
Leu His Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Gln
    165     170     175
Val Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu Arg Leu Ser Cys
    180     185     190
Val Asp Thr His Val Asn Glu Leu Thr Leu Met Ile Thr Ser Ser Ile
    195     200     205
Phe Val Leu Ile Pro Leu Ile Leu Ile Leu Thr Ser Tyr Gly Ala Ile
    210     215     220
Val Arg Ala Val Leu Arg Met Gln Ser Thr Thr Gly Leu Gln Lys Val
    225     230     235     240
Phe Gly Thr Cys Gly Ala His Leu Met Ala Val Ser Leu Phe Phe Ile
    245     250     255
Pro Ala Met Cys Ile Tyr Leu Gln Pro Pro Ser Gly Asn Ser Gln Asp
    260     265     270
Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu

```


275 280 285
 Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Val Val Arg Gly Ala Val
 290 295 300
 Lys Arg Leu Met Gly Trp Glu
 305 310

<210> 1814
 <211> 88
 <212> PRT
 <213> Unknown (H38g732 protein)

<220>
 <223> Synthetic construct

<400> 1814
 Phe Ile His Ala Leu Ser Val Ile Glu Ser Ile Ile Val Leu Ala Met
 1 5 10 15
 Ala Phe Glu Arg Tyr Val Ala Ile Cys His Pro Leu Cys His Ala Glu
 20 25 30
 Val Leu Asn Ser Thr Val Thr Ala His Ile Gly Ile Val Ala Gly Val
 35 40 45
 Arg Gly Ser Leu Phe Phe Ser Pro Leu Ala Leu Leu Ile Lys Thr Leu
 50 55 60
 Gly Leu Cys His Ser Tyr Val Leu Ser His Ser Tyr Ser Leu His Gln
 65 70 75 80
 Asp Val Ala Asn Leu Ser Tyr Ala
 85

<210> 1815
 <211> 159
 <212> PRT
 <213> Unknown (H38g733 protein)

<220>
 <223> Synthetic construct

<400> 1815
 Val Ala Ile Cys Asn Pro Leu Arg Tyr Leu Thr Val Met Asn Pro Gln
 1 5 10 15
 Leu Cys Leu Trp Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His
 20 25 30
 Ser Ile Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro
 35 40 45
 Asn Glu Leu Asp Asn Phe Tyr Cys Asp Val Leu Gln Ile Ile Lys Leu
 50 55 60
 Ala Cys Met Asp Thr Tyr Val Val Glu Val Leu Val Ile Ala Asn Ser
 65 70 75 80
 Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala
 85 90 95
 Ile Ile Leu Ile Thr Leu Arg Thr Arg Phe Cys Gln Gly Gln Asn Lys
 100 105 110
 Val Leu Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe
 115 120 125
 Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val
 130 135 140
 Asp Lys Ile Phe Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu
 145 150 155

<210> 1816
 <211> 316
 <212> PRT

<213> Unknown (H38g734 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1816

```

Met Ser Ala Pro Asn His Ser Thr Ala Asn His Asp Met Phe Val Leu
 1          5          10          15
Ile Gly Val Pro Gly Leu Lys Glu Leu His Val Trp Ile Ser Ile Pro
          20          25          30
Phe Cys Leu Met Tyr Leu Val Ala Val Ser Gly Asn Gly Leu Leu Val
          35          40          45
Cys Val Val Ala Val Glu His Ser Leu His Glu Pro Met Tyr Leu Phe
          50          55          60
Leu Ser Met Leu Ala Phe Trp Asp Leu Ile Leu Ser Thr Ser Ala Val
          65          70          75          80
Pro Lys Ala Leu Ser Ile Phe Trp Phe Asp Asp Val Asp Ile Ser Phe
          85          90          95
Gly Gly Cys Val Thr Gln Leu Phe Phe Met His Phe Ala Phe Val Ala
          100          105          110
Glu Ser Gly Ile Leu Leu Thr Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Tyr Pro Leu Arg Tyr Ser Thr Ile Leu Ser His Ser Val Ile Gly
          130          135          140
Lys Ile Gly Gly Val Val Phe Arg Ser Phe Ala Thr Val Phe Ser
          145          150          155          160
Ile Val Phe Leu Val Lys Arg Leu Pro Phe Cys Arg Thr Asn Ile Ile
          165          170          175
Ala His Thr Phe Cys Glu His Met Gly Leu Ala Lys Leu Gly Cys Ser
          180          185          190
Glu Ile Thr Ile Asn Ile Trp Tyr Gly Ile Ser Val Pro Leu Leu Ser
          195          200          205
Val Thr Leu Asp Met Val Thr Ile Val Ile Ser Xaa Gly Leu Ile Val
          210          215          220
Gln Ala Val Phe Arg Leu Pro Ser Leu Gly Ala Trp Met Lys Ala Leu
          225          230          235          240
Ser Thr Cys Gly Ser His Gly Ser Val Ile Leu Met Phe Cys Leu Pro
          245          250          255
Gly Ile Phe Thr Val Ile Val Gln Arg Phe Ala Xaa Lys Phe Pro Lys
          260          265          270
Tyr Val His Ile Leu Leu Ala Asn Leu Tyr Val Leu Val Pro Pro Met
          275          280          285
Met Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gln Lys Gly
          290          295          300
Val Ala Leu Val Phe Ser Pro Lys Gly Lys Cys Cys
          305          310          315

```

<210> 1817

<211> 364

<212> PRT

<213> Unknown (H38g735 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(364)

<223> Xaa = Any Amino Acid

<400> 1817

```

Met Pro Leu Thr Asn Glu Ser His Pro Glu Glu Phe Ile Leu Leu Gly
 1           5           10           15
Phe Ala Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe Thr Ser Leu Leu
      20           25           30
Ile Met Tyr Pro Ile Ala Val Met Gly Asn Ile Thr Ile Ile Leu Met
      35           40           45
Ser Arg Leu Asp Ser Arg Leu His Ser Pro Met Tyr Phe Phe Leu Thr
      50           55           60
Asn Leu Ser Phe Leu Asp Met Cys Tyr Thr Thr Ser Ile Val Pro Gln
      65           70           75           80
Met Leu Phe Asn Leu Gly Ser Ser Lys Lys Thr Ile Ser Tyr Met Gly
      85           90           95
Cys Ala Val Gln Leu Tyr Phe Phe His Ile Met Gly Gly Thr Glu Cys
      100          105          110
Leu Leu Leu Ala Ile Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Arg
      115          120          125
Pro Leu His Tyr Thr Leu Ile Met Asn Gln Arg Val Cys Ile His Xaa
      130          135          140
Phe Pro Pro Cys Trp Leu Ile Gly Ile Ile Tyr Ala Val Ser Glu Ala
      145          150          155          160
Thr Ala Thr Leu Gln Leu Pro Leu Cys Gly Ser Asn Lys Leu Asp His
      165          170          175
Leu Val Cys Glu Ile Pro Val Leu Ile Lys Ile Ala Cys Gly Glu Lys
      180          185          190
Gly Ser Asn Glu Leu Thr Leu Ser Val Val Cys Ile Phe Met Leu Ala
      195          200          205
Val Pro Leu Cys Leu Ile Leu Ala Ser Tyr Ala Ser Ile Gly Ser Ala
      210          215          220
Val Phe Lys Ile Lys Ser Ser Lys Gly Arg Lys Lys Ala Phe Gly Thr
      225          230          235          240
Cys Ser Ser His Leu Ile Val Val Phe Leu Phe Tyr Gly Pro Ala Ile
      245          250          255
Ser Met Tyr Leu Gln Pro Pro Ser Ser Ile Ser Arg Asp Gln Pro Lys
      260          265          270
Phe Met Ala Leu Phe Tyr Gly Val Val Thr Pro Ser Leu Asn Pro Phe
      275          280          285
Ile Tyr Thr Leu Arg Asn Lys Asn Val Lys Gly Ala Leu Arg Asn Leu
      290          295          300
Val Arg Ser Ile Phe Ser Phe Lys Xaa Xaa Trp Val Asp Ile Thr Met
      305          310          315          320
Lys Leu Leu Asn Ser Xaa Ser Arg Leu Leu Trp Phe Tyr Leu Thr Asn
      325          330          335
Ser Cys Leu Ile Ile Lys Tyr Arg Phe Thr Cys Ser Cys Lys Ile Cys
      340          345          350
Tyr Val Ser Glu Thr Leu Cys Lys His Val Gln Gln
      355          360

```

<210> 1818

<211> 166

<212> PRT

<213> Unknown (H38g736 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(166)

<223> Xaa = Any Amino Acid

<400> 1818
 Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr Ile Leu Leu Ala Met
 1 5 10 15
 Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg His Ala Ala
 20 25 30
 Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly Ile Val Ala Val Val
 35 40 45
 Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu Ile Lys Arg Leu
 50 55 60
 Ala Phe Cys His Ser Asn Val Leu Ser His Ser Tyr Cys Val His Gln
 65 70 75 80
 Asp Val Leu Lys Leu Ala Tyr Ala Asp Thr Leu Pro Asn Val Val Tyr
 85 90 95
 Gly Leu Thr Ala Ile Leu Leu Ala Met Gly Val Asp Ala Met Phe Ile
 100 105 110
 Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val Leu Gln Leu Pro Ser
 115 120 125
 Lys Ser Xaa Arg Ala Lys Ala Phe Gly Thr Cys Val Val His Ile Gly
 130 135 140
 Val Val Leu Gly Leu Tyr Val Pro Leu Ile Gly Thr Ser Ser Gly His
 145 150 155 160
 Arg Phe Gly Asn Lys Leu
 165

<210> 1819
 <211> 312
 <212> PRT
 <213> Unknown (H38g737 protein)

<220>
 <223> Synthetic construct

<400> 1819
 Met Met Ile Lys Lys Asn Ala Ser Ser Glu Asp Phe Phe Ile Leu Leu
 1 5 10 15
 Gly Phe Ser Asn Trp Pro Gln Leu Glu Val Val Leu Phe Val Val Ile
 20 25 30
 Leu Ile Phe Tyr Leu Met Thr Leu Thr Gly Asn Leu Phe Ile Ile Ile
 35 40 45
 Leu Ser Tyr Val Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Leu Asp Leu Cys His Thr Thr Ser Ser Ile Pro
 65 70 75 80
 Gln Leu Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Ala
 85 90 95
 Gly Cys Met Val Gln Leu Tyr Phe Val Leu Ala Leu Gly Ile Ala Glu
 100 105 110
 Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys
 115 120 125
 Arg Pro Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys His Leu
 130 135 140
 Leu Ala Ala Ala Ser Trp Val Ile Gly Phe Thr Ile Ser Ala Leu His
 145 150 155 160
 Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Leu Val Asp
 165 170 175
 His Phe Phe Cys Glu Val Pro Ala Leu Leu Arg Leu Ser Cys Val Asp
 180 185 190
 Thr His Ala Asn Glu Leu Thr Leu Met Val Met Ser Ser Ile Phe Val
 195 200 205
 Leu Ile Pro Leu Ile Leu Ile Leu Thr Ala Tyr Gly Ala Ile Ala Arg

210	215	220
Ala Val Leu Ser Met Gln Ser Thr Thr Gly Leu Gln Lys Val Phe Arg		
225	230	235
Thr Cys Gly Ala His Leu Met Val Val Ser Leu Phe Phe Ile Pro Val		240
	245	250
Met Cys Met Tyr Leu Gln Pro Pro Ser Glu Asn Ser Pro Asp Gln Gly		255
	260	265
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu Asn Pro		270
	275	280
Leu Ile Tyr Thr Leu Arg Asn Lys His Val Lys Gly Ala Ala Lys Arg		285
	290	295
Leu Leu Gly Trp Glu Trp Gly Lys		300
305	310	

<210> 1820

<211> 151

<212> PRT

<213> Unknown (H38g738 protein)

<220>

<223> Synthetic construct

<400> 1820

Arg Pro Leu Cys Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu		
1	5	10
Pro Ala Leu Leu Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu		15
	20	25
Asn Gln Met Phe Ala Ala Arg Val Val Ile Leu Leu Arg Gly Val Ala		30
	35	40
Val Ile Leu Ala Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met		45
	50	55
Arg Phe Asn Gly Gly Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His		60
	65	70
Leu Thr Ala Val Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu		75
	85	90
Gln Pro Ala Gln Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu		95
	100	105
Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu		110
	115	120
Arg Asn Lys Lys Met Lys Gly Ala Pro Arg Arg Leu Leu Arg Ser Leu		125
	130	135
Gly Arg Gly Gln Ala Gly Gln		140
145	150	

<210> 1821

<211> 341

<212> PRT

<213> Unknown (H38g739 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(341)

<223> Xaa = Any Amino Acid

<400> 1821

Met Met Glu Lys Val Asn Ala Ser Ser Glu Gly Tyr Phe Ile Leu Val		
1	5	10
Gly Phe Ser Asn Trp Pro Tyr Leu Glu Val Val Leu Phe Val Val Ile		15
	20	25
		30

```

Leu Ile Phe Cys Leu Met Thr Leu Ile Gly Asn Leu Phe Ile Ile Ile
   35           40           45
Leu Thr Tyr Leu Asp Ser His Leu His Thr Pro Leu Tyr Phe Phe Leu
   50           55           60
Ser Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser Ile Pro
   65           70           75           80
Gln Leu Leu Val Ser Leu Trp Gly Val Glu Lys Thr Ile Ser Tyr Ala
   85           90           95
Gly Cys Met Val Gln Leu Tyr Phe Phe Leu Thr Leu Gly Thr Thr Glu
  100           105           110
Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala Val Cys
  115           120           125
Arg Pro Leu His Tyr Thr Val Leu Met His Ser Arg Phe Cys His Leu
  130           135           140
Leu Ala Val Ala Ser Trp Val Ser Gly Phe Thr Asn Pro Ala Leu His
  145           150           155           160
Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Gln Ile Asp
  165           170           175
His Phe Phe Cys Glu Val Pro Ala Leu Leu Xaa Leu Ser Phe Val Asn
  180           185           190
Thr Arg Glu Asn Lys Leu Thr Leu Met Ile Thr Ser Ser Ile Phe Val
  195           200           205
Leu Leu Leu Leu Thr Leu Ile Phe Thr Ser Tyr Gly Ala Ile Ala Gln
  210           215           220
Ala Val Leu Arg Met Gln Ser Thr Thr Gly Leu Gln Lys Val Phe Gly
  225           230           235           240
Thr Cys Gly Ala His His Met Val Val Ser Leu Phe Phe Ile Pro Ala
  245           250           255
Met Cys Met Tyr Leu Gln Pro Pro Ser Gly Asn Ser Gln Asp Gln Gly
  260           265           270
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu Asn Pro
  275           280           285
Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Arg Gly Val Val Lys Arg
  290           295           300
Leu Arg Gly Trp Glu Xaa Ala Cys Val Cys Val Ile Leu Thr Ile Xaa
  305           310           315           320
Trp Ser Leu Ser Ser Gln Xaa Phe Ile His Leu Phe Ile Tyr Gln Pro
  325           330           335
Phe Phe Tyr Ser Leu
  340

```

<210> 1822

<211> 219

<212> PRT

<213> Unknown (H38g740 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(219)

<223> Xaa = Any Amino Acid

<400> 1822

```

Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
   1           5           10           15
Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
  20           25           30
Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Asp Ser Ile Leu
  35           40           45
Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Lys Cys His Pro Leu

```

```

      50              55              60
Tyr His Ser Ala Ile Met Asn Pro Cys Leu Cys Gly Phe Leu Leu Leu
65              70              75              80
Leu Ser Ile Phe Phe Ser Leu Ser Leu Leu Asp Ala Gln Leu Tyr Asn
      85              90
Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn
      100              105              110
Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr
      115              120              125
Phe Asn Asn Asn Ile Ile Leu Tyr Phe Pro Asp Ala Ile Phe Gly Phe
      130              135              140
Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys Ile Val Ser Ser
145              150              155              160
Ile Leu Arg Val Ser Ser Ser Gly Gly Arg Tyr Lys Ala Leu Ser Thr
      165              170              175
Cys Gly Ser His Val Ser Val Val Cys Xaa Val Tyr Gly Thr Gly Val
      180              185              190
Gly Gly Tyr Leu Ser Ser Asp Val Ser Phe Ser Pro Arg Lys Gly Ala
      195              200              205
Val Ala Ser Val Met Tyr Ala Val Val Thr Pro
      210              215

```

<210> 1823

<211> 324

<212> PRT

<213> Unknown (H38g741 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1823

```

Met Ile Ile Ile Cys Asn Asp Ser His Ser Asp Phe Ile Leu Leu Gly
1              5              10              15
Phe Ser Asn Lys Pro His Leu Glu Lys Ile Leu Phe Val Ile Ile Phe
      20              25              30
Ile Phe Tyr Phe Leu Thr Leu Ala Gly Asn Met Val Ile Val Leu Val
      35              40              45
Ser Leu Lys Asp Pro Lys Leu His Ile Pro Met Tyr Phe Phe Leu Ser
50              55              60
Asn Leu Ser Leu Val Asp Leu Cys Leu Thr Ser Ser Cys Val Pro Gln
65              70              75              80
Met Leu Ile Asn Phe Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ile Gly
      85              90              95
Cys Ala Ile Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Tyr
      100              105              110
Val Leu Leu Val Val Met Ala Val Asp Cys Tyr Val Ala Val Cys His
      115              120              125
Pro Leu Gln Asn Thr Met Ile Met His Pro Lys Leu Cys Leu Gln Leu
130              135              140
Ala Ile Leu Ala Trp Gly Thr Gly Leu Ala Gln Ser Leu Ile Gln Ser
145              150              155              160
Pro Ala Thr Leu Arg Leu Pro Phe Cys Ser Gln Arg Met Val Asp Asp
      165              170              175
Val Val Cys Glu Val Pro Ala Leu Ile Gln Leu Ser Ser Thr Asp Thr
      180              185              190
Thr Tyr Ser Glu Ile Gln Met Ser Ile Ala Ser Val Val Leu Leu Val
195              200              205

```

```

Met Pro Leu Ile Ile Ile Leu Ser Ser Ser Gly Ala Ile Ala Lys Ala
  210                215                220
Val Leu Arg Ile Lys Ser Thr Ala Gly Gln Lys Lys Ala Phe Gly Thr
  225                230                235                240
Cys Ile Ser His Leu Leu Val Val Ser Leu Phe Tyr Gly Thr Val Thr
                245                250                255
Gly Val Tyr Leu Gln Pro Lys Asn His Tyr Pro His Glu Trp Gly Lys
  260                265                270
Phe Leu Thr Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Leu
  275                280                285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Ile Arg Leu
  290                295                300
Gly Arg Arg Thr Trp Asp Ser Gln Asn Asn Xaa Gln Gly Xaa His Met
  305                310                315                320
Phe Thr Phe Ala

```

<210> 1824

<211> 218

<212> PRT

<213> Unknown (H38g742 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(218)

<223> Xaa = Any Amino Acid

<400> 1824

```

Leu Pro Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Met Val
  1                5                10                15
Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr
  20                25                30
Gln Ile Pro Phe Phe Val Leu Phe Val Cys Ile Asp Asp Met Leu Leu
  35                40                45
Thr Val Met Ala Tyr Asn Xaa Phe Val Ala Ile Cys His Pro Leu His
  50                55                60
Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu Val Leu Val
  65                70                75                80
Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val
  85                90                95
Leu Gln Gln Leu Thr Phe Phe Lys Asn Val Glu Ile Ser Xaa Phe Phe
  100               105               110
Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Ile
  115               120               125
Ile Asn Asn Ile Leu Cys Ile Leu Asp Ile Pro Ile Phe Gly Phe Leu
  130               135               140
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Ser Ser Ile
  145               150               155               160
Pro Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys
  165               170               175
Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Leu Val
  180               185               190
Gly Tyr Leu Ser Ser Ala Val Leu Pro Ser Pro Arg Lys Ser Met Val
  195               200               205
Ala Ser Val Met Tyr Thr Val Val Thr Pro
  210               215

```

<210> 1825

<211> 124

<212> PRT
 <213> Unknown (H38g743 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(124)
 <223> Xaa = Any Amino Acid

<400> 1825
 Phe Leu Leu Xaa Ala Asn Tyr Ser Ala Glu Glu Arg Phe Leu Leu Leu
 1 5 10 15
 Gly Phe Ser Asp Trp Pro Ser Leu Gln Pro Val Leu Phe Ala Leu Val
 20 25 30
 Leu Leu Cys Tyr Leu Leu Thr Leu Thr Gly Asn Ser Ala Leu Val Leu
 35 40 45
 Leu Ala Glu Lys Asp Pro Arg Leu Gln Thr Pro Arg Cys Met Asn Tyr
 50 55 60
 Phe Leu Cys His Leu Ala Leu Val Asp Ala Gly Phe Thr Thr Ser Val
 65 70 75 80
 Val Pro Pro Leu Leu Ala Asn Leu Arg Gly Pro Ala Leu Leu Xaa Pro
 85 90 95
 Arg Ser His Cys Thr Ala Gln Leu Cys Ala Ser Leu Ala Leu Gly Ser
 100 105 110
 Ala Glu Cys Val Leu Leu Ala Val Met Ala Leu Glu
 115 120

<210> 1826
 <211> 216
 <212> PRT
 <213> Unknown (H38g744 protein)

<220>
 <223> Synthetic construct

<400> 1826
 Ile Leu Glu Ile Ser Phe Thr Thr Val Ser Ile Pro Lys Phe Leu Gly
 1 5 10 15
 Asn Ile Ile Ser Gly Asp Lys Thr Ile Ser Phe Asn Asn Cys Ile Val
 20 25 30
 Gln Leu Phe Phe Phe Ile Leu Leu Gly Val Thr Glu Phe Tyr Leu Leu
 35 40 45
 Ala Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
 50 55 60
 Tyr Leu Ser Ile Met Asn Arg Arg Val Cys Thr Leu Leu Val Phe Thr
 65 70 75 80
 Ser Trp Leu Val Ser Phe Leu Ile Ile Phe Pro Ala Leu Met Leu Leu
 85 90 95
 Leu Lys Leu Asp Tyr Cys Arg Ser Asn Ile Ile Asp His Phe Thr Cys
 100 105 110
 Asp Tyr Phe Pro Leu Leu Gln Leu Ala Cys Ser Asp Thr Lys Phe Leu
 115 120 125
 Glu Val Met Gly Phe Ser Cys Ala Ala Phe Thr Leu Met Phe Thr Leu
 130 135 140
 Ala Leu Ile Phe Leu Ser Tyr Ile Tyr Ile Ile Arg Thr Ile Leu Arg
 145 150 155 160
 Ile Pro Ser Thr Ser Gln Arg Thr Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Met Val Val Ile Ser Ile Ser Tyr Gly Ser Cys Ile Phe Met Tyr
 180 185 190

Ile Lys Pro Ser Ala Lys Asp Arg Val Ser Leu Ser Lys Gly Val Ala
 195 200 205
 Ile Leu Asn Thr Ser Val Ala Pro
 210 215

<210> 1827
 <211> 219
 <212> PRT
 <213> Unknown (H38g745 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(219)
 <223> Xaa = Any Amino Acid

<400> 1827
 Phe Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
 35 40 45
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe Leu Asp Leu
 65 70 75 80
 Leu Ser Phe Phe Phe Ser Leu Ser Leu Leu Asp Ser Gln Leu His Asn
 85 90 95
 Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn
 100 105 110
 Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr
 115 120 125
 Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe
 130 135 140
 Leu Gln Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser
 145 150 155 160
 Ile Leu Arg Val Ser Ser Ser Gly Gly Asn Tyr Lys Ala Phe Ser Thr
 165 170 175
 Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr Gly Val
 180 185 190
 Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala
 195 200 205
 Val Ala Ser Val Met Tyr Met Val Val Thr Pro
 210 215

<210> 1828
 <211> 268
 <212> PRT
 <213> Unknown (H38g746 protein)

<220>
 <223> Synthetic construct

<400> 1828
 Met Met Ala Leu Ile Phe Thr Asp Ser His Leu Gln Ser Pro Met Tyr
 1 5 10 15
 Phe Phe Leu Asn Val Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val
 20 25 30
 Val Thr Pro Lys Leu Leu Val Asn Phe Leu Val Ser Asp Lys Ser Ile

```

      35              40              45
Ser Phe Glu Gly Cys Val Val Gln Leu Ala Phe Phe Val Val His Val
  50              55              60
Thr Ala Glu Ser Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Phe Leu
  65              70              75              80
Ala Ile Cys Gln Pro Leu His Tyr Gly Ser Ile Met Thr Arg Gly Thr
      85              90              95
Cys Leu Gln Leu Val Ala Val Ser Tyr Ala Phe Gly Gly Ala Asn Ser
      100              105              110
Ala Ile Gln Thr Gly Asn Val Phe Ala Leu Pro Phe Cys Gly Pro Asn
      115              120              125
Gln Leu Thr His Tyr Tyr Cys Asp Ile Pro Pro Leu Leu His Leu Ala
      130              135              140
Cys Ala Asn Thr Ala Thr Ala Arg Val Val Leu Tyr Val Phe Ser Ala
      145              150              155              160
Leu Val Thr Leu Leu Pro Ala Ala Val Ile Leu Thr Ser Tyr Cys Leu
      165              170              175
Val Leu Val Ala Ile Gly Arg Met Arg Ser Val Ala Gly Arg Glu Lys
      180              185              190
Asp Leu Ser Thr Cys Ala Ser His Phe Leu Ala Ile Ala Ile Phe Tyr
      195              200              205
Gly Thr Val Val Phe Thr Tyr Val Gln Pro His Gly Ser Thr Asn Asn
      210              215              220
Thr Asn Gly Gln Val Val Ser Val Phe Tyr Thr Ile Ile Ile Pro Met
      225              230              235              240
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala
      245              250              255
Leu Gln Arg Lys Leu Gln Val Asn Ile Phe Pro Gly
      260              265

```

<210> 1829

<211> 316

<212> PRT

<213> Unknown (H38g747 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1829

```

Met Asp Leu Gly Asn Gln Thr Arg Val Ser Glu Phe Leu Leu Leu Gly
  1              5              10              15
Phe Ser Gln Asp Leu Glu Asp Gln Gln Leu Leu Phe Ala Leu Phe Leu
      20              25              30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      35              40              45
Ile Ser Ser Asp Ser His Leu His Thr Pro Arg Tyr Phe Phe Leu Ser
      50              55              60
Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Thr Ala Val Pro Lys
      65              70              75              80
Met Leu Val Asn Ile Gln Val Gln Ser Asn Ala Ile Ser Tyr Ala Asp
      85              90              95
Cys Ile Ala Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr
      100              105              110
Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115              120              125
Pro Leu Tyr Tyr Cys Val Thr Arg Asn Pro Cys Leu Cys Gly Leu Leu
      130              135              140

```

Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser
 145 150 155 160
 Leu Leu Val Leu Arg Val Ser Phe Cys Thr Ser Xaa Val Ile Gln His
 165 170 175
 Phe Tyr Cys Glu Leu Ala Gln Val Leu Arg Leu Thr Cys Ser Asp Thr
 180 185 190
 His Val Asn Tyr Ile Leu Leu Tyr Val Val Ala Gly Leu Leu Asp Phe
 195 200 205
 Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Tyr
 210 215 220
 Ile Leu Arg Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Phe Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
 245 250 255
 Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser Trp Trp Gly Met
 260 265 270
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Cys Leu Arg Asn Arg Asp Ile Lys Arg Thr Leu Glu Thr Leu
 290 295 300
 Leu Gly Arg Met Leu Tyr Ala Gln Xaa Arg Gly His
 305 310 315

<210> 1830

<211> 309

<212> PRT

<213> Unknown (H38g748 protein)

<220>

<223> Synthetic construct

<400> 1830

Met Glu Asn Cys Thr Glu Val Thr Lys Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Ser Val Pro Glu Leu Gln Ile Pro Leu Phe Ile Leu Phe Thr Phe Ile
 20 25 30
 Tyr Leu Leu Thr Leu Cys Gly Asn Leu Gly Met Met Leu Leu Ile Leu
 35 40 45
 Met Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Leu Val Asp Phe Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Met
 65 70 75 80
 Ala Gly Phe Leu Arg Gly Asp Lys Val Ile Ser Tyr Asn Ala Cys Ala
 85 90 95
 Val Gln Met Phe Phe Phe Val Ala Leu Ala Thr Val Glu Asn Tyr Leu
 100 105 110
 Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Thr Thr Met Thr Ala Ser Val Gly Ala Cys Leu Ala Leu
 130 135 140
 Gly Ser Tyr Val Cys Gly Phe Leu Asn Ala Ser Phe His Ile Gly Gly
 145 150 155 160
 Ile Phe Ser Leu Ser Phe Cys Lys Ser Asn Leu Val His His Phe Phe
 165 170 175
 Cys Asp Val Pro Ala Val Met Ala Leu Ser Cys Ser Asp Lys His Thr
 180 185 190
 Ser Glu Val Ile Leu Val Phe Thr Ser Ser Phe Asn Ile Phe Phe Val
 195 200 205
 Leu Leu Val Ile Phe Ile Ser Tyr Leu Phe Ile Phe Ile Thr Ile Leu
 210 215 220
 Lys Met His Ser Ala Lys Gly His Gln Lys Ala Leu Ser Thr Cys Ala

225 230 235 240
 Ser His Phe Thr Ala Val Ser Val Phe Tyr Gly Thr Val Ile Phe Ile
 245 250 255
 Tyr Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Met Ala
 260 265 270
 Ser Val Phe Tyr Ala Met Ile Ile Pro Met Leu Asn Pro Val Val Tyr
 275 280 285
 Ser Leu Arg Asn Arg Glu Val Gln Asn Ala Phe Lys Lys Val Leu Arg
 290 295 300
 Arg Gln Lys Phe Leu
 305

<210> 1831

<211> 313

<212> PRT

<213> Unknown (H38g749 protein)

<220>

<223> Synthetic construct

<400> 1831

Met His Thr Met Val Glu Asn His Thr Gln Val Thr Trp Phe Arg Leu
 1 5 10 15
 Leu Gly Leu Thr Glu Gln Glu Glu Leu Arg Gly Ile Leu Phe Val Leu
 20 25 30
 Phe Leu Leu Met His Ser Val Thr Val Met Gly Asn Leu Gly Met Ile
 35 40 45
 Thr Leu Ile His Ala Asp Pro Gln Leu His Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Val Leu Ser Phe Ile Asp Ser Ser Phe Ser Thr Val Asp Thr
 65 70 75 80
 Pro Arg Leu Leu Glu Ser Phe Leu Ile Ser Ser Gln Ser Ile Ser Phe
 85 90 95
 Ala Gly Cys Met Val Gln Met Ala Leu Met Ile Leu His Gly Thr Ala
 100 105 110
 Glu Cys Leu Leu Leu Ala Ile Met Ala Tyr Asp Arg Phe Thr Ala Ile
 115 120 125
 Cys His Pro Leu Leu Tyr His Thr Ile Ile Ser Gln Cys Leu Cys Ala
 130 135 140
 Leu Leu Val Val Thr Cys Tyr Thr Val Ser Val Ala Asn Ser Ala Leu
 145 150 155 160
 Leu Thr Gly Cys Ile Phe Lys Leu Pro Tyr Cys Gly Pro Asn Val Ile
 165 170 175
 Asn His Tyr Phe Cys Asp Ile Pro Pro Val Leu Gln Leu Ala Gly Ala
 180 185 190
 Asp Thr Tyr Glu Val Glu Thr Ile Ile Phe Ser Leu Cys Ala Leu Leu
 195 200 205
 Ile Leu Phe Thr Ile Thr Ile Ile Pro Val Ser Tyr Ala Tyr Ile Leu
 210 215 220
 Val Thr Ile Cys Arg Met Arg Ser Leu Gln Ala Gln Ser Lys Ala Leu
 225 230 235 240
 Ser Thr Cys Ala Ser His Leu Thr Ile Ile Cys Leu Phe Tyr Ser Thr
 245 250 255
 Ile Thr Phe Met Tyr Ala Gln Pro Ser Ser His Asn Ser Met Glu His
 260 265 270
 Asn Lys Val Met Ser Val Phe Tyr Thr Val Val Ile Arg Arg Leu Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Tyr Ala Leu Lys
 290 295 300
 Arg Arg Cys Leu Cys Lys Leu Ser Ser
 305 310

<210> 1832
 <211> 314
 <212> PRT
 <213> Unknown (H38g750 protein)

<220>
 <223> Synthetic construct

<400> 1832
 Met Glu Asn Lys Thr Glu Val Thr Gln Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Asn Asp Ser Glu Leu Gln Val Pro Leu Phe Ile Thr Phe Pro Phe Ile
 20 25 30
 Tyr Ile Ile Thr Leu Val Gly Asn Leu Gly Ile Ile Val Leu Ile Phe
 35 40 45
 Trp Asp Ser Cys Leu His Asn Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Leu Val Asp Phe Cys Tyr Ser Ser Ala Val Thr Pro Ile Val Met
 65 70 75 80
 Ala Gly Phe Leu Ile Glu Asp Lys Val Ile Ser Tyr Asn Ala Cys Ala
 85 90 95
 Ala Gln Met Tyr Ile Phe Val Ala Phe Ala Thr Val Glu Asn Tyr Leu
 100 105 110
 Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Thr Thr Met Thr Thr Thr Val Cys Ala Arg Leu Ala Ile
 130 135 140
 Gly Ser Tyr Leu Cys Gly Phe Leu Asn Ala Ser Ile His Thr Gly Asp
 145 150 155 160
 Thr Phe Ser Leu Ser Phe Cys Lys Ser Asn Glu Val His His Phe Phe
 165 170 175
 Cys Asp Ile Pro Ala Val Met Val Leu Ser Cys Ser Asp Arg His Ile
 180 185 190
 Ser Glu Leu Val Leu Ile Tyr Val Val Ser Phe Asn Ile Phe Ile Ala
 195 200 205
 Leu Leu Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Ile Thr Ile Leu
 210 215 220
 Lys Met His Ser Ala Ser Val Tyr Gln Lys Pro Leu Ser Thr Cys Ala
 225 230 235 240
 Ser His Phe Ile Ala Val Gly Ile Phe Tyr Gly Thr Ile Ile Phe Met
 245 250 255
 Tyr Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Met Ala
 260 265 270
 Pro Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Val Tyr
 275 280 285
 Ser Leu Arg Asn Lys Glu Val Lys Ser Ala Phe Lys Lys Val Val Glu
 290 295 300
 Lys Ala Lys Leu Ser Val Gly Trp Ser Val
 305 310

<210> 1833
 <211> 312
 <212> PRT
 <213> Unknown (H38g751 protein)

<220>
 <223> Synthetic construct

<400> 1833
 Met Asn Asn Ser Asp Thr Arg Ile Ala Gly Cys Phe Leu Thr Gly Ile

```

1           5           10           15
Pro Gly Leu Glu Gln Leu His Ile Trp Leu Ser Ile Pro Phe Cys Ile
20           25           30
Met Tyr Ile Ala Ala Leu Glu Gly Asn Gly Ile Leu Ile Cys Val Ile
35           40           45
Leu Ser Gln Ala Ile Leu His Glu Pro Met Tyr Ile Phe Leu Ser Met
50           55           60
Leu Ala Ser Ala Asp Val Leu Leu Ser Thr Thr Thr Met Pro Lys Ala
65           70           75           80
Leu Ala Asn Leu Trp Leu Gly Tyr Ser His Ile Ser Phe Asp Gly Cys
85           90           95
Leu Thr Gln Lys Phe Phe Ile His Phe Leu Phe Ile His Ser Ala Val
100          105          110
Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu
115          120          125
Arg Tyr Val Thr Ile Leu Thr Ser Lys Val Ile Gly Lys Ile Val Thr
130          135          140
Ala Thr Leu Ser Arg Ser Phe Ile Ile Met Phe Pro Ser Ile Phe Leu
145          150          155          160
Leu Glu His Leu His Tyr Cys Gln Ile Asn Ile Ile Ala His Thr Phe
165          170          175
Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ser Asp Ile Ser Ile
180          185          190
Asn Val Trp Tyr Gly Leu Ala Ala Ala Leu Leu Ser Thr Gly Leu Asp
195          200          205
Ile Met Leu Ile Thr Val Ser Tyr Ile His Ile Leu Gln Ala Val Phe
210          215          220
Arg Leu Leu Ser Gln Asp Ala Arg Ser Lys Ala Leu Ser Thr Cys Gly
225          230          235          240
Ser His Ile Cys Val Ile Leu Leu Phe Tyr Val Pro Ala Leu Phe Ser
245          250          255
Val Phe Ala Tyr Arg Phe Gly Gly Arg Ser Ile Pro Cys Tyr Val His
260          265          270
Ile Leu Leu Ala Ser Leu Tyr Val Val Ile Pro Pro Met Leu Asn Pro
275          280          285
Val Ile Tyr Gly Val Arg Thr Lys Pro Ile Leu Glu Gly Ala Lys Gln
290          295          300
Met Phe Ser Asn Leu Ala Lys Gly
305          310

```

<210> 1834

<211> 332

<212> PRT

<213> Unknown (H38g752 protein)

<220>

<223> Synthetic construct

<400> 1834

```

Ser Ile Leu Phe Leu Tyr Phe Ser Leu Leu Gln Ala Ser Ser Asp Phe
1           5           10           15
Leu Ile Thr Leu Met Lys Asn Cys Thr Glu Val Thr Glu Phe Ile Leu
20           25           30
Leu Gly Leu Thr Asn Ala Pro Glu Leu Gln Val Pro Leu Leu Ile Met
35           40           45
Phe Thr Leu Ile Tyr Leu Val Asn Val Val Gly Asn Leu Gly Met Ile
50           55           60
Val Leu Ile Val Trp Asp Ile His Leu His Thr Pro Met Tyr Phe Phe
65           70           75           80
Leu Ser His Leu Ser Leu Val Asp Phe Cys Tyr Ser Ser Ala Val Thr
85           90           95

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Pro Thr Val Ile Ala Gly Leu Val Ile Gly Asp Lys Val Ile Ser Tyr
      100                      105                      110
Asn Ala Cys Ala Ala Gln Met Phe Phe Phe Ala Ala Phe Ala Thr Val
      115                      120                      125
Glu Asn Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Asp Ala Val
      130                      135                      140
Cys Lys Pro Leu His Tyr Thr Thr Thr Met Thr Thr Ser Val Cys Ala
      145                      150                      155                      160
Cys Leu Ala Ile Ile Cys Tyr Val Cys Gly Phe Leu Asn Ala Ser Ile
      165                      170                      175
His Ile Gly Glu Thr Phe Ser Leu Ser Phe Cys Met Ser Asn Glu Val
      180                      185                      190
His Cys Phe Phe Cys Asp Val Pro Pro Val Met Ala Leu Ser Cys Cys
      195                      200                      205
Asp Arg His Val Asn Glu Leu Val Leu Ile Tyr Val Ala Ser Phe Asn
      210                      215                      220
Ile Phe Ser Ala Ile Leu Val Ile Leu Ile Ser Tyr Leu Phe Ile Phe
      225                      230                      235                      240
Ile Thr Ile Leu Lys Met His Ser Ala Ser Gly Tyr Gln Lys Ala Leu
      245                      250                      255
Ser Thr Cys Ala Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr
      260                      265                      270
Ile Ile Phe Met Tyr Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr
      275                      280                      285
Asp Lys Leu Ala Ser Val Phe Tyr Thr Met Ile Ile Pro Met Leu Asn
      290                      295                      300
Pro Leu Val Tyr Ser Leu Arg Asn Asn Glu Val Lys Ser Ala Phe Lys
      305                      310                      315                      320
Lys Val Ile Glu Lys Ala Lys Leu Ser Leu Leu Leu
      325                      330

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<210> 1835

<211> 318

<212> PRT

<213> Unknown (H38g753 protein)

<220>

<223> Synthetic construct

<400> 1835

```

Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe
  1      5      10      15
Leu Thr Gly Ile Pro Gly Leu Glu Ala His Phe Trp Ile Ala Ile
      20      25      30
Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu
      35      40      45
Ile Leu Val Ile Ala Met Asp Asn Ala Leu His Ala Pro Met Tyr Leu
      50      55      60
Phe Leu Cys Leu Leu Ser Leu Thr Asp Leu Ala Leu Ser Ser Thr Thr
      65      70      75      80
Val Pro Lys Met Leu Ala Ile Leu Trp Leu His Ala Gly Glu Ile Ser
      85      90      95
Phe Gly Gly Cys Leu Ala Gln Met Phe Cys Val His Ser Ile Tyr Ala
      100     105     110
Leu Glu Ser Ser Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
      115     120     125
Ile Cys Asn Pro Leu Arg Tyr Thr Thr Ile Leu Asn His Ala Val Ile
      130     135     140
Gly Arg Ile Gly Phe Val Gly Leu Phe Arg Ser Val Ala Ile Val Ser
      145     150     155     160
Pro Phe Ile Phe Leu Leu Arg Arg Leu Pro Tyr Cys Gly His Arg Val

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      165      170      175
Met Thr His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys
      180      185      190
Ala Asn Ile Thr Val Asn Ile Val Tyr Gly Leu Thr Val Ala Leu Leu
      195      200      205
Ala Met Gly Leu Asp Ser Ile Leu Ile Ala Ile Ser Tyr Gly Phe Ile
      210      215      220
Leu His Ala Val Phe His Leu Pro Ser His Asp Ala Gln His Lys Ala
      225      230      235      240
Leu Ser Thr Cys Gly Ser His Ile Gly Ile Ile Leu Val Phe Tyr Ile
      245      250      255
Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Glu Val
      260      265      270
Pro Lys His Val His Ile Phe Leu Ala Asn Leu Tyr Val Leu Val Pro
      275      280      285
Pro Val Leu Asn Pro Ile Leu Tyr Gly Ala Arg Thr Lys Glu Ile Arg
      290      295      300
Ser Arg Leu Leu Lys Leu Leu His Leu Gly Lys Thr Ser Ile
      305      310      315

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<210> 1836

<211> 330

<212> PRT

<213> Unknown (H38g754 protein)

<220>

<223> Synthetic construct

<400> 1836

```

His Ile Glu Pro Gly Asn Asp Thr Gln Ile Ser Glu Phe Leu Leu Leu
1      5      10      15
Gly Leu Ser Asp Lys Pro Glu Leu Gln Pro Phe Leu Phe Gly Leu Phe
      20      25      30
Phe Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Thr Ile Ser Asp Ser His Leu His Thr Pro Val Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Phe Ala Asp Ile Cys Phe Ile Ser Thr Thr Ile Pro
      65      70      75      80
Lys Met Leu Val Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala
      85      90      95
Gly Cys Ile Thr Gln Met Cys Phe Phe Val Leu Leu Glu Ala Leu Asp
      100      105      110
Ser Leu Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys
      115      120      125
His Pro Leu His Tyr Met Val Ile Met Ser Pro Trp Phe Cys Gly Leu
      130      135      140
Leu Val Leu Ala Ser Trp Ile Ile Met Ser Pro Trp Leu Cys Gly Leu
      145      150      155      160
Leu Val Leu Ala Ser Trp Ile Ile Ser Asp Leu Asp Ser Ser Leu His
      165      170      175
Ser Leu Met Val Leu Ser Leu Pro Phe Cys Thr Asp Phe Gln Ile Pro
      180      185      190
His Phe Val Tyr Glu Leu Asn Gln Val Ile Arg Leu Ala Gly Ser Asp
      195      200      205
Thr Phe Leu Asn Asp Met Ala Met Tyr Phe Ala Val Gly Pro Leu Gly
      210      215      220
Gly Val Pro Leu Ala Gly Ile Leu Tyr Leu Tyr Cys Lys Ile Val Phe
      225      230      235      240
Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser
      245      250      255

```

Thr Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Arg Ser
 260 265 270
 Leu Gly Val Tyr Phe Ser Ser Ala Pro Thr Gln Asn Ser His Ser Gly
 275 280 285
 Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
 290 295 300
 Phe Ile Cys Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Asn Gln
 305 310 315 320
 Phe Ile Arg Val Val Pro Phe Phe Arg Lys
 325 330

<210> 1837

<211> 312

<212> PRT

<213> Unknown (H38g755 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1837

Thr Thr Ser Ile Asp Asp Asn Thr Glu Val Asn Glu Phe Ile Xaa Leu
 1 5 10 15
 Gly Leu Thr Lys Ala Pro Glu Leu Gln Val His Leu Phe Val Leu Phe
 20 25 30
 Asn Phe Ile Tyr Leu Phe Thr Leu Ser Gly Asn Leu Gly Met Met Leu
 35 40 45
 Leu Ile Leu Leu Asp Ser Arg Leu His Thr Ser Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Val Asp Phe Cys Tyr Ser Glu Thr Val Thr Pro
 65 70 75 80
 Lys Met Met Ala Gly Leu Leu Ile Ala His Lys Val Ile Ser Tyr Asn
 85 90 95
 Val Cys Ala Ala Gln Met Phe Phe Phe Ala Val Phe Ala Thr Val Glu
 100 105 110
 Ser Tyr Phe Leu Thr Ser Val Ala Tyr Asp Cys Tyr Arg Val Met Cys
 115 120 125
 Lys Pro Leu His Tyr Thr Thr Thr Met Thr Thr Asn Val Cys Ala Ser
 130 135 140
 Leu Ala Ile Ala Cys Tyr Val Leu Gly Leu Leu Thr Ala Ala Val Asp
 145 150 155 160
 Ile Gly Asp Ile Cys Met Ser Asn Glu Ile His His Phe Phe Cys Asp
 165 170 175
 Ile Leu Ala Val Met Thr Leu Thr Cys Ser Asn Lys His Ile Asn Glu
 180 185 190
 Leu Ile Leu Val Leu Leu Gln Ala Ile Phe Phe Thr Leu Leu Val Ile
 195 200 205
 Leu Ile Ser Cys Leu Phe Val Phe Val Phe Val Thr Ile Leu Lys Met
 210 215 220
 His Leu Phe Lys Ser Tyr Lys Lys Val Leu Ser Thr Tyr Gly Ser His
 225 230 235 240
 Leu Thr Ala Val Pro Leu Phe Tyr Glu Thr Val Leu Ile Thr Tyr Val
 245 250 255
 Gln Pro Ser Ser Ser His Phe Met Asn Thr Glu Lys Ile Val Ser Val
 260 265 270
 Phe His Ile Met Val Ile Pro Met Leu Ile Pro Val Val Tyr Ser Leu
 275 280 285
 Arg Asn Asn Glu Val Lys Ser Ala Phe Lys Thr Val Val Glu Glu Thr

290 295 300
 Lys Tyr Phe Leu Gly Leu Val Phe
 305 310

<210> 1838
 <211> 315
 <212> PRT
 <213> Unknown (H38g756 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 1838
 Met Gly Gly Phe Gly Thr Asn Ile Ser Ser Thr Thr Ser Phe Thr Leu
 1 5 10 15
 Thr Gly Phe Pro Glu Met Lys Gly Leu Glu His Trp Leu Ala Ala Leu
 20 25 30
 Leu Leu Leu Cys Ala Ile Ser Phe Leu Gly Asn Ile Leu Ile Leu
 35 40 45
 Phe Ile Ile Lys Glu Glu Gln Ser Leu His Gln Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Leu Phe Ser Val Asn Asp Leu Gly Val Ser Phe Ser Thr Leu
 65 70 75 80
 Pro Thr Val Leu Ala Ala Val Cys Phe His Ala Pro Glu Thr Thr Phe
 85 90 95
 Asp Ala Cys Leu Ala Gln Thr Phe Phe Ile His Phe Ser Ser Trp Thr
 100 105 110
 Glu Phe Gly Ile Leu Leu Ala Met Ser Phe Asp His Tyr Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Arg Tyr Ala Thr Val Leu Thr Asp Val Arg Val Ala
 130 135 140
 His Asn Gly Ile Ser Ile Val Ile Arg Ser Phe Cys Met Val Phe Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Lys Arg Leu Pro Phe Cys Lys Ala Ser Val Val
 165 170 175
 Leu Ala His Ser Tyr Cys Leu His Ala Asp Leu Ile Arg Leu Pro Cys
 180 185 190
 Gly Asp Thr Thr Ile Asn Ser Met Tyr Gly Leu Phe Ile Val Ile Ser
 195 200 205
 Ala Phe Gly Val Asp Ser Leu Leu Ile Leu Leu Ser Tyr Val Leu Ile
 210 215 220
 Leu His Ser Val Leu Ala Ile Ala Ser Arg Gly Glu Arg Leu Lys Thr
 225 230 235 240
 Leu Asn Thr Cys Val Ser His Ile Tyr Ala Val Leu Ile Phe Tyr Val
 245 250 255
 Pro Met Val Ser Val Ser Met Val His Arg Phe Gly Arg His Ala Pro
 260 265 270
 Glu Tyr Val His Lys Phe Met Ser Ser Leu Tyr Leu Pro Met Leu Tyr
 275 280 285
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile Arg Arg Arg Leu His
 290 295 300
 Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Lys
 305 310 315

<210> 1839
 <211> 329
 <212> PRT

<213> Unknown (H38g757 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1839

```

Met Glu Pro Glu Asn Asp Thr Arg Ile Ser Glu Phe Arg Leu Leu Gly
 1           5           10          15
Phe Ser Glu Glu Pro Arg Leu Gln Arg Phe Arg Phe Leu Phe Gly Val
      20           25           30
Phe Leu Ser Met Tyr Leu Ile Ile Val Phe Gly Asn Leu Leu Ile Ile
      35           40           45
Leu Val Ile Ile Leu Cys Ser His Leu His Thr Ser Met Tyr Phe Phe
      50           55           60
Leu Ser Asn Leu Ser Phe Val Asp Ile Cys Phe Ala Ser Thr Arg Val
      65           70           75           80
Pro Lys Met Leu Val Asn Ile Gln Ala Gln Ser Lys Val Ile Thr Ser
      85           90           95
Ala Gly Cys Ile Thr Gln Met Tyr Phe Phe Ile His Phe Val Gly Leu
      100          105          110
Asp Ser Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile
      115          120          125
Cys His Pro Leu Tyr Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly
      130          135          140
Leu Leu Val Leu Val Ser Trp Ile Thr Ser Val Leu His Ser Leu Leu
      145          150          155          160
His Ser Leu Met Val Leu Gln Leu Ser Leu Cys Arg Glu Leu Glu Ile
      165          170          175
Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser
      180          185          190
Asp Thr Phe Leu Asn Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu
      195          200          205
Gly Gly Gly Ser Leu Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Thr Val
      210          215          220
Ser Ser Ile Cys Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe
      225          230          235          240
Ser Thr Cys Pro Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr
      245          250          255
Ser Leu Gly Val Tyr Leu Ser Ser Ala Ala Ser His Asn Ser His Ser
      260          265          270
Gly Ala Ile Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
      275          280          285
Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys
      290          295          300
Asn Ser Leu Gly Gly Lys Leu Glu Lys Gly Gln Leu Ser Leu Gly Leu
      305          310          315          320
Lys Leu Tyr Pro Xaa Leu Gln Gly Ser
      325

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<210> 1840

<211> 320

<212> PRT

<213> Unknown (H38g758 protein)

<220>

<223> Synthetic construct

<400> 1840

```

Met Glu Arg Gly Asn Gln Thr Glu Val Gly Asn Phe Leu Leu Leu Gly
 1           5           10           15
Phe Ala Glu Asp Ser Asp Met Gln Leu Leu Leu His Gly Leu Phe Leu
 20           25           30
Ser Met Tyr Leu Val Thr Ile Ile Gly Asn Leu Leu Ile Ile Leu Thr
 35           40           45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50           55           60
Asn Leu Ser Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys
 65           70           75           80
Met Leu Val Asn Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly
 85           90           95
Cys Leu Thr Gln Ile Phe Phe Phe Ile Ala Phe Gly Cys Leu Asp Asn
 100          105          110
Leu Leu Leu Thr Met Thr Ala Tyr Asp Arg Phe Val Ala Ile Cys Tyr
 115          120          125
Pro Leu His Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu
 130          135          140
Val Leu Gly Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr
 145          150          155          160
Leu Thr Ile Leu Arg Leu Ser Ser Cys Thr Asn Met Glu Ile Pro His
 165          170          175
Phe Phe Cys Asp Pro Ser Glu Val Leu Lys Leu Ala Cys Ser Asp Thr
 180          185          190
Phe Ile Asn Asn Ile Val Met Cys Phe Val Thr Ile Val Leu Gly Val
 195          200          205
Phe Pro Leu Cys Gly Ile Leu Phe Ser Tyr Ser Gln Ile Phe Ser Ser
 210          215          220
Val Leu Arg Val Ser Ser Ala Arg Gly Gln His Lys Ala Phe Thr Thr
 225          230          235          240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
 245          250          255
Gly Val Tyr Leu Ser Ser Ala Val Thr Pro Pro Ser Arg Thr Ser Leu
 260          265          270
Ala Ala Ser Val Met His Thr Met Val Thr Pro Met Leu Asn Pro Phe
 275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Ser Leu Gly Arg Leu
 290          295          300
Leu Leu Arg Ala Thr Ser Leu Lys Glu Gly Thr Ile Ala Lys Leu Ser
 305          310          315          320

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<210> 1841

<211> 328

<212> PRT

<213> Unknown (H38g759 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1841

```

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu
 1           5           10           15
Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys
 20           25           30
Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala
 35           40           45

```

Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys
 50 55 60
 Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu
 100 105 110
 Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys
 115 120 125
 His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe
 130 135 140
 Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln Leu
 145 150 155 160
 Gln Asn Leu Ile Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile
 165 170 175
 Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys
 180 185 190
 Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe
 195 200 205
 Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val
 210 215 220
 Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Ser Tyr Lys Ala Phe
 225 230 235 240
 Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr
 245 250 255
 Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys
 260 265 270
 Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu Trp
 290 295 300
 Gln Pro Cys Ser Arg Thr Ala Ala Gln Ser Pro Ser Gln Tyr Leu His
 305 310 315 320
 Leu Phe His Ser Phe Cys Arg Met
 325

<210> 1842

<211> 210

<212> PRT

<213> Unknown (H38g760 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(210)

<223> Xaa = Any Amino Acid

<400> 1842

Ser Val Lys Tyr Leu Asn Glu Ser Phe Pro Glu Asp Phe Ile Leu Met
 1 5 10 15
 Gly Phe Val Lys Tyr Pro Trp Leu Asp Phe Leu Leu Phe Cys Val Leu
 20 25 30
 Leu Thr Phe Tyr Met Phe Thr Leu Leu Gly Asn Ser Ala Ile Ile Leu
 35 40 45
 Val Ser Gln Leu Asp Ser Gln Leu His Ser Pro Met Tyr Phe Leu Leu
 50 55 60
 Thr Ser Leu Ser Val Leu Tyr Leu Cys Phe Thr Thr Thr Thr Val Pro
 65 70 75 80
 Gln Met Leu Phe Asn Leu Gly Gly Thr Asn Lys Asn Ile Thr Xaa Ile

```

      85      90      95
Gly Cys Met Ala Gln Ala Tyr Val Phe His Trp Leu Ala Cys Ile Glu
      100      105      110
Cys Val Leu Leu Gly Ile Val Ala Leu Asp Cys Tyr Val Ala Val Cys
      115      120      125
Lys Pro Pro Arg Tyr Thr Ile Ile Ile Asp His Lys Val Cys Leu His
      130      135      140
Leu Ser Ser Thr Ala Trp Leu Ile Gly Leu Ala Asn Ser Leu Leu Gln
      145      150      155      160
Ser Thr Ile Thr Ile Gln Leu Pro Leu Xaa Arg Cys Ile Ala Gln Ile
      165      170      175
Phe Leu Xaa Leu Glu Ser Val Thr Xaa Gln Ser Leu Thr Val Thr Tyr
      180      185      190
Leu Xaa Asp Leu Leu Gln His Ser Ile Xaa Gly Gln Leu His Ala Gly
      195      200      205
Glu Leu
      210

```

<210> 1843

<211> 315

<212> PRT

<213> Unknown (H38g761 protein)

<220>

<223> Synthetic construct

<400> 1843

```

Met Glu Pro Glu Lys Gln Thr Glu Ile Ser Glu Phe Phe Leu Gln Gly
1      5      10      15
Leu Ser Glu Lys Pro Glu His Gln Thr Leu Leu Phe Thr Met Phe Leu
      20      25      30
Ser Thr Tyr Leu Val Thr Ile Ile Gly Asn Ala Leu Ile Ile Leu Ala
      35      40      45
Ile Ile Thr Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
      50      55      60
Asn Leu Ser Leu Val Asp Thr Leu Leu Ser Ser Thr Thr Val Pro Lys
      65      70      75      80
Met Leu Ala Asn Ile Gln Ala Gln Ser Arg Ala Ile Pro Phe Val Gly
      85      90      95
Cys Leu Thr Gln Met Tyr Ala Phe His Leu Phe Gly Thr Met Asp Ser
      100      105      110
Phe Leu Leu Ala Val Met Ala Ile Asp Arg Phe Val Ala Ile Val His
      115      120      125
Pro Gln Arg Tyr Leu Val Leu Met Cys Ser Pro Val Cys Gly Leu Leu
      130      135      140
Leu Gly Ala Ser Trp Met Ile Thr Asn Leu Gln Ser Leu Ile His Thr
      145      150      155      160
Cys Leu Met Ala Gln Leu Thr Phe Cys Ala Gly Ser Glu Ile Ser His
      165      170      175
Phe Phe Cys Asp Leu Met Pro Leu Leu Lys Leu Ser Gly Ser Asp Thr
      180      185      190
His Thr Asn Glu Leu Val Ile Phe Ala Phe Gly Ile Val Val Gly Thr
      195      200      205
Ser Pro Phe Ser Cys Ile Leu Leu Ser Tyr Ile Arg Ile Phe Trp Thr
      210      215      220
Val Phe Lys Ile Pro Ser Thr Arg Gly Lys Trp Lys Ala Phe Ser Thr
      225      230      235      240
Cys Gly Leu His Leu Thr Val Val Ser Leu Ser Tyr Gly Thr Ile Phe
      245      250      255
Ala Val Tyr Leu Gln Pro Thr Ser Pro Ser Ser Ser Gln Lys Asp Lys
      260      265      270

```

Ala Ala Ala Leu Met Cys Gly Val Phe Ile Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Ile Arg Asn Lys Asp Met Lys Ala Ala Leu Gly Lys Leu
 290 295 300
 Ile Gly Lys Val Ala Val Pro Cys Pro Arg Pro
 305 310 315

<210> 1844
 <211> 316
 <212> PRT
 <213> Unknown (H38g762 protein)

<220>
 <223> Synthetic construct

<400> 1844
 Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Val Asp Gly Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys Leu
 20 25 30
 Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala Leu
 35 40 45
 Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu Gly
 50 55 60
 His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro Arg
 65 70 75 80
 Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln Ala
 85 90 95
 Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu Ser
 100 105 110
 Tyr Leu Leu Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys Arg
 115 120 125
 Pro Leu Arg Tyr Gly Ala Leu Val Thr Pro Trp Ala Cys Ala Ser Leu
 130 135 140
 Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His Thr
 145 150 155 160
 Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg Pro
 165 170 175
 Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp Thr
 180 185 190
 Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val Leu
 195 200 205
 Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val Ala
 210 215 220
 Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Tyr Cys Gly Ala
 225 230 235 240
 His Leu Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser Val Leu Ser
 245 250 255
 Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr Asp Arg Leu
 260 265 270
 Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn Pro Phe Ile
 275 280 285
 Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Arg Gly Leu
 290 295 300
 Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala
 305 310 315

<210> 1845
 <211> 312
 <212> PRT
 <213> Unknown (H38g763 protein)

<220>

<223> Synthetic construct

<400> 1845

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1          5          10          15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser
      20          25          30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
      35          40          45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
      50          55          60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
      65          70          75          80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
      85          90          95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
      100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys
      115          120          125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
      130          135          140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
      145          150          155          160
Ala Phe Leu Val Asn Leu Ala Phe Cys Gly Pro Asn Val Leu Asp Ser
      165          170          175
Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr
      180          185          190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
      195          200          205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr
      210          215          220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
      225          230          235          240
Ser Ala His Ser Thr Val Val Leu Leu Phe Phe Gly Pro Pro Met Phe
      245          250          255
Val Tyr Thr Arg Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
      260          265          270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
      275          280          285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
      290          295          300
Leu Val Ile Tyr Lys Arg Ile Ser
      305          310

```

<210> 1846

<211> 318

<212> PRT

<213> Unknown (H38g764 protein)

<220>

<223> Synthetic construct

<400> 1846

```

Met Trp Gln Lys Asn Gln Thr Ser Leu Ala Asp Phe Ile Leu Glu Gly
 1          5          10          15
Leu Phe Asp Asp Ser Leu Thr His Leu Phe Leu Phe Ser Leu Thr Met
      20          25          30
Val Val Phe Leu Ile Ala Val Ser Gly Asn Thr Leu Thr Ile Leu Leu
      35          40          45

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Ile Cys Ile Asp Pro Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50          55          60
Gln Leu Ser Leu Met Asp Leu Met His Val Ser Thr Thr Ile Leu Lys
65          70          75          80
Met Ala Thr Asn Tyr Leu Ser Gly Lys Lys Ser Ile Ser Phe Val Gly
          85          90          95
Cys Ala Thr Gln His Phe Leu Tyr Leu Cys Leu Gly Gly Ala Glu Cys
          100          105          110
Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
          115          120          125
Pro Leu Arg Tyr Ala Val Leu Met Asn Lys Lys Val Gly Leu Met Met
          130          135          140
Ala Val Met Ser Trp Leu Gly Ala Ser Val Asn Ser Leu Ile His Met
145          150          155          160
Ala Ile Leu Met His Phe Pro Phe Cys Gly Pro Arg Lys Val Tyr His
          165          170          175
Phe Tyr Cys Glu Phe Pro Ala Val Val Lys Leu Val Cys Gly Asp Ile
          180          185          190
Thr Val Tyr Glu Thr Thr Val Tyr Ile Ser Ser Ile Leu Leu Leu Leu
          195          200          205
Pro Ile Phe Leu Ile Ser Thr Ser Tyr Val Phe Ile Leu Gln Ser Val
210          215          220
Ile Gln Met Arg Ser Ser Gly Ser Lys Arg Asn Ala Phe Ala Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Ser Leu Trp Phe Gly Ala Cys Ile Phe
          245          250          255
Ser Tyr Met Arg Pro Arg Ser Gln Cys Thr Leu Leu Gln Asn Lys Val
          260          265          270
Gly Ser Val Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Ser Leu Ile
          275          280          285
Tyr Thr Leu Arg Asn Lys Asp Val Ala Lys Ala Leu Arg Arg Val Leu
          290          295          300
Arg Arg Asp Val Ile Thr Gln Cys Ile Gln Arg Leu Gln Leu
305          310          315

```

<210> 1847

<211> 105

<212> PRT

<213> Unknown (H38g765 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(105)

<223> Xaa = Any Amino Acid

<400> 1847

```

Thr Leu Cys Ala Thr Ala Xaa Leu Asp His Phe Ile Cys Glu Leu Pro
 1          5          10          15
Ala Leu Leu Lys Leu Ala Arg Gly Gly Ile Gly Asp Thr Thr Glu Asn
          20          25          30
Gln Met Phe Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val
          35          40          45
Ile Leu Ala Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg
          50          55          60
Phe Ser Gly Gly Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu
65          70          75          80
Thr Ala Val Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln
          85          90          95
Pro Ala Gln Arg Asn Asn Gln Ala Arg

```

100

105

<210> 1848
 <211> 104
 <212> PRT
 <213> Unknown (H38g766 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(104)
 <223> Xaa = Any Amino Acid

<400> 1848
 Ile His Ala Leu Ser Ala Ile Glu Ser Thr Ile Leu Leu Ala Met Ala
 1 5 10 15
 Phe Asn Arg Tyr Val Ala Ile Cys His Pro Leu Arg His Ala Ala Val
 20 25 30
 Leu Asn Asn Thr Val Thr Ala Gln Ile Gly Ile Val Ala Val Val Arg
 35 40 45
 Gly Ser Leu Phe Phe Phe Pro Leu Leu Ile Lys Arg Leu Ala
 50 55 60
 Phe Cys His Ser Asn Val Leu Ser His Ser Tyr Cys Val His Gln Asp
 65 70 75 80
 Val Met Lys Leu Ala Tyr Ala Asp Asn Leu Pro Asn Val Val Tyr Gly
 85 90 95
 Leu Asn Xaa Pro Phe Trp Leu Val
 100

<210> 1849
 <211> 320
 <212> PRT
 <213> Unknown (H38g767 protein)

<220>
 <223> Synthetic construct

<400> 1849
 Met Glu Thr Gly Asn Gln Thr His Ala Gln Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Phe Ser Ala Thr Ser Glu Ile Gln Phe Ile Leu Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Phe Thr Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile Cys Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ala Asp Leu Cys Phe Thr Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Leu Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr Ala Gly
 85 90 95
 Cys Leu Ser Gln Ile Phe Phe Phe Thr Ser Phe Gly Cys Leu Asp Asn
 100 105 110
 Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His
 115 120 125
 Pro Leu His Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu
 130 135 140
 Val Leu Gly Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr
 145 150 155 160
 Leu Thr Val Leu Arg Leu Ser Phe Cys Thr Lys Met Glu Ile Pro His
 165 170 175

```

Phe Phe Cys Asp Leu Leu Glu Val Leu Lys Leu Ala Cys Ser Asp Thr
      180      185      190
Phe Ile Asn Asn Val Val Ile Tyr Phe Ala Thr Gly Val Leu Gly Val
      195      200      205
Ile Ser Phe Thr Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Val Phe Ser
      210      215      220
Ile Leu Arg Ile Ser Ser Ala Gly Arg Lys His Lys Ala Phe Ser Thr
      225      230      235      240
Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Phe
      245      250      255
Gly Val Tyr Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu
      260      265      270
Val Ala Ser Val Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu Arg Asn Thr Asp Met Lys Arg Ala Leu Gly Arg Leu
      290      295      300
Leu Ser Arg Ala Thr Phe Phe Asn Gly Asp Ile Thr Ala Gly Leu Ser
      305      310      315      320

```

<210> 1850

<211> 312

<212> PRT

<213> Unknown (H38g768 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1850

```

Met Gly Asp Asn Gln Ser Arg Val Thr Glu Phe Ile Leu Val Gly Phe
  1      5      10      15
Gln Leu Ser Val Glu Met Glu Val Leu Leu Phe Trp Ile Phe Ser Leu
      20      25      30
Leu Tyr Leu Phe Ser Leu Leu Ala Asn Gly Met Ile Leu Gly Leu Ile
      35      40      45
Cys Leu Asp Pro Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Ser His
      50      55      60
Leu Ala Val Ile Asp Ile Tyr Tyr Ala Ser Ser Asn Leu Leu Asn Met
      65      70      75      80
Leu Glu Asn Leu Val Lys His Lys Lys Asn Tyr Pro Phe Ile Ser Cys
      85      90      95
Ile Met Gln Met Ala Leu Tyr Leu Thr Phe Ala Ala Ala Val Cys Met
      100      105      110
Ile Leu Val Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro
      115      120      125
Leu His Tyr Thr Val Ile Met Asn Trp Arg Val Cys Thr Val Leu Ala
      130      135      140
Ile Thr Ser Trp Ala Cys Gly Phe Ser Leu Ala Leu Ile Asn Leu Ile
      145      150      155      160
Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Gln Glu Val Asn His Phe
      165      170      175
Phe Gly Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp
      180      185      190
Ile Asn Glu Ile Phe Val Phe Ala Gly Gly Val Phe Val Leu Val Gly
      195      200      205
Pro Leu Ser Leu Met Leu Ile Ser Tyr Met Arg Ile Leu Leu Ala Ile
      210      215      220
Leu Lys Ile Gln Ser Lys Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys

```

<210> 1851
<211> 319
<212> PRT
<213> Unknown (H38g769 protein)

<400>	1851															
Met	Glu	Pro	Gly	Asn	Asp	Thr	Gln	Ile	Ser	Glu	Phe	Leu	Leu	Leu	Gly	
1				5					10					15		
Phe	Ser	Gln	Glu	Pro	Gly	Leu	Gln	Pro	Phe	Leu	Phe	Gly	Leu	Phe	Leu	
		20						25					30			
Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala	
		35					40					45				
Thr	Ile	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	
	50					55					60					
Asn	Leu	Ser	Phe	Ala	Asp	Ile	Cys	Val	Thr	Ser	Thr	Thr	Ile	Pro	Lys	
65					70					75					80	
Met	Leu	Met	Asn	Ile	Gln	Thr	Gln	Asn	Lys	Val	Ile	Thr	Tyr	Ile	Ala	
			85						90					95		
Cys	Leu	Met	Gln	Met	Tyr	Phe	Phe	Ile	Leu	Phe	Ala	Gly	Phe	Glu	Asn	
			100					105					110			
Phe	Leu	Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His	
		115					120					125				
Pro	Leu	His	Tyr	Met	Val	Ile	Met	Asn	Pro	His	Leu	Cys	Gly	Leu	Leu	
	130					135					140					
Val	Leu	Ala	Ser	Trp	Thr	Met	Ser	Ala	Leu	Tyr	Ser	Leu	Leu	Gln	Ile	
145					150					155					160	
Leu	Met	Val	Val	Arg	Leu	Ser	Phe	Cys	Thr	Ala	Leu	Glu	Ile	Pro	His	
			165						170					175		
Phe	Phe	Cys	Glu	Leu	Asn	Gln	Val	Ile	Gln	Leu	Ala	Cys	Ser	Asp	Ser	
		180						185					190			
Phe	Leu	Asn	His	Met	Val	Ile	Tyr	Phe	Thr	Val	Ala	Leu	Leu	Gly	Gly	
	195					200					205					
Gly	Pro	Leu	Thr	Gly	Ile	Leu	Tyr	Ser	Tyr	Ser	Lys	Ile	Ile	Ser	Ser	
	210				215						220					
Ile	His	Ala	Ile	Ser	Ser	Ala	Gln	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr	
225					230					235					240	
Cys	Ala	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly	Ala	Ile	Leu	
			245						250					255		
Gly	Val	Tyr	Leu	Ser	Ser	Ala	Ala	Thr	Arg	Asn	Ser	His	Ser	Ser	Ala	
		260						265					270			
Thr	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	
	275					280						285				
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Ile	Lys	Arg	Ala	Leu	Gly	Ile	His	
	290				295						300					
Leu	Leu	Trp	Gly	Thr	Met	Lys	Gly	Gln	Phe	Phe	Lys	Lys	Cys	Pro		
305					310					315						

<210> 1852
 <211> 74
 <212> PRT
 <213> Unknown (H38g770 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(74)
 <223> Xaa = Any Amino Acid

<400> 1852
 Gly Asp Thr Thr Glu Asn Gln Met Phe Ala Ala Arg Val Val Ile Leu
 1 5 10 15
 Leu Leu Pro Tyr Asp Val Ile Leu Ala Ser Xaa Gly Ala Val Ala Arg
 20 25 30
 Ala Val Cys Cys Met Arg Phe Ser Gly Gly Pro Arg Arg Ala Leu Gly
 35 40 45
 Thr Cys Gly Ser His Pro Thr Ala Val Trp Leu Phe Xaa Gly Ser Gly
 50 55 60
 Lys Xaa Thr Tyr Leu Gln Ala Ala Gln Leu
 65 70

<210> 1853
 <211> 309
 <212> PRT
 <213> Unknown (H38g771 protein)

<220>
 <223> Synthetic construct

<400> 1853
 Met Lys Ser Trp Asn Asn Thr Ile Ile Leu Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Ile Ser Glu Glu Pro Glu Leu Gln Ala Phe Leu Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Val Gly Ile Cys Phe Val Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Ile Gln Thr His Asn Lys Val Ile Thr Tyr Ala Gly
 85 90 95
 Cys Ile Thr Gln Met Cys Phe Phe Leu Phe Val Gly Leu Asp Asn
 100 105 110
 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu
 130 135 140
 Val Leu Ala Ser Trp Ile Met Ser Val Leu Asn Ser Met Leu Gln Ser
 145 150 155 160
 Leu Met Val Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His
 165 170 175
 Phe Phe Cys Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr
 180 185 190
 Phe Leu Asn Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly
 195 200 205
 Gly Pro Leu Thr Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser

210 215 220
 Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Cys Leu
 245 250 255
 Gly Val Tyr Leu Ser Ser Ala Ala Thr His Asn Ser His Thr Gly Ala
 260 265 270
 Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys His Ile Lys Gly Ala Met Lys Thr Phe
 290 295 300
 Phe Arg Gly Lys Gln
 305

<210> 1854
 <211> 82
 <212> PRT
 <213> Unknown (H38g772 protein)

<220>
 <223> Synthetic construct

<400> 1854
 Met Val Thr Glu Phe Leu Pro Leu Gly Phe Leu Leu Gly Pro Arg Ile
 1 5 10 15
 Gln Met Leu Leu Leu Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Pro
 20 25 30
 Leu Gly Asn Gly Thr Ile Pro Gly Leu Ile Ser Leu Asp Ser Arg Leu
 35 40 45
 His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Val Val Asn Ile
 50 55 60
 Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu Val Asn Leu Leu His
 65 70 75 80
 Pro Ala

<210> 1855
 <211> 216
 <212> PRT
 <213> Unknown (H38g773 protein)

<220>
 <223> Synthetic construct

<400> 1855
 Leu Met Asp Leu Lys Leu Ile Cys Thr Thr Val Pro Lys Met Ala Phe
 1 5 10 15
 Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly Cys Val Thr
 20 25 30
 Gln Ile Phe Phe Tyr Ile Ser Leu Ser Gly Ser Glu Cys Phe Leu Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Leu Arg
 50 55 60
 Tyr Thr Asn Leu Met Asn Pro Lys Ile Cys Gly Leu Met Ala Thr Phe
 65 70 75 80
 Ser Trp Ile Leu Gly Ser Thr Asp Gly Ile Ile Asp Ala Val Ala Thr
 85 90 95
 Phe Ser Phe Ser Phe Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys
 100 105 110
 Glu Phe Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr Ser Ile Phe
 115 120 125

Glu Glu Val Ile Phe Ile Cys Cys Ile Val Met Leu Val Phe Pro Val
 130 135 140
 Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala Val Ile His
 145 150 155 160
 Met Gly Ser Gly Glu Gly Arg Cys Lys Ala Phe Thr Thr Cys Ser Ser
 165 170 175
 His Leu Met Val Val Gly Met Tyr Tyr Gly Ala Ala Leu Phe Met Tyr
 180 185 190
 Ile Arg Pro Thr Ser Asp His Ser Pro Thr Gln Asp Lys Met Val Ser
 195 200 205
 Val Phe Tyr Thr Ile Leu Thr Pro
 210 215

<210> 1856
 <211> 305
 <212> PRT
 <213> Unknown (H38g774 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(305)
 <223> Xaa = Any Amino Acid

<400> 1856
 Met Lys Pro Gly Asn Asp Thr Arg Ile Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Ala Glu Pro Glu Leu Gln Pro Phe Phe Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ala Asp Ile Ser Phe Val Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly
 85 90 95
 Cys Ile Thr Gln Met Cys Phe Phe Leu Leu Phe Ala Val Leu Asp Ser
 100 105 110
 Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu Tyr Tyr Thr Ile Ile Met Asn Pro Gln Phe Tyr Ser Trp Ile
 130 135 140
 Leu Ser Val Leu Asn Ser Leu Leu Gln Ser Leu Met Val Leu Pro Leu
 145 150 155 160
 Pro Phe Tyr Thr Asp Ile Ala Ile Pro His Phe Phe Cys Glu Leu Asn
 165 170 175
 Gln Ile Ile Cys Ile Ala Cys Ser Asp Thr Phe Leu Asn Asp Ile Met
 180 185 190
 Ile Tyr Cys Ala Thr Val Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile
 195 200 205
 Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser
 210 215 220
 Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser
 225 230 235 240
 Val Val Ser Leu Phe Tyr Gly Thr Ser Leu Gly Met Tyr Leu Ser Ser
 245 250 255
 Ala Ala Thr His Asn Ser Pro Ser Ser Ala Thr Ala Ser Val Met Tyr
 260 265 270
 Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn

275 280 285
 Lys Asp Leu Lys Asp Ala Leu Lys Arg Phe Phe Arg Arg Lys Gln Xaa
 290 295 300
 Lys
 305

<210> 1857
 <211> 120
 <212> PRT
 <213> Unknown (H38g775 protein)

<220>
 <223> Synthetic construct

<400> 1857
 Phe Ser Leu Ser His Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn
 1 5 10 15
 Thr Val Pro Arg Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile
 20 25 30
 Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala
 35 40 45
 Val Thr Glu Cys Phe Leu Leu Val Val Lys Ser Asn Asp Leu Tyr Val
 50 55 60
 Ala Ile Cys His Pro Ser Arg Tyr Leu Ala Ile Met Thr Trp Arg Val
 65 70 75 80
 Cys Ile Thr Leu Ala Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser
 85 90 95
 Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln
 100 105 110
 Lys Ile Tyr His Phe Phe Cys Glu
 115 120

<210> 1858
 <211> 214
 <212> PRT
 <213> Unknown (H38g776 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(214)
 <223> Xaa = Any Amino Acid

<400> 1858
 Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asn Met Leu
 35 40 45
 Pro Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu
 50 55 60
 Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 65 70 75 80
 Leu Ser Phe Phe Leu Ser Phe Ser Gln Leu His Asn Leu Ile Ala Leu
 85 90 95
 Gln Met Thr Cys Phe Lys Asn Val Gly Ile Pro Asn Phe Leu Cys Asp
 100 105 110
 Pro Ser Gln Leu Pro His Leu Thr Cys Cys Asp Thr Phe Thr Asn His
 115 120 125

```

Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser
  130                      135                      140
Gly Thr Leu Phe Ser Tyr His Val Ile Val Ser Ser Ile Leu Arg Val
  145                      150                      155                      160
Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Tyr Gly Ser His
                      165                      170                      175
Leu Ser Asp Val Ser Xaa Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu
                      180                      185                      190
Ser Ser Asp Val Ser Ser Ser Pro Arg Lys Thr Ala Val Ala Ser Val
                      195                      200                      205
Met Tyr Ala Val Val Thr
  210

```

<210> 1859
 <211> 166
 <212> PRT
 <213> Unknown (H38g777 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(166)
 <223> Xaa = Any Amino Acid

```

<400> 1859
Val Lys Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly Phe Phe
  1                      5                      10                      15
Leu Ser Pro Arg Ile His Met Leu Leu Phe Gly Leu Phe Tyr Leu Phe
                      20                      25                      30
Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser
                      35                      40                      45
Leu Asp Ser Ile Leu His Thr Pro Met Tyr Phe Phe Leu Xaa His Leu
                      50                      55                      60
Ser Val Val Asn Ile Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu
                      65                      70                      75                      80
Val Asn Leu Leu His Ser Ala Lys Pro Ile Tyr Phe Ala Gly Cys Met
                      85                      90                      95
Thr Tyr Thr Phe Leu Phe Leu Arg Phe Ala His Thr Glu Cys Leu Leu
                      100                      105                      110
Leu Val Leu Met Ser Tyr Asp Trp Tyr Val Ala Ile Leu Thr Pro Leu
                      115                      120                      125
Arg Tyr Ile Ile Ile Met Thr Trp Lys Val Phe Ile Ile Ser Ala Ile
                      130                      135                      140
Thr Ser Trp Thr Cys Gly Ser Phe Leu Ser Met Val His Val Ser Leu
                      145                      150                      155                      160
Ile Leu Arg Leu Pro Phe
                      165

```

<210> 1860
 <211> 93
 <212> PRT
 <213> Unknown (H38g778 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(93)
 <223> Xaa = Any Amino Acid

<400> 1860

Gln Met Ser Leu Phe Val Ile Phe Ala Ser Ala Glu Cys Asn Leu Phe
 1 5 10 15
 Lys Leu Ala Leu Ala Tyr Arg Pro Xaa Cys Tyr Cys His Leu Cys Thr
 20 25 30
 His Pro Phe Tyr His Ile Asp His Val Xaa Glu Ala Ile Ile Phe Phe
 35 40 45
 Leu Val Ala Gly Cys Tyr Leu Gly Gly Leu Val Lys Met Val Thr Val
 50 55 60
 Thr Thr Ser Ile Thr Gln Leu Ser Leu Cys Gln Pro Cys Val His Leu
 65 70 75 80
 His Phe Phe Cys Asp Ile Pro Ser Phe Cys Ser Tyr Ser
 85 90

<210> 1861

<211> 215

<212> PRT

<213> Unknown (H38g779 protein)

<220>

<223> Synthetic construct

<400> 1861

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
 1 5 10 15
 Asn Met Gln Ser Gln Val Pro Thr Ile Ser Tyr Ala Asp Cys Leu Thr
 20 25 30
 Gln Leu Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu
 35 40 45
 Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60
 Tyr Thr Ser Ile Met Ser Thr Lys Phe Cys Ala Leu Leu Val Leu Leu
 65 70 75 80
 Leu Trp Met Leu Thr Ile Ser His Ala Leu Leu His Thr Leu Leu Met
 85 90 95
 Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu His Phe Phe Cys
 100 105 110
 Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr Tyr Val Asn
 115 120 125
 Glu Leu Met Ile Phe Ile Met Gly Gly Ile Ile Ser Ile Ile Pro Phe
 130 135 140
 Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser Ile Leu Lys
 145 150 155 160
 Val Pro Ser Ser Gln Asp Ile His Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190
 Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Asn Glu Ile Ser Met Ala
 195 200 205
 Met Met Tyr Thr Val Val Ala
 210 215

<210> 1862

<211> 219

<212> PRT

<213> Unknown (H38g780 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(219)

<223> Xaa = Any Amino Acid

<400> 1862

```

Ser Asn Leu Ser Phe Thr Asp Leu Xaa Phe Ser Ser Val Thr Met Pro
 1          5          10          15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala
 20          25          30
Gly Cys Leu Thr Gln Met Tyr Phe Leu Leu Phe Phe Gly Asp Leu Glu
 35          40          45
Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 50          55          60
Phe Pro Leu His Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser
 65          70          75          80
Leu Val Leu Leu Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His
 85          90          95
Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro
100          105          110
His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp
115          120          125
Ile His Ile Asn Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val
130          135          140
Ile Leu Pro Phe Leu Leu Ile Thr Val Ser Tyr Ala Arg Ile Ile Ser
145          150          155          160
Ser Ile Leu Lys Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser
165          170          175
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile
180          185          190
Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp
195          200          205
Thr Val Met Ser Met Met Tyr Thr Val Val Thr
210          215

```

<210> 1863

<211> 314

<212> PRT

<213> Unknown (H38g781 protein)

<220>

<223> Synthetic construct

<400> 1863

```

Met Glu Asn Asn Thr Glu Val Thr Glu Phe Ile Leu Val Gly Leu Thr
 1          5          10          15
Asp Asp Pro Glu Leu Gln Ile Pro Leu Phe Ile Val Phe Leu Phe Ile
 20          25          30
Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Met Ile Glu Leu Ile Leu
 35          40          45
Leu Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50          55          60
Ser Leu Val Asp Phe Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Met
 65          70          75          80
Val Gly Phe Leu Thr Gly Asp Lys Phe Ile Leu Tyr Asn Ala Cys Ala
 85          90          95
Thr Gln Phe Phe Phe Val Ala Phe Ile Thr Ala Glu Ser Phe Leu
100          105          110
Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ala Ala Leu Cys Lys Pro Leu
115          120          125
His Tyr Thr Thr Thr Met Thr Thr Asn Val Cys Ala Cys Leu Ala Ile
130          135          140
Gly Ser Tyr Ile Cys Gly Phe Leu Asn Ala Ser Ile His Thr Gly Asn

```

```

145          150          155          160
Thr Phe Arg Leu Ser Phe Cys Arg Ser Asn Val Val Glu His Phe Phe
          165          170          175
Cys Asp Ala Pro Pro Leu Leu Thr Leu Ser Cys Ser Asp Asn Tyr Ile
          180          185          190
Ser Glu Met Val Ile Phe Phe Val Val Gly Phe Asn Asp Leu Phe Ser
          195          200          205
Ile Leu Val Ile Leu Ile Ser Tyr Leu Phe Ile Phe Ile Thr Ile Met
          210          215          220
Lys Met Arg Ser Pro Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ala
225          230          235          240
Ser His Leu Thr Ala Val Ser Ile Phe Tyr Gly Thr Gly Ile Phe Met
          245          250          255
Tyr Leu Arg Pro Asn Ser Ser His Phe Met Gly Thr Asp Lys Met Ala
          260          265          270
Ser Val Phe Tyr Ala Ile Val Ile Pro Met Leu Asn Pro Leu Val Tyr
          275          280          285
Ser Leu Arg Asn Lys Glu Val Lys Ser Ala Phe Lys Lys Thr Val Gly
          290          295          300
Lys Ala Lys Ala Ser Ile Gly Phe Ile Phe
305          310

```

<210> 1864

<211> 189

<212> PRT

<213> Unknown (H38g782 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(189)

<223> Xaa = Any Amino Acid

<400> 1864

```

Ala Thr Lys Glu Leu Cys Phe Leu Gly Val Tyr Ile Pro Lys Gly Asp
1          5          10          15
Ala Cys Trp Lys Xaa Leu Xaa Leu Gly Leu His Leu Leu Leu Gly
          20          25          30
Xaa Gln Val Val Ser Met Val Gly Asn Leu Ala Leu Ile Ala Leu Ile
          35          40          45
Gly Xaa Asn Ser Tyr Leu His His Pro Gln Ala Leu Phe Ser Phe Thr
          50          55          60
Gln Ser Phe Pro Asp Leu Tyr Cys Pro Val Cys Thr Pro Arg Met Leu
65          70          75          80
Met Thr Phe Val Ser Lys Lys Asn Ile Phe Tyr Val Arg Cys Met Thr
          85          90          95
Gln Leu Ser Gln Leu Phe Phe Leu Phe Ile Val Leu Ser Ile Lys Tyr
          100          105          110
His Val Leu Met Phe Ile Ala Cys Gly Cys Leu Val Ala Ile Tyr Asn
          115          120          125
Pro Ser Leu His Glu Val Thr Met Ser Pro Gln Val Arg Glu Met Arg
          130          135          140
Glu Ser Gly Phe Ala Gly Thr Thr Ala His Thr Gly His Ile Leu Arg
145          150          155          160
Pro Asn Leu Cys Asn Ile Asp Val Ile Asn His His Leu Thr Asp Ser
          165          170          175
Leu Leu Val Leu Xaa Val Ser Cys Thr Ser Thr Cys Ala
          180          185

```

<210> 1865

<211> 311
 <212> PRT
 <213> Unknown (H38g783 protein)

<220>
 <223> Synthetic construct

<400> 1865
 Met Thr Gly Gly Gly Asn Ile Thr Glu Ile Thr Tyr Phe Ile Leu Leu
 1 5 10 15
 Gly Phe Ser Asp Phe Pro Arg Ile Ile Lys Val Leu Phe Thr Ile Phe
 20 25 30
 Leu Val Ile Tyr Ile Thr Ser Leu Ala Trp Asn Leu Ser Leu Ile Val
 35 40 45
 Leu Ile Arg Met Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Ile Asp Val Cys Tyr Ile Ser Ser Thr Val Pro
 65 70 75 80
 Lys Met Leu Ser Asn Leu Leu Gln Glu Gln Gln Thr Ile Thr Phe Val
 85 90 95
 Gly Cys Ile Ile Gln Tyr Phe Ile Phe Ser Thr Met Gly Leu Ser Glu
 100 105 110
 Ser Cys Leu Met Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Ser Ser Ile Met Ser Pro Thr Leu Cys Val Trp
 130 135 140
 Met Val Leu Gly Ala Tyr Met Thr Gly Leu Thr Ala Ser Leu Phe Gln
 145 150 155 160
 Ile Gly Ala Leu Leu Gln Leu His Phe Cys Gly Ser Asn Val Ile Arg
 165 170 175
 His Phe Phe Cys Asp Met Pro Gln Leu Leu Ile Leu Ser Cys Thr Asp
 180 185 190
 Thr Phe Phe Val Gln Val Met Thr Ala Ile Leu Thr Met Phe Phe Gly
 195 200 205
 Ile Ala Ser Ala Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Gly Ile
 210 215 220
 Ser Ile Met Lys Ile Thr Ser Ala Lys Gly Arg Pro Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Ala Val Ser Leu Phe Tyr Thr Ser Gly
 245 250 255
 Ile Phe Val Tyr Leu Arg Ser Ser Ser Gly Gly Ser Ser Ser Phe Asp
 260 265 270
 Arg Phe Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Lys Arg
 290 295 300
 Leu Gln Lys Arg Lys Cys Cys
 305 310

<210> 1866
 <211> 312
 <212> PRT
 <213> Unknown (H38g784 protein)

<220>
 <223> Synthetic construct

<400> 1866
 Met Thr Gly Glu Arg Asn Ser Thr Arg Ile Thr Lys Phe Ile Leu Leu
 1 5 10 15
 Gly Phe Ser Glu Phe Pro Lys Asn Pro Ile Phe Leu Phe Ser Ile Phe

```

      20      25      30
Leu Gly Ile Tyr Leu Leu Thr Val Ser Trp Asn Ile Asn Leu Ile Thr
      35      40      45
Leu Ile Arg Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Phe Leu Asp Ile Cys Tyr Val Ser Thr Ile Ala Pro
      65      70      75      80
Lys Met Leu Ser Asp Phe Phe Lys Lys His Lys Phe Ile Ser Phe Met
      85      90      95
Gly Cys Ser Met Gln Tyr Phe Phe Phe Ser Ser Leu Gly Leu Thr Glu
      100      105      110
Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys
      115      120      125
Asn Pro Leu Leu Tyr Arg Ala Ile Met Phe Pro Thr Leu Cys Val Gln
      130      135      140
Met Val Ala Gly Ser Cys Ile Thr Gly Phe Leu Gly Ser Phe Ile Gln
      145      150      155      160
Leu Cys Ala Leu Leu Gln Leu His Phe Cys Gly Pro Asn Val Ile Asn
      165      170      175
His Phe Phe Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser Cys Ser Asp
      180      185      190
Thr Phe Phe Gln Val Met Thr Ser Val Leu Thr Val Ile Phe Gly
      195      200      205
Leu Thr Ser Val Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Ile Ala
      210      215      220
Thr Ile Leu Lys Ile Thr Ser Ala Glu Gly Arg Ala Lys Ser Phe Asn
      225      230      235      240
Thr Cys Ala Ser His Leu Thr Ala Val Ile Leu Phe Phe Gly Ser Gly
      245      250      255
Ile Phe Val Tyr Met Tyr Pro Asn Ala Gly Asp Ser Leu Ser Gln Asn
      260      265      270
Lys Leu Ala Ser Val Leu Tyr Thr Val Thr Ile Pro Met Leu Asn Pro
      275      280      285
Val Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Asn Arg
      290      295      300
Trp Lys Lys Arg Ile Phe Ser Trp
      305      310

```

<210> 1867

<211> 444

<212> PRT

<213> Unknown (H38g785 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(444)

<223> Xaa = Any Amino Acid

<400> 1867

```

Met Thr Val Glu Arg Ser Ser Met Thr Ile Thr Lys Phe Ile Leu Leu
1      5      10      15
Gly Phe Ser Glu Tyr Ser Lys Thr Thr Ile Phe Leu Phe Ser Val Phe
      20      25      30
Leu Gly Ile Tyr Leu Leu Thr Met Ser Xaa Asn Val Ser Leu Ile Ala
      35      40      45
Leu Ile Arg Thr Asp Ser His Leu His Ala Pro Val Tyr Phe Phe Leu
      50      55      60
Ser Asn Pro Ser Phe Leu Asp Ile Cys Cys Val Ser Thr Ile Ala Pro
      65      70      75      80

```

Lys Met Pro Ser Asp Phe Phe Lys Lys His Lys Phe Ile Ser Phe Met
 85 90 95
 Gly Cys Thr Met Gln Tyr Phe Ser Ser Leu Asn Val Thr Glu Cys Cys
 100 105 110
 Leu Leu Thr Ala Met Ala Tyr Asp Xaa Tyr Ala Ala Ile Cys Asp Pro
 115 120 125
 Leu Leu Tyr Thr Ala Ile Met Ser Pro Ala Leu Cys Met Pro Met Val
 130 135 140
 Ala Gly Ser Cys Thr Thr Gly Tyr Phe Val Ser Phe Ile Gln Leu Cys
 145 150 155 160
 Ala Leu Leu Leu Leu His Phe Cys Glu Ser Asn Ser Ser His Phe Phe
 165 170 175
 Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser Cys Ser His Thr Val Phe
 180 185 190
 Phe Phe Ser Ser His Asp His Tyr Ala His Ser Asn Leu Tyr Thr His
 195 200 205
 Leu Tyr Leu Gly Tyr His Asp Asn Leu Trp Leu Tyr His Cys Gln His
 210 215 220
 Ser Ser Leu Leu Trp Asp Ala Pro Cys Asn Thr Ser Ser Leu Ala Trp
 225 230 235 240
 Val Xaa Leu Ser Ala Val Phe Trp Lys Leu Trp Leu Ile Ile Asp Met
 245 250 255
 Leu Pro Phe Val Thr Leu Cys Ser Thr Trp Pro Ser Met Ser Pro Thr
 260 265 270
 Ser Val Cys Thr Xaa Trp Leu Glu Pro Val Xaa Leu Leu Ser Leu Ala
 275 280 285
 His Leu Ser Asn Tyr Val Leu Cys Phe Ser Ser Ile Ser Val Gly Gln
 290 295 300
 Ile Val Asn His Phe Phe Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser
 305 310 315 320
 Cys Tyr Asp Thr Phe Phe Cys Gln Val Met Thr Ser Met Leu Thr Val
 325 330 335
 Val Phe Gly Leu Thr Ser Val Leu Val Ile Met Ile Phe Tyr Gly Tyr
 340 345 350
 Val Ile Ala Thr Ile Leu Lys Ile Ile Ser Val Glu Gly Arg Ser Lys
 355 360 365
 Val Phe Asn Thr Gly Gly Ser His Leu Ile Ala Val Thr Leu Phe Tyr
 370 375 380
 Cys Ser Arg Ile Phe Val Tyr Met Cys Ser His Ser Asp Ala Ser Leu
 385 390 395 400
 Ser Arg Asn Lys Val Asp Ser Ile Val Tyr Thr Val Val Ile Pro Arg
 405 410 415
 Leu Asn Pro Leu Ile Tyr Ser Leu Ser Asp Lys Xaa Ile Lys Asp Ala
 420 425 430
 Leu Lys Arg Trp Thr Lys Arg Ile Phe Ser Trp Pro
 435 440

<210> 1868

<211> 310

<212> PRT

<213> Unknown (H38g786 protein)

<220>

<223> Synthetic construct

<400> 1868

Met Gly Glu Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly Phe
 1 5 10 15
 Leu Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
 20 25 30
 Phe Tyr Ile Phe Thr Leu Leu Gly Asn Gly Ala Ile Leu Gly Leu Ile


```

      35              40              45
Ser Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
  50              55              60
Leu Ala Val Val Asp Ile Ala Tyr Thr Arg Asn Thr Val Pro Gln Met
  65              70              75              80
Leu Ala Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys
      85              90              95
Met Thr Gln Thr Phe Leu Cys Leu Ser Phe Gly His Ser Glu Cys Leu
      100              105              110
Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
      115              120              125
Leu Arg Tyr Ser Val Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
      130              135              140
Val Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Leu Ala His Val Val
      145              150              155              160
Leu Ile Leu Arg Leu Pro Phe Ser Gly Pro His Glu Ile Asn His Phe
      165              170              175
Phe Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala Asp Thr Trp
      180              185              190
Leu Asn Gln Val Val Ile Phe Ala Ala Cys Val Phe Phe Leu Val Gly
      195              200              205
Pro Pro Ser Leu Val Leu Val Ser Tyr Ser His Ile Leu Ala Ala Ile
      210              215              220
Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys
      225              230              235              240
Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Ile
      245              250              255
Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val
      260              265              270
Phe Phe Leu Phe Tyr Ser Phe Phe Asn Pro Thr Leu Asn Pro Leu Ile
      275              280              285
Tyr Ser Leu Arg Asn Gly Glu Val Lys Gly Ala Leu Arg Arg Ala Leu
      290              295              300
Gly Lys Glu Ser His Ser
      305              310

```

<210> 1869

<211> 314

<212> PRT

<213> Unknown (H38g787 protein)

<220>

<223> Synthetic construct

<400> 1869

```

Met Glu Arg Gln Asn Gln Ser Cys Val Val Glu Phe Ile Leu Leu Gly
  1              5              10              15
Phe Ser Asn Tyr Pro Glu Leu Gln Gly Gln Leu Phe Val Ala Phe Leu
      20              25              30
Val Ile Tyr Leu Val Thr Leu Ile Gly Asn Ala Ile Ile Ile Val Ile
      35              40              45
Val Ser Leu Asp Gln Ser Leu His Val Pro Met Tyr Leu Phe Leu Leu
      50              55              60
Asn Leu Ser Val Val Asp Leu Ser Phe Ser Ala Val Ile Met Pro Glu
      65              70              75              80
Met Leu Val Val Leu Ser Thr Glu Lys Thr Thr Ile Ser Phe Gly Gly
      85              90              95
Cys Phe Ala Gln Met Tyr Phe Ile Leu Leu Phe Gly Gly Ala Glu Cys
      100              105              110
Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Phe Ala Ala Ile Cys His
      115              120              125

```

Pro Leu Asn Tyr Gln Met Ile Met Asn Lys Gly Val Phe Met Lys Leu
 130 135 140
 Ile Ile Phe Ser Trp Ala Leu Gly Phe Met Leu Gly Thr Val Gln Thr
 145 150 155 160
 Ser Trp Val Ser Ser Phe Pro Phe Cys Gly Leu Asn Glu Ile Asn His
 165 170 175
 Ile Ser Cys Glu Thr Pro Ala Val Leu Glu Leu Ala Cys Ala Asp Thr
 180 185 190
 Phe Leu Phe Glu Ile Tyr Ala Phe Thr Gly Thr Phe Leu Ile Ile Leu
 195 200 205
 Val Pro Phe Leu Leu Ile Leu Leu Ser Tyr Ile Arg Val Leu Phe Ala
 210 215 220
 Ile Leu Lys Met Pro Ser Thr Thr Gly Arg Gln Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ala His Leu Thr Ser Val Thr Leu Phe Tyr Gly Thr Ala Ser
 245 250 255
 Met Thr Tyr Leu Gln Pro Lys Ser Gly Tyr Ser Pro Glu Thr Lys Lys
 260 265 270
 Val Met Ser Leu Ser Tyr Ser Leu Leu Thr Pro Leu Leu Asn Leu Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Ser Glu Met Lys Arg Ala Leu Met Lys Leu
 290 295 300
 Trp Arg Arg Arg Val Val Leu His Thr Ile
 305 310

<210> 1870

<211> 331

<212> PRT

<213> Unknown (H38g788 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1870

Met Val Thr Glu Phe Leu Leu Leu Gly Phe Leu Leu Gly Pro Arg Ile
 1 5 10 15
 Gln Met Leu Leu Phe Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu
 20 25 30
 Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu
 35 40 45
 His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Val Val Asn Ile
 50 55 60
 Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu Val Asn Leu Leu His
 65 70 75 80
 Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys Met Thr Xaa Thr Phe Leu
 85 90 95
 Phe Leu Ser Phe Ala His Thr Glu Cys Leu Leu Leu Val Leu Met Ser
 100 105 110
 Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Phe Ile Ile
 115 120 125
 Met Thr Trp Lys Val Cys Ile Thr Leu Ala Ile Thr Ser Trp Thr Cys
 130 135 140
 Gly Ser Leu Leu Ala Met Val His Val Ser Leu Ile Leu Arg Leu Pro
 145 150 155 160
 Phe Cys Gly Pro Arg Glu Ile Asn His Phe Phe Cys Glu Ile Leu Ser
 165 170 175
 Val Leu Arg Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val Ile

```

      180      185      190
Phe Ala Ala Cys Met Phe Ile Leu Val Gly Pro Leu Cys Leu Val Leu
      195      200      205
Val Ser Tyr Ser His Ile Leu Ala Ala Ile Leu Arg Ile Gln Ser Gly
      210      215      220
Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val
      225      230      235      240
Val Gly Leu Phe Phe Gly Ser Ala Ser Val Met Tyr Met Ala Pro Lys
      245      250      255
Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Phe Leu Phe Tyr Ser
      260      265      270
Ser Phe Asn Pro Met Leu Asn Pro Leu Ile Tyr Asn Leu Arg Asn Val
      275      280      285
Glu Val Lys Gly Ala Leu Arg Arg Ala Leu Cys Lys Glu Ser His Ser
      290      295      300
Xaa Glu Val Xaa His Leu Asn Cys Gln Pro Gln Leu Ser Arg Gly Leu
      305      310      315      320
Leu Met Pro Asn Tyr Cys Leu Asn Pro Glu Lys
      325      330

```

<210> 1871

<211> 310

<212> PRT

<213> Unknown (H38g789 protein)

<220>

<223> Synthetic construct

<400> 1871

```

Met Gly Asp Asn Ile Thr Ser Ile Thr Glu Phe Leu Leu Leu Gly Phe
  1      5      10      15
Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
      20      25      30
Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
      35      40      45
Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
      50      55      60
Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met
      65      70      75      80
Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
      85      90      95
Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu
      100      105      110
Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
      115      120      125
Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
      130      135      140
Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val
      145      150      155      160
Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
      165      170      175
Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
      180      185      190
Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
      195      200      205
Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
      210      215      220
Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Cys Thr Cys
      225      230      235      240
Phe Ser His Leu Cys Val Ile Gly Leu Phe Tyr Gly Thr Ala Ile Ile
      245      250      255

```

Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
 260 265 270
 Leu Pro Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu
 290 295 300
 Gly Val Glu Arg Ala Leu
 305 310

<210> 1872

<211> 314

<212> PRT

<213> Unknown (H38g790 protein)

<220>

<223> Synthetic construct

<400> 1872

Met Lys Arg Gln Asn Gln Ser Cys Val Val Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asn Phe Pro Glu Leu Gln Val Gln Leu Phe Gly Val Phe Leu
 20 25 30
 Val Ile Tyr Val Val Thr Leu Met Gly Asn Ala Ile Ile Thr Val Ile
 35 40 45
 Ile Ser Leu Asn Gln Ser Leu His Val Pro Met Tyr Leu Phe Leu Leu
 50 55 60
 Asn Leu Ser Val Val Glu Val Ser Phe Ser Ala Val Ile Thr Pro Glu
 65 70 75 80
 Met Leu Val Val Leu Ser Thr Glu Lys Thr Met Ile Ser Phe Val Gly
 85 90 95
 Cys Phe Ala Gln Met Tyr Phe Ile Leu Leu Phe Gly Gly Thr Glu Cys
 100 105 110
 Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Phe Ala Ala Ile Cys His
 115 120 125
 Pro Leu Asn Tyr Pro Val Ile Met Asn Arg Gly Val Phe Met Lys Leu
 130 135 140
 Val Ile Phe Ser Trp Ile Ser Gly Ile Met Val Ala Thr Val Gln Thr
 145 150 155 160
 Thr Trp Val Phe Ser Phe Pro Phe Cys Gly Pro Asn Glu Ile Asn His
 165 170 175
 Leu Phe Cys Glu Thr Pro Pro Val Leu Glu Leu Val Cys Ala Asp Thr
 180 185 190
 Phe Leu Phe Glu Ile Tyr Ala Phe Thr Gly Thr Ile Leu Ile Val Met
 195 200 205
 Val Pro Phe Leu Leu Ile Leu Leu Ser Tyr Ile Arg Val Leu Phe Ala
 210 215 220
 Ile Leu Lys Met Pro Ser Thr Thr Gly Arg Gln Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ser Val Thr Leu Phe Tyr Gly Thr Ala Asn
 245 250 255
 Met Thr Tyr Leu Gln Pro Lys Ser Gly Tyr Ser Pro Glu Thr Lys Lys
 260 265 270
 Leu Ile Ser Leu Ala Tyr Thr Leu Leu Thr Pro Leu Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Ser Glu Met Lys Arg Thr Leu Ile Lys Leu
 290 295 300
 Trp Arg Arg Lys Val Ile Leu His Thr Phe
 305 310

<210> 1873

<211> 312

<212> PRT

<213> Unknown (H38g791 protein)

<220>

<223> Synthetic construct

<400> 1873

```

Met Ser Ala Asn Thr Ser Met Val Thr Glu Phe Leu Leu Leu Gly Phe
 1           5           10           15
Ser His Leu Ala Asp Leu Gln Gly Leu Leu Phe Ser Val Phe Leu Thr
      20           25           30
Ile Tyr Leu Leu Thr Val Ala Gly Asn Phe Leu Ile Val Val Leu Val
 35           40           45
Ser Thr Asp Ala Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu Arg Thr
 50           55           60
Leu Ser Ala Leu Glu Ile Gly Tyr Thr Ser Val Thr Val Pro Leu Leu
 65           70           75           80
Leu His His Leu Leu Thr Gly Arg Arg His Ile Ser Arg Ser Gly Cys
      85           90           95
Ala Leu Gln Met Phe Phe Phe Leu Phe Phe Gly Ala Thr Glu Cys Cys
      100           105           110
Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro
      115           120           125
Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala
      130           135           140
Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro
 145           150           155           160
Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe
      165           170           175
Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser
      180           185           190
Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys
      195           200           205
Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile
      210           215           220
Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys
 225           230           235           240
Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe
      245           250           255
Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu
      260           265           270
Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile
      275           280           285
Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile
      290           295           300
Gln Lys Thr Val Pro Met Glu Ile
 305           310

```

<210> 1874

<211> 276

<212> PRT

<213> Unknown (H38g792 protein)

<220>

<223> Synthetic construct

<400> 1874

```

Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ala
 1           5           10           15
Ile Ser Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
      20           25           30

```

Leu Ser Phe Val Asp Ile Cys Phe Ala Ser Thr Met Val Pro Lys Met
 35 40 45
 Leu Val Asn Ile Gln Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys
 50 55 60
 Ile Thr Gln Met Cys Phe Phe Val Leu Phe Ile Val Leu Asp Ser Leu
 65 70 75 80
 Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro
 85 90 95
 Leu His Tyr Thr Val Ile Met Ser Pro Gln Leu Cys Gly Leu Leu Val
 100 105 110
 Leu Val Ser Trp Ile Met Ser Val Leu Asn Ser Met Leu Gln Ser Leu
 115 120 125
 Val Thr Leu Gln Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe
 130 135 140
 Phe Cys Glu Leu Asn Glu Met Ile His Leu Ala Cys Ser Asp Thr Phe
 145 150 155 160
 Val Asn Asn Met Val Met His Phe Ala Ala Val Leu Leu Asp Gly Gly
 165 170 175
 Pro Leu Val Gly Ile Leu Tyr Ser Tyr Cys Arg Ile Val Ser Ser Ile
 180 185 190
 Arg Ala Ile Ser Ser Thr Gln Gly Lys Tyr Lys Ala Leu Ser Thr Cys
 195 200 205
 Ala Ser His Leu Ser Val Val Ser Ile Phe Tyr Gly Thr Gly Leu Gly
 210 215 220
 Val Tyr Leu Ser Ser Thr Met Thr Gln Asn Leu His Ser Thr Ala Val
 225 230 235 240
 Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile
 245 250 255
 Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Thr Gln Phe Phe
 260 265 270
 Arg Gly Lys Gln
 275

<210> 1875

<211> 317

<212> PRT

<213> Unknown (H38g793 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1875

Ser Ile Thr Trp Glu Asn His Ser Val Leu Met Glu Phe Val Phe Leu
 1 5 10 15
 Ala Tyr Pro Ser Cys Pro Glu Leu His Ile Leu Ser Phe Leu Gly Val
 20 25 30
 Ser Leu Val Tyr Gly Leu Ile Ile Thr Gly Asn Ile Leu Ile Val Val
 35 40 45
 Ser Ile His Thr Glu Thr Cys Leu Cys Thr Ser Met Tyr Tyr Phe Leu
 50 55 60
 Gly Ser Leu Ser Gly Ile Glu Ile Cys Tyr Thr Ala Val Val Val Pro
 65 70 75 80
 His Ile Leu Ala Asn Thr Leu Gln Ser Glu Lys Thr Ser Leu Ser Val
 85 90 95
 Gly Cys Ala Thr Gln Met Ala Phe Phe Ile Ala Leu Gly Ser Ala Asp
 100 105 110
 Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys

115	120	125
His Pro Leu Gln Tyr Pro Leu Leu Met Thr Leu Thr Leu Cys Val His		
130	135	140
Leu Val Val Ala Ser Val Ile Ser Gly Leu Phe Leu Ser Leu Gln Leu		
145	150	155
Val Ala Phe Ile Phe Ser Leu Pro Phe Cys Gln Ala Gln Gly Ile Glu		160
165	170	175
His Phe Phe Cys Asp Val Pro Pro Val Met His Val Val Cys Ala Gln		
180	185	190
Ser His Ile His Glu Gln Ser Val Leu Val Ala Ala Ile Leu Ala Ile		
195	200	205
Ala Val Pro Phe Phe Leu Ile Thr Thr Ser Tyr Thr Phe Ile Val Ala		
210	215	220
Ala Leu Leu Lys Ile His Ser Ala Ala Gly Arg His Arg Ala Phe Ser		
225	230	235
Thr Cys Ser Ser His Leu Thr Val Val Leu Leu Gln Tyr Gly Cys Cys		240
245	250	255
Ala Phe Met Tyr Leu Cys Pro Ser Ser Ser Tyr Asn Pro Lys Gln Asp		
260	265	270
Arg Phe Ile Ser Leu Val Tyr Thr Leu Gly Thr Pro Leu Leu Asn Pro		
275	280	285
Leu Ile Tyr Ala Leu Arg Asn Ser Glu Met Lys Gly Ala Val Gly Arg		
290	295	300
Val Leu Thr Arg Asn Cys Leu Ser Gln Asn Ser Xaa Glu		
305	310	315

<210> 1876

<211> 309

<212> PRT

<213> Unknown (H38g794 protein)

<220>

<223> Synthetic construct

<400> 1876

Met Glu Pro Glu Asn Asp Thr Gly Ile Ser Glu Phe Val Leu Leu Gly		
1	5	10
Leu Ser Glu Glu Pro Glu Leu Gln Pro Phe Leu Phe Gly Leu Phe Leu		15
20	25	30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala		
35	40	45
Thr Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser		
50	55	60
Asn Leu Ser Phe Ala Asp Ile Cys Phe Ile Ser Thr Thr Ile Pro Lys		
65	70	75
Met Leu Ile Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly		
85	90	95
Cys Ile Thr Gln Met Cys Phe Phe Val Leu Phe Gly Gly Leu Asp Ser		
100	105	110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His		
115	120	125
Pro Leu His Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu		
130	135	140
Val Leu Ala Ser Trp Met Ile Ala Ala Leu Asn Ser Leu Ser Gln Ser		
145	150	155
Leu Met Val Leu Trp Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His		
165	170	175
Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr		
180	185	190
Phe Leu Asn Asp Met Gly Met Tyr Phe Ala Ala Gly Leu Leu Ala Gly		
195	200	205

Gly Pro Leu Val Gly Ile Leu Cys Ser Tyr Ser Lys Ile Val Ser Ser
 210 215 220
 Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Cys Cys Thr Gly Leu
 245 250 255
 Gly Val Tyr Leu Thr Ser Ala Ala Thr His Asn Ser His Thr Ser Ala
 260 265 270
 Thr Ala Ser Val Met Tyr Thr Val Ala Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys Met Ser
 290 295 300
 Phe Arg Gly Lys Gln
 305

<210> 1877

<211> 314

<212> PRT

<213> Unknown (H38g795 protein)

<220>

<223> Synthetic construct

<400> 1877

Met Glu Asn Asn Thr Glu Val Ser Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Asn Ala Pro Glu Leu Gln Val Pro Leu Phe Ile Met Phe Thr Leu Ile
 20 25 30
 Tyr Leu Ile Thr Leu Thr Gly Asn Leu Gly Met Ile Ile Leu Ile Leu
 35 40 45
 Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Leu Ala Gly Ile Gly Tyr Ser Ser Ala Val Thr Pro Lys Val Leu
 65 70 75 80
 Thr Gly Leu Leu Ile Glu Asp Lys Ala Ile Ser Tyr Ser Ala Cys Ala
 85 90 95
 Ala Gln Met Phe Phe Cys Ala Val Phe Ala Thr Val Glu Asn Tyr Leu
 100 105 110
 Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Asn Pro Leu
 115 120 125
 His Tyr Thr Thr Thr Met Thr Thr Arg Val Cys Ala Cys Leu Ala Ile
 130 135 140
 Gly Cys Tyr Val Ile Gly Phe Leu Asn Ala Ser Ile Gln Ile Gly Asp
 145 150 155 160
 Thr Phe Arg Leu Ser Phe Cys Met Ser Asn Val Ile His His Phe Phe
 165 170 175
 Cys Asp Lys Pro Ala Val Ile Thr Leu Thr Cys Ser Glu Lys His Ile
 180 185 190
 Ser Glu Leu Ile Leu Val Leu Ile Ser Ser Phe Asn Val Phe Phe Ala
 195 200 205
 Leu Leu Val Thr Leu Ile Ser Tyr Leu Phe Ile Leu Ile Thr Ile Leu
 210 215 220
 Lys Arg His Thr Gly Lys Gly Tyr Gln Lys Pro Leu Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Ile Ala Ile Phe Leu Phe Tyr Ile Thr Val Ile Ile Met
 245 250 255
 Tyr Ile Arg Pro Ser Ser Ser His Ser Met Asp Thr Asp Lys Ile Ala
 260 265 270
 Ser Val Phe Tyr Thr Met Ile Ile Pro Met Leu Ser Pro Ile Val Tyr
 275 280 285
 Thr Leu Arg Asn Lys Asp Val Lys Asn Ala Phe Met Lys Val Val Glu

290 295 300
 Lys Ala Lys Tyr Ser Leu Asp Ser Val Phe
 305 310

<210> 1878
 <211> 315
 <212> PRT
 <213> Unknown (H38g796 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 1878
 Met Xaa Asn Asn Ser Lys Phe Thr Asp Phe Ile Leu Val Gly Leu Thr
 1 5 10 15
 Asn Ala Thr Glu Leu Gln Ile Pro Leu Phe Ile Leu Phe Ile Leu Ile
 20 25 30
 His Leu Leu Ile Leu Thr Arg Asn Leu Glu Ile Ile Leu Leu Ile Leu
 35 40 45
 Leu Asp Ser Cys Leu His Ile Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Leu Leu Gly Tyr Leu Thr Val Thr Pro Arg Val Thr Ala Ser Arg
 65 70 75 80
 Ala Gly Tyr Leu Glu Gly Arg Arg Leu Ser Ser Ser Tyr Asn Ala Cys
 85 90 95
 Ala Ala Gln Met Phe Phe Phe Val Ala Leu Ala Thr Val Glu Asn Met
 100 105 110
 Leu Leu Thr Ser Met Ala Tyr Asp His Tyr Ile Ala Val Cys Lys Pro
 115 120 125
 Leu His Tyr Thr Thr Thr Thr Ile Ala Ser Val Cys Ala His Leu Val
 130 135 140
 Ile Gly Ser Tyr Val Cys Gly Phe Leu Asn Ala Ser Leu Arg Ile Gly
 145 150 155 160
 Asp Ile Phe Ser Leu Ser Phe Cys Lys Ser Asn Leu Val His His Leu
 165 170 175
 Phe Cys Asp Val Pro Pro Val Met Ala Val Ser Cys Ser Gly Lys His
 180 185 190
 Ile Ser Lys Lys Ile Leu Val Phe Met Ser Ser Phe Asn Val Phe Leu
 195 200 205
 Ala Leu Leu Val Ile Leu Thr Ser Tyr Leu Phe Ile Phe Ile Thr Ile
 210 215 220
 Leu Lys Met His Ser Ala Gln Gly His Leu Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Ala Ser His Leu Ile Ala Val Ser Ile Phe Tyr Gly Thr Thr Ile Phe
 245 250 255
 Met His Leu Gln Pro Ser Ser Ser His Ser Met Asp Thr Asp Glu Met
 260 265 270
 Ala Ser Leu Phe Tyr Ala Val Phe Ile Ser Met Leu Asn Leu Val Phe
 275 280 285
 Tyr Ser Leu Arg Ser Lys Glu Val Lys Asn Ala Phe Lys Lys Ala Val
 290 295 300
 Glu Lys Ala Lys Phe Phe Leu Glu Leu Xaa Phe
 305 310 315

<210> 1879
 <211> 314
 <212> PRT

<213> Unknown (H38g797 protein)

<220>

<223> Synthetic construct

<400> 1879

```

Met Asp Asn Ser Asn Trp Thr Ser Val Ser His Phe Val Leu Leu Gly
 1           5           10           15
Ile Ser Thr His Pro Glu Glu Gln Ile Pro Leu Phe Leu Val Phe Ser
           20           25           30
Leu Met Tyr Ala Ile Asn Ile Ser Gly Asn Leu Ala Ile Ile Thr Leu
           35           40           45
Ile Leu Ser Ala Pro Arg Leu His Ile Pro Met Tyr Ile Phe Leu Ser
           50           55           60
Asn Leu Ala Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys
65           70           75           80
Met Leu Gln Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr Thr Gly
           85           90           95
Cys Leu Ala Gln Thr Tyr Phe Phe Ile Cys Phe Ala Val Met Glu Asn
           100          105          110
Phe Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His
           115          120          125
Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val Lys Met
           130          135          140
Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu His Thr
145          150          155          160
Phe Leu Met Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile Pro His
           165          170          175
Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr Ser Thr
           180          185          190
Tyr Leu Asn Thr Leu Met Ile His Thr Glu Gly Ala Val Val Ile Ser
           195          200          205
Gly Ala Leu Ala Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile Leu Val
           210          215          220
Val Leu Arg Ile Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly Thr Leu Ser
           245          250          255
Trp Val Tyr Phe Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys Gly Arg
           260          265          270
Ile Ile Thr Val Val Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
           275          280          285
Ile Tyr Ser Leu Arg Asn Gly Asp Val Lys Gly Gly Phe Met Lys Trp
           290          295          300
Met Ser Arg Met Gln Thr Phe Phe Phe Arg
305          310

```

<210> 1880

<211> 316

<212> PRT

<213> Unknown (H38g798 protein)

<220>

<223> Synthetic construct

<400> 1880

```

Met Val Asn Gln Ser Ser Pro Met Gly Phe Leu Leu Leu Gly Phe Ser
 1           5           10           15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
           20           25           30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Val

```

```

      35              40              45
Leu Tyr Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asp Leu
  50              55              60
Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
  65              70              75              80
Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Gly Cys Ser
      85              90              95
Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
      100              105              110
Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
      115              120              125
His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
      130              135              140
Val Ala Trp Val Met Ser Leu Val Gln Ser Ile Val Gln Thr Pro Ser
      145              150              155              160
Thr Leu His Leu Pro Phe Cys Pro His Gln Gln Ile Asp Asp Phe Leu
      165              170              175
Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp Thr Ser Tyr
      180              185              190
Asn Glu Ile Gln Leu Ala Val Ser Ser Val Ile Phe Val Val Val Pro
      195              200              205
Leu Ser Leu Ile Leu Ala Ser Tyr Gly Ala Thr Ala Gln Ala Val Leu
      210              215              220
Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
      225              230              235              240
Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
      245              250              255
Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
      260              265              270
Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
      275              280              285
Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
      290              295              300
Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
      305              310              315

```

<210> 1881

<211> 324

<212> PRT

<213> Unknown (H38g799 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1881

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20              25              30
Leu Ser Leu Ser Met Tyr Met Val Thr Val Leu Arg Asn Leu Leu Ser
      35              40              45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Cys Phe
      50              55              60
Phe Leu Ser Lys Leu Cys Xaa Ala Asp Ile Gly Phe Thr Leu Ala Met
      65              70              75              80
Val Pro Lys Met Ile Val Asn Met Gln Ser His Ser Arg Val Ile Ser
      85              90              95

```

```

Tyr Glu Gly Cys Leu Thr Arg Met Ser Phe Phe Val Leu Phe Ala Cys
      100      105      110
Met Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
      115      120      125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130      135      140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Pro Leu Asp Ser Gln
      145      150      155      160
Leu His Ser Trp Ile Val Leu Leu Phe Thr Ile Ile Lys Asn Val Glu
      165      170      175
Ile Thr Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys
      180      185      190
Ser Asp Ser Val Ile Asn Asn Ile Phe Ile Tyr Phe Asp Ser Thr Met
      195      200      205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
      210      215      220
Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Gly
      225      230      235      240
Phe Ser Thr Cys Gly Ser Tyr Leu Ala Val Val Cys Xaa Phe Asp Gly
      245      250      255
Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
      260      265      270
Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
      275      280      285
Asn Leu Phe Ile Tyr Ser Leu Gly Lys Arg Asp Ile Gln Ser Val Leu
      290      295      300
Arg Arg Leu Cys Ser Arg Thr Val Glu Ser Pro Xaa Tyr Val Pro Ser
      305      310      315      320
Phe Phe Leu Cys

```

<210> 1882

<211> 158

<212> PRT

<213> Unknown (H38g800 protein)

<220>

<223> Synthetic construct

<400> 1882

```

Met Glu Pro Glu Asn Gly Thr Arg Ile Leu Gly Phe Leu Leu Leu Gly
  1      5      10      15
Leu Ser Glu Glu Pro Glu Leu Gln Pro Val Met Phe Gly Leu Phe Leu
      20      25      30
Ser Met Tyr Leu Thr Thr Val Phe Gly Asn Leu Leu Ile Ile Leu Ala
      35      40      45
Ile Cys Ser Gly Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys
      65      70      75      80
Thr Leu Ser Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly
      85      90      95
Cys Ile Thr Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser
      100      105      110
Leu Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His
      115      120      125
Pro Leu His Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu
      130      135      140
Val Leu Ala Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile
      145      150      155

```

<210> 1883
 <211> 318
 <212> PRT
 <213> Unknown (H38g801 protein)

<220>
 <223> Synthetic construct

<400> 1883

```

Met Met Ser Phe Ala Pro Asn Ala Ser His Ser Pro Val Phe Leu Leu
 1          5          10          15
Leu Gly Phe Ser Arg Ala Asn Ile Ser Tyr Thr Leu Leu Phe Phe Leu
          20          25          30
Phe Leu Ala Ile Tyr Leu Thr Thr Ile Leu Gly Asn Val Thr Leu Val
          35          40          45
Leu Leu Ile Ser Trp Asp Ser Arg Leu His Ser Pro Met Tyr Tyr Leu
          50          55          60
Leu Arg Gly Leu Ser Val Ile Asp Met Gly Leu Ser Thr Val Thr Leu
          65          70          75          80
Pro Gln Leu Leu Ala His Leu Val Ser His Tyr Pro Thr Ile Pro Ala
          85          90          95
Ala Arg Cys Leu Ala Gln Phe Phe Phe Tyr Ala Phe Gly Val Thr
          100          105          110
Asp Thr Leu Val Ile Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Asp Pro Leu His Tyr Ala Leu Val Met Asn His Gln Arg Cys Ala
          130          135          140
Cys Leu Leu Ala Leu Ser Trp Val Val Ser Ile Leu His Thr Met Leu
          145          150          155          160
Arg Val Gly Leu Val Leu Pro Leu Cys Trp Thr Gly Asp Ala Gly Gly
          165          170          175
Asn Val Asn Leu Pro His Phe Phe Cys Asp His Arg Pro Leu Leu Arg
          180          185          190
Ala Ser Cys Ser Asp Ile His Ser Asn Glu Leu Ala Ile Phe Phe Glu
          195          200          205
Gly Gly Phe Leu Met Leu Gly Pro Cys Ala Leu Ile Val Leu Ser Tyr
          210          215          220
Val Arg Ile Gly Ala Ala Ile Leu Arg Leu Pro Ser Ala Ala Gly Arg
          225          230          235          240
Arg Arg Ala Val Ser Thr Cys Gly Ser His Leu Thr Met Val Gly Phe
          245          250          255
Leu Tyr Gly Thr Ile Ile Cys Val Tyr Phe Gln Pro Pro Phe Gln Asn
          260          265          270
Ser Gln Tyr Gln Asp Met Val Ala Ser Val Met Tyr Thr Ala Ile Thr
          275          280          285
Pro Leu Ala Asn Pro Phe Val Tyr Ser Leu His Asn Lys Asp Val Lys
          290          295          300
Gly Ala Leu Cys Arg Leu Leu Glu Trp Val Lys Val Asp Pro
          305          310          315

```

<210> 1884
 <211> 307
 <212> PRT
 <213> Unknown (H38g802 protein)

<220>
 <223> Synthetic construct

<400> 1884

```

Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr
 1          5          10          15

```

Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile
 20 25 30
 Tyr Phe Ile Ser Val Thr Gly Asn Gly Ala Val Leu Met Ile Val Ile
 35 40 45
 Ser Asp Pro Arg Leu His Ser Leu Met Tyr Phe Phe Leu Gly Asn Leu
 50 55 60
 Ser Tyr Leu Asp Ile Cys Tyr Ser Thr Val Thr Leu Pro Lys Met Leu
 65 70 75 80
 Gln Asn Phe Leu Ser Thr His Lys Ala Ile Ser Phe Leu Gly Cys Ile
 85 90 95
 Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ser Met Leu
 100 105 110
 Phe Ala Val Met Ala Phe Asp Leu Ser Val Ala Ile Cys Lys Pro Leu
 115 120 125
 Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile
 130 135 140
 Thr Ile Trp Val Ile Gly Phe Phe His Ala Leu Leu His Ser Val Met
 145 150 155 160
 Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile His His Phe Leu
 165 170 175
 Cys Asp Ile Lys Pro Leu Leu Lys Leu Ala Cys Gly Asn Thr Glu Leu
 180 185 190
 Asn Gln Trp Leu Leu Ser Thr Val Thr Gly Thr Ile Ala Met Gly Pro
 195 200 205
 Phe Phe Leu Thr Leu Leu Ser Tyr Phe Tyr Ile Ile Thr Tyr Leu Phe
 210 215 220
 Phe Lys Thr Arg Ser Cys Ser Met Leu Cys Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Ala Ser His Phe Met Val Val Ile Leu Phe Tyr Ala Pro Val Leu Phe
 245 250 255
 Thr Tyr Ile His Pro Ala Leu Glu Ser Phe Met Asp Gln Asp Arg Ile
 260 265 270
 Val Ala Ile Met Tyr Thr Val Val Thr Pro Val Leu Asn Pro Leu Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly Arg Val Ile
 290 295 300
 Arg Arg Leu
 305

<210> 1885
 <211> 320
 <212> PRT
 <213> Unknown (H38g803 protein)

<220>
 <223> Synthetic construct

 <221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

<400> 1885
 Gln Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Met Gly Leu
 1 5 10 15
 Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser Leu Ser
 20 25 30
 Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val
 35 40 45
 Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 50 55 60
 Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro Lys Ile

```

65          70          75          80
Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Val Gly Cys
      85          90          95
Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu Asp Met
      100        105        110
Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro
      115        120        125
Leu His Tyr Pro Val Ile Val Asn Ala His Leu Arg Val Phe Leu Val
      130        135        140
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Xaa
145          150          155          160
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
      165        170        175
Val Cys Glu Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Ile
      180        185        190
Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu
      195        200        205
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Cys Lys Ile Val Pro Ser Ile
      210        215        220
Leu Arg Ile Ser Thr Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys
225          230          235          240
Gly Ser His Leu Ala Leu Val Cys Leu Phe Tyr Gly Ala Gly Ile Gly
      245        250        255
Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val
      260        265        270
Val Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile
      275        280        285
Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Thr Leu Arg Arg Leu Leu
      290        295        300
Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu Cys
305          310          315          320

```

<210> 1886

<211> 328

<212> PRT

<213> Unknown (H38g804 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1886

```

Met Ala Pro Gly Asn Gly Ser Phe Val Thr Glu Phe Ile Leu Ala Gly
 1          5          10          15
Leu Thr His Gln Pro Asp Leu Gln Ser Pro Leu Phe Phe Leu Phe Leu
      20        25        30
Val Ile Tyr Val Val Thr Leu Leu Gly Asn Leu Gly Leu Val Thr Leu
      35        40        45
Ile Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
      50        55        60
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Ile Pro Lys
65          70          75          80
Met Leu Met Asn Phe Ile Ser Glu Lys Asn Ile Met Ser Phe Lys Gly
      85        90        95
Cys Met Thr Gln Leu Ser Phe Tyr Xaa Phe Phe Val Val Ile Ser Glu
      100       105       110
Gly Tyr Val Leu Thr Ser Met Ala Tyr Asp Arg Val Ala Ile Cys Thr
      115       120       125

```

Pro Leu Leu Tyr His Ile Ala Met Ser Pro Thr Val Cys Ser Ser Leu
 130 135 140
 Met Phe Gly Ser Tyr Leu Met Pro Phe Ser Gly Ala Met Ala His Thr
 145 150 155 160
 Gly Cys Met Leu Arg Leu Thr Phe Cys Asp Ala Asn Thr Ile Asp His
 165 170 175
 Tyr Phe Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
 180 185 190
 Tyr Ile Asn Glu Leu Val Val Phe Thr Val Val Gly Ile Asn Ile Ile
 195 200 205
 Val Pro Thr Val Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser
 210 215 220
 Ile Leu His Ile Ser Ser Lys Glu Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala
 245 250 255
 Phe Met Tyr Leu Asn Pro Ser Ser Ala Gly Ser Met Asp Lys Arg Lys
 260 265 270
 Leu Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Phe Ala Leu Arg Lys Ala
 290 295 300
 Leu Ser Ser Arg Lys Leu Xaa Xaa Val Ile Val Cys Val Cys Val Tyr
 305 310 315 320
 Ser His Lys Thr Gly Ile Phe Cys
 325

<210> 1887

<211> 310

<212> PRT

<213> Unknown (H38g805 protein)

<220>

<223> Synthetic construct

<400> 1887

Met Gly Arg Asn Asn Leu Thr Arg Pro Ser Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Arg Pro Glu Asp Gln Lys Pro Leu Phe Ala Val Phe Leu
 20 25 30
 Pro Ile Tyr Leu Ile Thr Val Ile Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile Arg Ser Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Ile Leu Ser Phe Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Ser Glu
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Ala Phe Gly Asn Thr Asp Ser
 100 105 110
 Tyr Leu Leu Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Phe His Tyr Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu
 130 135 140
 Leu Val Leu Ser Phe Cys Ile Pro His Phe His Ser Leu Leu His Ile
 145 150 155 160
 Leu Leu Thr Asn Gln Leu Ile Phe Cys Ala Ser Asn Val Ile His His
 165 170 175
 Phe Phe Cys Asp Asp Gln Pro Val Leu Lys Leu Ser Cys Ser Ser His
 180 185 190
 Phe Val Lys Glu Ile Thr Val Met Thr Glu Gly Leu Ala Val Ile Met


```

      195              200              205
Thr Pro Phe Ser Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Thr
  210              215              220
Val Leu Lys Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Phe Ser Thr
  225              230              235              240
Cys Gly Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile Ser
      245              250              255
Tyr Leu Tyr Phe Gln Pro Leu Ser Asn Tyr Thr Val Lys Asp Gln Ile
      260              265              270
Ala Thr Ile Ile Tyr Thr Val Leu Thr Pro Met Leu Asn Pro Phe Ile
      275              280              285
Tyr Ser Leu Arg Asn Lys Asp Met Lys Gln Gly Leu Ala Lys Leu Met
      290              295              300
His Arg Met Lys Cys Gln
305              310

```

<210> 1888

<211> 315

<212> PRT

<213> Unknown (H38g806 protein)

<220>

<223> Synthetic construct

<400> 1888

```

Met Glu Ile Val Ser Thr Gly Asn Glu Thr Ile Thr Glu Phe Val Leu
  1              5              10              15
Leu Gly Phe Tyr Asp Ile Pro Glu Leu His Phe Leu Phe Phe Ile Val
      20              25              30
Phe Thr Ala Val Tyr Val Phe Ile Ile Ile Gly Asn Met Leu Ile Ile
      35              40              45
Val Ala Val Val Ser Ser Gln Arg Leu His Lys Pro Met Tyr Ile Phe
      50              55              60
Leu Ala Asn Leu Ser Phe Leu Asp Ile Leu Tyr Thr Ser Ala Val Met
      65              70              75              80
Pro Lys Met Leu Glu Gly Phe Leu Gln Glu Ala Thr Ile Ser Val Ala
      85              90              95
Gly Cys Leu Leu Gln Phe Phe Ile Phe Gly Ser Leu Ala Thr Ala Glu
      100              105              110
Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys
      115              120              125
Tyr Pro Leu His Tyr Pro Leu Leu Met Gly Pro Arg Arg Tyr Met Gly
      130              135              140
Leu Val Val Thr Thr Trp Leu Ser Gly Phe Val Val Asp Gly Leu Val
      145              150              155              160
Val Ala Leu Val Ala Gln Leu Arg Phe Cys Gly Pro Asn His Ile Asp
      165              170              175
Gln Phe Tyr Cys Asp Phe Met Leu Phe Val Gly Leu Ala Cys Ser Asp
      180              185              190
Pro Arg Val Ala Gln Val Thr Thr Leu Ile Leu Ser Val Phe Cys Leu
      195              200              205
Thr Ile Pro Phe Gly Leu Ile Leu Thr Ser Tyr Ala Arg Ile Val Val
      210              215              220
Ala Val Leu Arg Val Pro Ala Gly Ala Ser Arg Arg Arg Ala Phe Ser
      225              230              235              240
Thr Cys Ser Ser His Leu Ala Val Val Thr Thr Phe Tyr Gly Thr Leu
      245              250              255
Met Ile Phe Tyr Val Ala Pro Ser Ala Val His Ser Gln Leu Leu Ser
      260              265              270
Lys Val Phe Ser Leu Leu Tyr Thr Val Val Thr Pro Leu Phe Asn Pro
      275              280              285

```

Val Ile Tyr Thr Met Arg Asn Lys Glu Val His Gln Ala Leu Arg Lys
 290 295 300
 Ile Leu Cys Ile Lys Gln Thr Glu Thr Leu Asp
 305 310 315

<210> 1889
 <211> 188
 <212> PRT
 <213> Unknown (H38g807 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(188)
 <223> Xaa = Any Amino Acid

<400> 1889
 His Trp Lys Ile Leu Arg Arg Asn Ser Lys Met Ile His Glu Ile Ile
 1 5 10 15
 Xaa Thr Leu Cys Gln Ile Leu Tyr Ser Glu Asp Lys Thr Cys Tyr Ile
 20 25 30
 Gln Ile Gln Ser Leu Phe Cys Thr Asp Leu Glu Ile Pro Asn Phe Phe
 35 40 45
 Cys Glu Leu Asn Xaa Val Val His Leu Ala Cys Ser Asp Thr Phe Leu
 50 55 60
 Lys Asp Ile Val Arg Tyr Cys Thr Thr Met Leu Leu Ser Gly Gly Pro
 65 70 75 80
 Ile Ala Gly Ile Phe Tyr Ser Phe Ser Lys Ile Ile Ser Ser Ile Cys
 85 90 95
 Ala Ile Pro Ser Ala Gln Gly Lys His Lys Ala Phe Pro Thr Cys Val
 100 105 110
 Ser His Leu Ser Asn Met Ser Leu Phe Tyr Cys Arg Ser Thr Gly Leu
 115 120 125
 Tyr Leu Ser Phe Ala Ala Thr His Asn Ser Cys Ser Asn Ala Thr Ala
 130 135 140
 Ser Val Arg His Thr Val Val Lys Pro Leu Leu Asn Val Phe Ile Leu
 145 150 155 160
 Lys Ser Ser Asn Lys Asp Ile Lys Xaa Ala Leu Lys Val Phe Phe Arg
 165 170 175
 Gly Lys Gln Trp Lys His His Phe Ser Lys Ser Ala
 180 185

<210> 1890
 <211> 313
 <212> PRT
 <213> Unknown (H38g808 protein)

<220>
 <223> Synthetic construct

<400> 1890
 Met Glu Lys Arg Asn Leu Thr Val Val Arg Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Pro Ser Ser Ala Glu Gln Gln His Leu Leu Ser Val Leu Phe Leu
 20 25 30
 Cys Met Tyr Leu Ala Thr Thr Leu Gly Asn Met Leu Ile Ile Ala Thr
 35 40 45
 Ile Gly Phe Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ala Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Gln

```

65              70              75              80
Met Val Val Asn Ile Leu Thr Gly Thr Lys Thr Ile Ser Phe Ala Gly
      85              90              95
Cys Leu Thr Gln Leu Phe Phe Phe Val Ser Phe Val Asn Met Asp Ser
      100              105              110
Leu Leu Leu Cys Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115              120              125
Pro Leu His Tyr Thr Ala Arg Met Asn Leu Cys Leu Cys Val Gln Leu
      130              135              140
Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His Ala Leu Leu His Thr
      145              150              155              160
Val Leu Ile Ala Gln Leu Ser Phe Cys Ala Ser Asn Ile Ile His His
      165              170              175
Phe Leu Cys Asp Leu Asn Pro Leu Leu Gln Leu Ser Cys Ser Asp Val
      180              185              190
Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly Asp Leu Leu Ala Leu
      195              200              205
Thr Pro Leu Val Cys Ile Leu Val Ser Tyr Gly Leu Ile Phe Ser Thr
      210              215              220
Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln Arg Ala Val Ser Thr
      225              230              235              240
Cys Ser Cys His Leu Ser Val Val Val Leu Phe Tyr Gly Thr Ala Ile
      245              250              255
Ala Val Tyr Phe Ser Pro Ser Ser Pro His Met Pro Glu Ser Asp Thr
      260              265              270
Leu Ser Thr Ile Met Tyr Ser Met Val Ala Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Thr Leu Arg Asn Arg Asp Met Lys Arg Gly Leu Gln Lys Met
      290              295              300
Leu Leu Lys Cys Thr Val Phe Gln Gln
305              310

```

<210> 1891

<211> 312

<212> PRT

<213> Unknown (H38g809 protein)

<220>

<223> Synthetic construct

<400> 1891

```

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
1              5              10              15
Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
      20              25              30
Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
      35              40              45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ala
      50              55              60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
65              70              75              80
Met Leu Val Asn Leu Gln Ser His Asn Lys Ala Ile Ser Tyr Ala Gly
      85              90              95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
      100              105              110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
      115              120              125
Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu
      130              135              140
Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr
      145              150              155              160

```

Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
 165 170 175
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile
 180 185 190
 Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys
 245 250 255
 Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
 290 295 300
 Asp Lys His Phe Lys Arg Leu Thr
 305 310

<210> 1892

<211> 317

<212> PRT

<213> Unknown (H38g810 protein)

<220>

<223> Synthetic construct

<400> 1892

Met Gly Met Ser Asn Leu Thr Arg Leu Ser Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Arg Ser Glu Asp Gln Arg Pro Leu Phe Ala Leu Phe Leu
 20 25 30
 Ile Ile Tyr Leu Val Thr Leu Met Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile His Ser Asp Pro Arg Leu Gln Asn Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Ile Leu Ser Phe Ala Asp Ile Cys Tyr Thr Thr Val Ile Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Tyr Ala Glu
 85 90 95
 Cys Leu Ala Gln Met Tyr Phe Phe Leu Val Phe Gly Asn Ile Asp Ser
 100 105 110
 Tyr Leu Leu Ala Ala Met Ala Ile Asn Arg Cys Val Ala Ile Cys Asn
 115 120 125
 Pro Phe His Tyr Val Thr Val Met Asn Arg Arg Cys Cys Val Leu Leu
 130 135 140
 Leu Ala Phe Pro Ile Thr Phe Ser Tyr Phe His Ser Leu Leu His Val
 145 150 155 160
 Leu Leu Val Asn Arg Leu Thr Phe Cys Thr Ser Asn Val Ile His His
 165 170 175
 Phe Phe Cys Asp Val Asn Pro Val Leu Lys Leu Ser Cys Ser Ser Thr
 180 185 190
 Phe Val Asn Glu Ile Val Ala Met Thr Glu Gly Leu Ala Ser Val Met
 195 200 205
 Ala Pro Phe Val Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Ala
 210 215 220
 Val Leu Lys Ile Pro Ser Ala Ala Gly Lys His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ser Ile Ser

<210> 1894

<211> 328
 <212> PRT
 <213> Unknown (H38g812 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(328)
 <223> Xaa = Any Amino Acid

<400> 1894

Ser	Val	Asp	Gln	Val	Asn	Asp	Ser	Leu	Val	Thr	Glu	Phe	Val	Leu	Leu	1	5	10	15
Gly	Leu	Ala	Gln	Ser	Leu	Glu	Met	Gln	Phe	Phe	Leu	Phe	Leu	Phe	Phe	20	25	30	
Ser	Leu	Phe	Tyr	Val	Gly	Ile	Ile	Leu	Gly	Asn	Leu	Phe	Ile	Val	Phe	35	40	45	
Thr	Val	Ile	Phe	Asp	Pro	His	Leu	His	Ser	Pro	Met	Tyr	Ile	Leu	Leu	50	55	60	
Ala	Asn	Leu	Ser	Leu	Ile	Asp	Leu	Ser	Leu	Ser	Ser	Thr	Thr	Val	Pro	65	70	75	80
Arg	Leu	Ile	Tyr	Asp	Leu	Phe	Thr	Asp	Cys	Lys	Val	Ile	Ser	Phe	His	85	90	95	
Asn	Cys	Met	Ile	Gln	Lys	Phe	Phe	Ile	His	Val	Thr	Gly	Gly	Val	Glu	100	105	110	
Met	Val	Leu	Leu	Ile	Val	Met	Glu	Tyr	Asp	Arg	Tyr	Thr	Ala	Ile	Cys	115	120	125	
Lys	Pro	Leu	His	Tyr	Pro	Thr	Ile	Met	Asn	Pro	Lys	Met	Cys	Met	Phe	130	135	140	
Leu	Val	Ala	Ala	Ala	Trp	Val	Ile	Gly	Val	Ile	His	Ala	Met	Ser	Gln	145	150	155	160
Phe	Val	Phe	Val	Ile	Asn	Xaa	Pro	Phe	Cys	Gly	Pro	Asn	Asn	Val	Gly	165	170	175	
Ser	Phe	Tyr	Cys	Asp	Phe	Pro	Arg	Val	Ile	Lys	Leu	Ala	Cys	Met	Asp	180	185	190	
Thr	Tyr	Gly	Leu	Glu	Phe	Val	Val	Thr	Ala	Asn	Ser	Gly	Phe	Ile	Ser	195	200	205	
Met	Gly	Thr	Phe	Phe	Phe	Leu	Ile	Val	Ser	Tyr	Ile	Phe	Ile	Leu	Val	210	215	220	
Thr	Val	Gln	Arg	His	Ser	Ser	Asn	Asp	Leu	Ser	Lys	Ala	Phe	Phe	Thr	225	230	235	240
Ser	Xaa	Ala	His	Ile	Thr	Val	Val	Val	Leu	Phe	Phe	Ala	Pro	Cys	Met	245	250	255	
Phe	Leu	Tyr	Val	Trp	Pro	Phe	Pro	Thr	Lys	Ser	Leu	Asp	Lys	Phe	Phe	260	265	270	
Ala	Ile	Met	Asn	Phe	Val	Val	Thr	Pro	Val	Leu	Asn	Pro	Ala	Ile	Tyr	275	280	285	
Thr	Leu	Arg	Asn	Lys	Asp	Met	Lys	Phe	Ala	Met	Arg	Arg	Leu	Asn	Gln	290	295	300	
His	Ile	Leu	Asn	Ser	Met	Glu	Thr	Thr	Xaa	His	Ile	Trp	Leu	Met	Arg	305	310	315	320
Ala	Gln	Asp	Lys	Cys	His	Gly	Pro									325			

<210> 1895
 <211> 272
 <212> PRT
 <213> Unknown (H38g813 protein)

<220>

<223> Synthetic construct

<400> 1895

```

Met Trp Ile Asn Asn Gln Ser S r Leu Asp Asp Phe Ile Leu Leu Gly
 1           5           10           15
Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Val Ile Phe Leu Val
      20           25           30
Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val Ser
 35           40           45
His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser Asn
 50           55           60
Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln Met
65           70           75           80
Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys
      85           90           95
Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile
      100           105           110
Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys Pro
 115           120           125
Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met Ala
 130           135           140
Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser Thr
145           150           155           160
Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His Phe
      165           170           175
Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile Arg
      180           185           190
Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Leu Met
 195           200           205
Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala Val
 210           215           220
Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr Cys
225           230           235           240
Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser
      245           250           255
Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys Ile
      260           265           270

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<210> 1896

<211> 315

<212> PRT

<213> Unknown (H38g814 protein)

<220>

<223> Synthetic construct

<400> 1896

```

Met Asn Val Ser Glu Pro Asn Ser Ser Phe Ala Phe Val Asn Glu Phe
 1           5           10           15
Ile Leu Gln Gly Phe Ser Cys Glu Trp Thr Ile Gln Ile Phe Leu Phe
      20           25           30
Ser Leu Phe Thr Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala
 35           40           45
Ile Ala Phe Val Leu Trp Cys Asp Arg Arg Leu His Thr Pro Met Tyr
 50           55           60
Met Phe Leu Gly Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser
65           70           75           80
Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser Glu Lys Lys Asn Ile
      85           90           95
Ser Phe Ala Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
      100           105           110

```

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Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala Phe Asp Gln Tyr Leu
    115                      120                      125
Ala Ile Cys Arg Pro Leu Leu Tyr Pro Asn Ile Met Thr Gly His Leu
    130                      135                      140
Tyr Ala Lys Leu Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe
    145                      150                      155                      160
Leu Ile Pro Ile Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn
    165                      170                      175
Ile Ile Asp His Val Val Cys Asp Pro Gly Pro Arg Phe Ala Leu Asp
    180                      185                      190
Cys Val Ser Ala Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser
    195                      200                      205
Leu Val Ile Phe Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu
    210                      215                      220
Val Leu Lys Ala Met Leu Gly Met Pro Ser Ser Thr Gly Arg His Lys
    225                      230                      235                      240
Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Cys Tyr
    245                      250                      255
Ser Ser Leu Met Val Met Tyr Val Ser Pro Gly Leu Gly His Ser Thr
    260                      265                      270
Gly Met Gln Lys Ile Glu Thr Leu Phe Tyr Ala Met Val Thr Pro Leu
    275                      280                      285
Phe Asn Pro Leu Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala
    290                      295                      300
Leu Arg Lys Val Leu Gly Ser Ser Asn Ile Ile
    305                      310                      315

```

<210> 1897

<211> 305

<212> PRT

<213> Unknown (H38g815 protein)

<220>

<223> Synthetic construct

<400> 1897

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Gly Leu
    1           5           10           15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
    20           25           30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
    35           40           45
His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu
    50           55           60
Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser
    65           70           75           80
Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
    85           90           95
Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
    100          105          110
Tyr Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu Asn Tyr Thr Thr Ile
    115          120          125
Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile
    130          135          140
Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Pro
    145          150          155          160
Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
    165          170          175
Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
    180          185          190
Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile

```



```

      195              200              205
Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp
 210              215              220
Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
 225              230              235              240
Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
      245              250              255
Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
      260              265              270
Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
      275              280              285
Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
      290              295              300
Phe
305

```

<210> 1898

<211> 318

<212> PRT

<213> Unknown (H38g816 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1898

```

Met Thr Leu Pro Ser Asp Asp Ser Thr Val Pro Val Ser Glu Phe Leu
 1              5              10              15
Leu Ile Cys Phe Pro Asn Phe Gln Ser Trp Gln His Leu Leu Ser Leu
      20              25              30
Pro Leu Ser Leu Met Phe Leu Leu Ala Met Gly Thr Asn Thr Thr Pro
      35              40              45
Pro Ile Thr Ile His Leu Glu Ala Ser Leu His Leu Pro Leu Tyr Tyr
      50              55              60
Leu Pro Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr Val
      65              70              75              80
Ile Pro Lys Val Leu Ala Ile Phe Trp Phe Asp Leu Arg Ser Ile Gly
      85              90              95
Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn Ser Phe Leu Pro
      100              105              110
Met Glu Ser Cys Thr Phe Met Val Lys Asp Tyr Asp His Tyr Val Ala
      115              120              125
Ile Cys His Pro Leu Gln Tyr Leu Ser Ile Ile Thr His Gln Phe Val
      130              135              140
Ala Lys Ala Ser Val Phe Ile Val Val Gln Asn Ala Leu Leu Leu Ser
      145              150              155              160
Pro Val Pro Ile Leu Ser Ala Gln Leu His Tyr Cys Arg Lys Asn Val
      165              170              175
Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser Arg Leu Ser Cys
      180              185              190
Asp Asn Phe Thr Leu Asn Arg Leu Tyr Gln Phe Val Ala Gly Trp Thr
      195              200              205
Phe Leu Gly Ser Asp Phe Ile Leu Ile Phe Leu Ser Tyr Thr Phe Ile
      210              215              220
Leu Arg Ala Val Leu Arg Phe Lys Val Glu Gly Val Ala Val Lys Ala
      225              230              235              240
Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu Phe Phe Ser Ile
      245              250              255

```

Leu Leu Val Val Val Leu Thr Asn Val Ala Arg Lys Lys Val Pro Met
 260 265 270
 Asp Ile Leu Ile Leu Phe Asn Val Leu His Pro Phe Ser Pro Pro Ala
 275 280 285
 Leu Asn Pro Ile Ile Cys Gly Phe Gln Thr Lys Glu Leu Lys Lys Glu
 290 295 300
 Phe Xaa Lys Leu Leu Gln Arg Gly Leu Xaa Lys His Gly Arg
 305 310 315

<210> 1899

<211> 317

<212> PRT

<213> Unknown (H38g817 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1899

Lys His Asn His Thr Ala Val Thr Lys Val Thr Glu Phe Ile Leu Met
 1 5 10 15
 Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro Leu Phe Gly Leu Phe
 20 25 30
 Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn Leu Gly Met Val Ile
 35 40 45
 Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Lys His Leu Ala Ile Thr Asp Leu Gly Tyr Ser Thr Val Ile Gly Pro
 65 70 75 80
 Gln Met Met Phe Ser Glu Thr Ser Tyr Val His Lys Glu His Asn Phe
 85 90 95
 Phe Tyr Asn Trp Tyr Ala Asn His Arg Ala Arg Phe Glu Arg Asn Ile
 100 105 110
 Ile Ser His Arg Gly Ile Leu Ser Ala Thr Asn Asn Glu Pro Tyr Lys
 115 120 125
 Pro Ile Thr Lys Gln Leu Leu Asn Pro Ile Ile Met Pro Glu Lys Ile
 130 135 140
 Arg Glu Glu Gln Ile Thr Val Pro Glu Leu Asp Lys Thr Cys Ala Pro
 145 150 155 160
 Leu Phe Leu Lys Arg Lys Xaa Val Lys Thr Val Ser Thr Asn Pro Asp
 165 170 175
 Thr Thr Asn Asn Cys His Gly Glu Gly Thr Ala Lys Met Xaa Ile Leu
 180 185 190
 Arg Ser Glu Lys Lys Lys Ile Thr Ile Ile Lys Ala Met Thr Ala Gly
 195 200 205
 Thr Asn Met Leu Ile Ser Leu Ser Ile Val Leu Ile Ser Tyr Met Phe
 210 215 220
 Ile Leu Val Ala Asn Leu Arg Met Asn Ser Arg Lys Gly Arg Tyr Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Met Phe Tyr
 245 250 255
 Gly Thr Leu Leu Phe Ile Tyr Leu Gln Pro Lys Ser Ser His Thr Leu
 260 265 270
 Ala Ile Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Leu Ile Pro Met
 275 280 285
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala
 290 295 300
 Leu Lys Arg Thr Leu Thr Asn Arg Phe Lys Ile Pro Ile

305

310

315

<210> 1900

<211> 220

<212> PRT

<213> Unknown (H38g818 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(220)

<223> Xaa = Any Amino Acid

<400> 1900

```

Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro
 1           5           10           15
Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Pro Tyr Ala
      20           25           30
Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 35           40           45
Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 50           55           60
Arg Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe
 65           70           75           80
Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
      85           90           95
Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Ser Asn Val Glu Ile Ala
      100           105           110
Asn Phe Val Tyr Glu Pro Ser Gln Leu Leu Asn Leu Asp Cys Ser Asp
 115           120           125
Thr Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Met Phe Gly Phe
 130           135           140
Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys Ile Val Pro Ser
 145           150           155           160
Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ala Thr
      165           170           175
Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr Gly Ile
      180           185           190
Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val
 195           200           205
Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met
 210           215           220

```

<210> 1901

<211> 311

<212> PRT

<213> Unknown (H38g819 protein)

<220>

<223> Synthetic construct

<400> 1901

```

Met Glu Lys Ser Asn Asn Ser Thr Leu Phe Ile Leu Leu Gly Phe Ser
 1           5           10           15
Gln Asn Lys Asn Ile Glu Val Leu Cys Phe Val Leu Phe Leu Phe Cys
      20           25           30
Tyr Ile Ala Ile Trp Met Gly Asn Leu Leu Ile Met Ile Ser Ile Thr
 35           40           45
Cys Thr Gln Leu Ile His Gln Pro Met Tyr Phe Phe Leu Asn Tyr Leu
 50           55           60

```

Ser Leu Ser Asp Leu Cys Tyr Thr Ser Thr Val Thr Pro Lys Leu Met
 65 70 75 80
 Val Asp Leu Leu Ala Glu Arg Lys Thr Ile Ser Tyr Asn Asn Cys Met
 85 90 95
 Ile Gln Leu Phe Thr Thr His Phe Phe Gly Gly Ile Glu Ile Phe Ile
 100 105 110
 Leu Thr Gly Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Ile Ile Met Ser Arg Gln Lys Cys Asn Thr Ile Ile Ile
 130 135 140
 Val Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu Leu
 145 150 155 160
 Thr Ile Phe Val Pro Phe Cys Gly Pro Asn Glu Ile Asp His Tyr Phe
 165 170 175
 Cys Asp Val Tyr Pro Leu Leu Lys Leu Ala Cys Ser Asn Ile His Met
 180 185 190
 Ile Gly Leu Leu Val Ile Ala Asn Ser Gly Leu Ile Ala Leu Val Thr
 195 200 205
 Phe Val Val Leu Leu Leu Ser Tyr Val Phe Ile Leu Tyr Thr Ile Arg
 210 215 220
 Ala Tyr Ser Ala Glu Arg Ser Lys Ala Leu Ala Thr Cys Ser Ser
 225 230 235 240
 His Val Ile Val Val Val Leu Phe Phe Ala Pro Ala Leu Phe Ile Tyr
 245 250 255
 Ile Arg Pro Val Thr Thr Phe Ser Glu Asp Lys Val Phe Ala Leu Phe
 260 265 270
 Tyr Thr Ile Ala Pro Met Phe Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Thr Glu Met Lys Asn Ala Met Arg Lys Val Trp Cys Cys Gln Ile
 290 295 300
 Leu Leu Lys Arg Asn Gln Leu
 305 310

<210> 1902

<211> 222

<212> PRT

<213> Unknown (H38g820 protein)

<220>

<223> Synthetic construct

<400> 1902

Arg Asn Phe Ser Phe Leu Glu Ile Ser Phe Thr Thr Val Cys Ile Pro
 1 5 10 15
 Arg Phe Leu Gly Ala Ile Ile Thr Arg Asn Lys Thr Ile Ser Tyr Asn
 20 25 30
 Asn Cys Ala Ala Gln Leu Phe Phe Ile Phe Met Gly Val Thr Glu
 35 40 45
 Phe Tyr Ile Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys
 50 55 60
 Lys Pro Leu His Tyr Thr Ser Ile Met Asn Arg Lys Leu Cys Thr Leu
 65 70 75 80
 Leu Val Leu Cys Ala Trp Leu Ser Gly Phe Pro Thr Ile Phe Pro Pro
 85 90 95
 Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Ala Ser Asn Val Ile Asp
 100 105 110
 His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu Ser Cys Ser Asp
 115 120 125
 Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala Leu Val Thr Leu
 130 135 140
 Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met Tyr Ile Ile Arg

```

145          150          155          160
Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys Lys Ala Phe Ser
          165          170          175
Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser Tyr Gly Ser Cys
          180          185          190
Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys Ala Ser Leu Thr
          195          200          205
Lys Gly Ile Ala Ile Leu Asn Thr Ser Val Ala Pro Met Leu
          210          215          220

```

<210> 1903

<211> 267

<212> PRT

<213> Unknown (H38g821 protein)

<220>

<223> Synthetic construct

<400> 1903

```

Ile Ile Leu Cys Phe Phe Ile Ile Gly Asn Ser Gln Asp Asn Ser Gln
1      5      10      15
Met Thr Leu Met Asp Asn Ile Ser Glu Val Thr Glu Phe Val Leu Val
          20      25      30
Gly Leu Thr Asp Val Leu Glu Leu Gln Val Pro Leu Phe Ile Ile Phe
          35      40      45
Thr Val Ile Tyr Leu Thr Thr Leu Val Gly Asn Phe Gly Met Ile Met
          50      55      60
Leu Ile Leu Leu Asp Ser Arg Leu His Ile Pro Met Tyr Phe Phe Leu
65      70      75      80
Gly Lys Leu Ser Leu Val Asp Ser Val Cys Ala Cys Leu Val Thr Gly
          85      90      95
Ser Tyr Ile Cys Gly Leu Phe Gln Ser Ser Ile His Val Ala Phe Thr
          100     105     110
Phe His Leu Ser Phe Cys His Ser Asn Val Val Asn His Phe Phe Cys
          115     120     125
Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Ile Tyr Ala His
          130     135     140
Glu Ile Val Leu Phe Ile Leu Ala Ala Phe Asn Ile Phe Phe Thr Leu
145     150     155     160
Leu Ile Ile Leu Asn Ser Tyr Val Phe Ile Phe Ile Ala Ile Leu Arg
          165     170     175
Met His Ser Ala Glu Gly Gln Lys Lys Val Phe Ser Thr Cys Ala Tyr
          180     185     190
His Leu Thr Thr Val Ser Ile Phe Tyr Gly Thr Ile Thr Phe Met Tyr
          195     200     205
Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp Lys Ile Ser Ser
          210     215     220
Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Val Tyr Ser
225     230     235     240
Leu Arg Asn Lys Glu Val Gln Ser Ala Phe Lys Val Val Ile Gly Lys
          245     250     255
Ala Lys Ser Ser Leu Gly Leu Ala Tyr Tyr Leu
          260     265

```

<210> 1904

<211> 316

<212> PRT

<213> Unknown (H38g822 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1904

```

Trp Xaa Pro Val Phe Asn Gln Ser Ala Pro Leu Gln Phe Val Phe Arg
 1          5          10          15
Val Phe Thr Thr Val Pro Glu Phe Gln Val Leu Leu Phe Leu Leu Phe
      20          25          30
Leu Leu Phe Tyr Leu Met Ile Leu Cys Gly Asn Thr Ala Ile Ile Trp
      35          40          45
Val Val Cys Thr Tyr Ser Val Leu Arg Thr Pro Met Tyr Phe Phe Leu
      50          55          60
Ser Asn Leu Ser Phe Val Glu Ile Cys Tyr Thr Thr Val Val Val Pro
65          70          75          80
Leu Met Leu Ser Asn Ile Phe Gly Ala Gln Lys Pro Ile Pro Leu Ala
      85          90          95
Gly Cys Gly Ala Gln Met Phe Phe Phe Leu Thr Leu Gly Gly Ala Asp
      100          105          110
Cys Phe Leu Leu Ala Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      115          120          125
His Pro Leu His Tyr Arg Leu Ile Met Thr Cys Asn Leu Cys Val Gln
      130          135          140
Met Leu Gly Gly Ala Val Gly Leu Ala Leu Phe Leu Ser Leu Gln Leu
145          150          155          160
Thr Ala Leu Ile Phe Thr Leu Pro Phe Cys Gly Tyr Arg Gln Glu Ile
      165          170          175
Asn His Phe Leu Cys Asp Val Pro Pro Val Leu Arg Leu Ala Cys Ala
      180          185          190
Ala Ile Arg Val His Gln Ala Val Leu Tyr Val Val Ser Ile Leu Val
      195          200          205
Leu Thr Val Pro Phe Leu Leu Ile Cys Val Ser Tyr Val Phe Ile Thr
      210          215          220
Cys Ala Ile Leu Ser Ile Arg Ser Ala Glu Gly Arg His Gln Ala Phe
225          230          235          240
Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Leu Gln Tyr Gly Cys
      245          250          255
Cys Ala Leu Ala Tyr Leu His Pro Gln Ser Ser Ser Ser Ala Asp Glu
      260          265          270
Asp Arg Gln Phe Ala Leu Val Tyr Thr Phe Ile Thr Pro Leu Leu Asn
      275          280          285
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Glu
      290          295          300
Lys Ser Ala Gln Tyr Gln Arg Asp Thr Xaa Val Leu
305          310          315

```

<210> 1905

<211> 312

<212> PRT

<213> Unknown (H38g823 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1905

```

Met Xaa Asn Ser Arg Glu Ala Ser Gln Phe Ile Phe Leu Gly Leu Ser

```

1	5	10	15
Asn Val Pro Glu Leu Gln Val Pro Phe Ile Met Phe Val Leu Ile			
20	25	30	
Tyr Leu Ile Asn Val Val Gly Asn Leu Gly Met Ile Ile Leu Ile Leu			
35	40	45	
Trp Tyr Ser Gln Leu His Asn Pro Met Tyr Phe Phe Phe Ser Asn Leu			
50	55	60	
Ser Leu Val Asp Phe Phe Tyr Ser Ser Val Val Thr Pro Lys Val Met			
65	70	75	80
Thr Gly Leu Leu Arg Glu Asp Lys Ile Ile Ser Tyr Thr Val Trp Ala			
85	90	95	
Thr Gln Thr Phe Phe Ser Asp Ser Phe Ala Ser Val Val Asn Leu Leu			
100	105	110	
Leu Ala Leu Met Ala Ser Gly His Tyr Ala Ala Val Cys Lys Pro Leu			
115	120	125	
His Tyr Thr Thr Thr Met Met Thr Ser Val Cys Thr Cys Leu Ala Ile			
130	135	140	
Gly Xaa Tyr Val Gly Gly Phe Leu Asn Ala Ser Ile His Thr Gly Glu			
145	150	155	160
Thr Phe Ser Leu Phe Cys Met Ser Ser Glu Val His His Phe Phe Cys			
165	170	175	
Glu Val Pro Ala Val Met Ala Leu Ser Cys Ser Asp Arg His Val Asn			
180	185	190	
Val Val Val Leu Val Tyr Val Thr Ser Phe Asn Ile Leu Phe Ala Leu			
195	200	205	
Leu Val Ile Leu Ile Ser Tyr Leu Leu Met Phe Ile Thr Ile Leu Lys			
210	215	220	
Met His Ser Thr Ala Gly Tyr Gln Lys Ala Leu Ala Ile Cys Ala Ser			
225	230	235	240
His Leu Thr Ala Val Ala Ile Phe Tyr Gly Thr Ile Ile Phe Met His			
245	250	255	
Ile Gln Pro Ser Ser Ser His Ser Ile Asp Thr Asp Lys Ile Ala Ala			
260	265	270	
Val Phe Tyr Thr Ile Val Phe Pro Met Val Asn His Val Val Xaa Arg			
275	280	285	
Leu Lys Asn Lys Val Lys Ser Thr Phe Lys Lys Ile Val Glu Lys Val			
290	295	300	
Lys Leu Ser Leu Gly Leu Xaa Val			
305	310		

<210> 1906

<211> 318

<212> PRT

<213> Unknown (H38g824 protein)

<220>

<223> Synthetic construct

<400> 1906

Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly			
1	5	10	15
Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu			
20	25	30	
Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu			
35	40	45	
Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg			
50	55	60	
Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg			
65	70	75	80
Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln			
85	90	95	

Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu
 100 105 110
 Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala
 130 135 140
 Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His
 145 150 155 160
 Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro
 165 170 175
 His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly
 180 185 190
 Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile
 195 200 205
 Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly
 210 215 220
 Ala Asn Leu Ala Met Gly Leu Thr Gln Ser Arg Arg Lys Val Phe Ser
 225 230 235 240
 Thr Cys Ser Ser His Arg Leu Val Val Ser Leu Phe Phe Gly Thr Ala
 245 250 255
 Ser Ile Thr Asn Asn Arg Pro Gln Ala Gly Ser Ser Glu Thr Thr Asp
 260 265 270
 Arg Val Ile Ser Leu Phe Asn Thr Val Ile Thr Pro Met Leu Asn Pro
 275 280 285
 Ile Ile Asn Thr His Gly Asn Lys Asp Val Arg Arg Ala Leu Arg Tyr
 290 295 300
 Leu Val Lys Arg Arg Arg Pro Ser Pro Gly Arg Gly Ser Gly
 305 310 315

<210> 1907

<211> 311

<212> PRT

<213> Unknown (H38g825 protein)

<220>

<223> Synthetic construct

<400> 1907

Met Glu Thr Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu
 1 5 10 15
 Gly Leu Ser Ser Asn Pro Lys Leu Gln Lys Pro Leu Phe Ala Ile Phe
 20 25 30
 Leu Ile Met Tyr Leu Leu Thr Ala Val Gly Asn Val Leu Ile Ile Leu
 35 40 45
 Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro
 65 70 75 80
 Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Ile Ile Ser Tyr Val
 85 90 95
 Gly Cys Leu Ile Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp
 100 105 110
 Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys
 115 120 125
 Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Trp His Cys Leu Leu
 130 135 140
 Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg
 145 150 155 160
 Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys
 165 170 175
 His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp


```

      180      185      190
Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
      195      200      205
Val Thr Pro Phe Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val
      210      215      220
Thr Val Leu Arg Ile Pro Ser Ala Ala Arg Lys Trp Lys Ala Phe Ser
225      230      235      240
Thr Cys Gly Ser His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val
      245      250      255
Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Gly
      260      265      270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275      280      285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys
      290      295      300
Leu Arg His Arg Ile Tyr Ser
305      310

```

<210> 1908
 <211> 131
 <212> PRT
 <213> Unknown (H38g826 protein)

<220>
 <223> Synthetic construct

```

<400> 1908
Met Lys Asn Lys Thr Val Leu Thr Glu Phe Ile Leu Leu Gly Leu Thr
  1      5      10      15
Asp Val Pro Glu Leu Gln Val Ala Val Phe Thr Phe Leu Phe Leu Ala
      20      25      30
Tyr Leu Leu Ser Ile Leu Gly Asn Leu Thr Ile Leu Ile Leu Thr Leu
      35      40      45
Leu Asp Ser His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe
      50      55      60
Ser Phe Leu Glu Ile Ser Phe Thr Asn Ile Phe Ile Pro Arg Val Leu
      65      70      75      80
Ile Ser Ile Thr Thr Gly Asn Lys Ser Ile Ser Phe Ala Gly Cys Phe
      85      90      95
Thr Gln Tyr Phe Phe Ala Met Phe Leu Gly Ala Thr Glu Phe Tyr Leu
      100      105      110
Leu Ala Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Leu Met
      115      120      125
Thr Met His
      130

```

<210> 1909
 <211> 311
 <212> PRT
 <213> Unknown (H38g827 protein)

<220>
 <223> Synthetic construct

```

<400> 1909
Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu
  1      5      10      15
Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro Leu Phe Ala Ile Phe
      20      25      30
Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn Val Leu Ile Ile Pro
      35      40      45

```

Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro
 65 70 75 80
 Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val
 85 90 95
 Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp
 100 105 110
 Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys
 115 120 125
 Asn Pro Leu His Tyr Asp Val Met Lys Pro Arg His Cys Leu Leu
 130 135 140
 Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg
 145 150 155 160
 Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys
 165 170 175
 His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp
 180 185 190
 Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
 195 200 205
 Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Met Val
 210 215 220
 Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile
 245 250 255
 Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp
 260 265 270
 Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys
 290 295 300
 Leu Gln Asp Arg Ile Tyr Arg
 305 310

<210> 1910

<211> 313

<212> PRT

<213> Unknown (H38g828 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1910

Met Pro Asn Lys Ile Val Val Thr Glu Phe Phe Leu Thr Arg Pro Asp
 1 5 10 15
 Gly Leu Gln Lys Ser Phe Gln Val Ala Val Phe Leu Leu Pro Asp Ala
 20 25 30
 Cys His Thr Leu Xaa Leu Ser Leu Gly Thr Xaa Ile Ile Ile Thr Met
 35 40 45
 Thr Leu Leu Asp Thr Arg Met Gln Thr Ser Met Tyr Leu Phe Leu Gln
 50 55 60
 Asn Leu Ser Cys Leu Glu Ile Trp Phe Gln Thr Val Ile Val Pro Lys
 65 70 75 80
 Met Leu Leu Asn Ile Ala Met Gly Thr Lys Thr Val Ser Phe Ala Gly
 85 90 95
 Cys Ile Thr Gln Asp Phe Phe His Ile Phe Leu Gly Ala Thr Glu Phe

```

      100      105      110
Phe Leu Leu Thr Ala Met Ala Tyr Asp Gln Tyr Ile Ala Ile Cys Lys
      115      120      125
Pro Leu His Tyr Pro Met Leu Ile Ser Ser Arg Val Cys Thr Gln Leu
      130      135      140
Ile Leu Thr Cys Trp Leu Leu Gly Phe Ser Phe Ile Ile Met Pro Val
      145      150      155      160
Ile Leu Thr Ser Gln Leu Pro Phe Cys Asp Thr His Ile Lys His Phe
      165      170      175
Phe Cys Asp Tyr Thr Pro Leu Met Glu Val Val Cys Ser Gly Pro Lys
      180      185      190
Val Leu Glu Met Val Asp Phe Thr Leu Ala Leu Val Ala Leu Phe Gly
      195      200      205
Thr Leu Val Leu Ile Thr Leu Ser Tyr Val Gln Ile Ile Gln Thr Ile
      210      215      220
Val Arg Ile Pro Ala Val Gln Glu Arg Lys Lys Ala Phe Ser Thr Cys
      225      230      235      240
Ser Ser His Val Ile Met Val Thr Met Cys Tyr Asp Ser Cys Phe Phe
      245      250      255
Met Tyr Val Lys Pro Ser Pro Gly Lys Trp Val Asp Val Asn Lys Gly
      260      265      270
Val Ser Leu Ile Asn Thr Ile Ile Ala Pro Leu Leu Asn Pro Phe Ile
      275      280      285
Cys Thr Leu Arg Asn Gln Gln Val Lys Gln Val Met Lys Asp Leu Val
      290      295      300
Arg Lys Met Thr Leu Ser Glu Asn Lys
      305      310

```

<210> 1911

<211> 317

<212> PRT

<213> Unknown (H38g829 protein)

<220>

<223> Synthetic construct

<400> 1911

```

Met Asn Ser Glu Asn Leu Thr Arg Ala Ala Val Ala Pro Ala Glu Phe
  1      5      10      15
Val Leu Leu Gly Ile Thr Asn Arg Trp Asp Leu Arg Val Ala Leu Phe
      20      25      30
Leu Thr Cys Leu Pro Val Tyr Leu Val Ser Leu Leu Gly Asn Met Gly
      35      40      45
Met Ala Leu Leu Ile Arg Met Asp Ala Arg Leu His Thr Pro Met Tyr
      50      55      60
Phe Phe Leu Ala Asn Leu Ser Leu Leu Asp Ala Cys Tyr Ser Ser Ala
      65      70      75      80
Ile Gly Pro Lys Met Leu Val Asp Leu Leu Leu Pro Arg Ala Thr Ile
      85      90      95
Pro Tyr Thr Ala Cys Ala Leu Gln Met Phe Val Phe Ala Gly Leu Ala
      100      105      110
Asp Thr Glu Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
      115      120      125
Ala Ile Arg Asn Pro Leu Leu Tyr Thr Thr Ala Met Ser Gln Arg Leu
      130      135      140
Cys Leu Ala Leu Leu Gly Ala Ser Gly Leu Gly Gly Ala Val Ser Ala
      145      150      155      160
Phe Val His Thr Thr Leu Thr Phe Arg Leu Ser Phe Cys Arg Ser Arg
      165      170      175
Lys Ile Asn Ser Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Ile Ser
      180      185      190

```

Cys Ser Asp Thr Ser Leu Asn Glu Leu Leu Leu Phe Ala Ile Cys Gly
 195 200 205
 Phe Ile Gln Thr Ala Thr Val Leu Ala Ile Thr Val Ser Tyr Gly Phe
 210 215 220
 Ile Ala Gly Ala Val Ile His Met Arg Ser Val Glu Gly Ser Arg Arg
 225 230 235 240
 Ala Ala Ser Thr Gly Gly Ser His Leu Thr Ala Val Ala Met Met Tyr
 245 250 255
 Gly Thr Leu Ile Phe Met Tyr Leu Arg Pro Ser Ser Ser Tyr Ala Leu
 260 265 270
 Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Ser
 275 280 285
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala
 290 295 300
 Leu Arg Gln Thr Trp Ser Arg Phe His Cys Pro Gly Gln
 305 310 315

<210> 1912

<211> 316

<212> PRT

<213> Unknown (H38g830 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1912

Met Val Ile Leu Ser Trp Glu Asn Gln Thr Met Arg Val Glu Phe Val
 1 5 10 15
 Leu Gln Gly Phe Ser Ser Ile Arg Gln Leu Asn Ile Phe Leu Phe Met
 20 25 30
 Ile Ile Leu Val Phe Tyr Ile Leu Thr Val Ser Gly Asn Ile Leu Ile
 35 40 45
 Val Leu Leu Val Leu Val Arg His His Leu His Thr Pro Met Tyr Phe
 50 55 60
 Leu Leu Val Asn Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Asn Ile
 65 70 75 80
 Ile Pro Lys Met Leu Leu Ile Ile Ile Ala Glu Xaa Lys Thr Ile Ser
 85 90 95
 Val Ala Gly Trp Leu Ala Gln Phe Tyr Phe Phe Gly Ser Leu Ala Ala
 100 105 110
 Thr Glu Cys Leu Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala
 115 120 125
 Ile Cys Gln Pro Leu Cys Tyr Arg Val Leu Met Thr Gly Pro Leu Cys
 130 135 140
 Ile Arg Leu Ala Ala Gly Ser Trp Phe Cys Cys Phe Leu Leu Thr Ala
 145 150 155 160
 Ile Thr Met Val Leu Leu Cys Arg Leu Thr Phe Cys Gly Pro Tyr Glu
 165 170 175
 Thr Asp His Phe Phe Cys Asp Phe Thr Pro Leu Val His Leu Ser Cys
 180 185 190
 Met Asp Thr Ser Val Thr Glu Thr Ile Ala Phe Ala Thr Ser Ser Ala
 195 200 205
 Val Thr Leu Ile Pro Phe Leu Leu Ile Val Ala Ser Tyr Ser Cys Val
 210 215 220
 Leu Ser Ala Ile Leu Arg Ile Pro Ser Cys Thr Gly Gln Lys Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Val Phe Tyr Gly

				245					250					255		
Thr	Leu	Ile	Ala	Thr	Tyr	Leu	Val	Pro	Ser	Ala	Asn	Ser	Ser	Gln	Leu	
			260					265					270			
Leu	Cys	Lys	Gly	Ser	Ser	Leu	Leu	Tyr	Ile	Ile	Leu	Thr	Pro	Met	Phe	
		275					280					285				
Asn	Pro	Ile	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	His	Glu	Ala	Leu	
		290				295					300					
Lys	Lys	Cys	Leu	Arg	Lys	Lys	Ser	Gly	Val	Cys	Leu					
305					310					315						

```
<210> 1913
<211> 309
<212> PRT
<213> Unknown (H38g831 protein)
```

<220>
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(309)
<223> Xaa = Any Amino Acid
```

<400> 1913																
Glu	Xaa	Met	Gly	Thr	Ser	Asn	Asn	Val	Thr	Glu	Phe	Val	Leu	Pro	Gly	
1				5					10					15		
Leu	Ser	Gln	Asp	Pro	Asp	Val	Gln	Lys	Ala	Leu	Phe	Val	Met	Phe	Leu	
			20					25					30			
Leu	Thr	Tyr	Asn	Val	Thr	Met	Val	Gly	Asn	Leu	Leu	Ile	Val	Val	Thr	
			35				40					45				
Ile	Ile	Ala	Ile	Ala	Ser	Leu	Asp	Ser	Pro	Val	Ser	Phe	Phe	Leu	Ala	
			50			55					60					
Cys	Leu	Ser	Phe	Ile	Asp	Ala	Val	Tyr	Ser	Thr	Ser	Phe	Ser	Pro	Lys	
65					70				75					80		
Leu	Met	Ile	Asp	Leu	Cys	Asp	Lys	Lys	Thr	Val	Ser	Phe	Leu	Ala		
				85				90					95			
Cys	Met	Gly	Gln	Leu	Phe	Ile	Asn	Tyr	Pro	Phe	Gly	Gly	Ile	Glu	Val	
			100					105					110			
Phe	Leu	Leu	Val	Gly	Met	Ala	Cys	Asp	His	Tyr	Val	Asp	Ile	Cys	Lys	
			115				120					125				
Leu	Leu	His	Tyr	Leu	Thr	Ile	Met	Asn	Trp	Gln	Val	Cys	Ile	Leu	Leu	
			130				135				140					
Phe	Met	Val	Ala	Val	Thr	Gly	Gly	Phe	Leu	His	Ser	Met	Phe	Gln	Ile	
145					150				155					160		
Val	Val	Val	Tyr	Ser	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Val	Ile	Asp	His	
				165					170				175			
Phe	Cys	Asp	Met	Tyr	Pro	Leu	Leu	Glu	Met	Val	Cys	Thr	Asp	Thr	Tyr	
			180					185					190			
Phe	Ile	Gly	Leu	Thr	Val	Ile	Ala	Asn	Gly	Gly	Ala	Val	Cys	Met	Val	
			195				200				205					
Ile	Phe	Ile	Leu	Leu	Leu	Ile	Ser	Tyr	Gly	Val	Ile	Leu	Asn	Ser	Leu	
			210				215				220					
Lys	Thr	Tyr	Ser	Gln	Glu	Gly	Gly	His	Lys	Ala	Leu	Ser	Thr	Cys	Ser	
225					230				235					240		
Ser	Asn	Ile	Thr	Val	Ser	Leu	Phe	Phe	Asp	Pro	Cys	Ile	Phe	Ile		
				245				250				255				
Tyr	Val	Arg	Pro	Asp	Ser	Asn	Phe	Pro	Ile	Asp	Lys	Phe	Met	Thr	Val	
			260					265					270			
Phe	Tyr	Thr	Ile	Ile	Thr	Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu	
			275				280				285					
Arg	Asn	Leu	Glu	Val	Arg	Ile	Ala	Val	Lys	Asn	Leu	Trp	Cys	Lys	Asn	
			290				295				300					

Xaa Thr Ile Val Arg
305

<210> 1914

<211> 318

<212> PRT

<213> Unknown (H38g832 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1914

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
 1          5          10          15
Leu Ser Ser Ser Trp Glu Met His Pro Phe Leu Phe Trp Phe Phe Ser
      20          25          30
Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
      35          40          45
Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
 50          55          60
Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
65          70          75          80
Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
      85          90          95
Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
      100          105          110
Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
      115          120          125
Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
      130          135          140
Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
      145          150          155          160
Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
      165          170          175
Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
      180          185          190
Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu
      195          200          205
Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser
      210          215          220
Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val
      225          230          235          240
Gly Ile Leu Phe Phe Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro Leu
      245          250          255
Pro Lys Thr Thr His Asp Xaa Tyr Leu Phe Ile Val Pro Leu Leu Ser
      260          265          270
Pro Leu Ser Arg Ile Tyr Thr Leu Arg Asn Lys Asp Met Asn Val Ser
      275          280          285
Met Glu Arg Leu Gly Lys Trp Ile Ala Gly Ser Ser Arg Met Ser Xaa
      290          295          300
Xaa Met Val Leu Ser Arg Val Gln Asp Asp Ser Val Ser Pro
305          310          315

```

<210> 1915

<211> 309

<212> PRT

<213> Unknown (H38g833 protein)

<220>

<223> Synthetic construct

<400> 1915

```

Met Glu Gly Ile Asn Lys Thr Ala Lys Met Gln Phe Phe Phe Arg Pro
 1           5           10           15
Phe Ser Pro Asp Pro Glu Val Gln Met Leu Ile Phe Val Val Phe Leu
          20           25           30
Met Met Tyr Leu Thr Ser Leu Gly Gly Asn Ala Thr Ile Ala Val Ile
          35           40           45
Val Gln Ile Asn His Ser Leu His Thr Pro Met Tyr Phe Phe Leu Ala
          50           55           60
Asn Leu Ala Val Leu Glu Ile Phe Tyr Thr Ser Ser Ile Thr Pro Leu
65           70           75           80
Ala Leu Ala Asn Leu Leu Ser Met Gly Lys Thr Pro Val Ser Ile Thr
          85           90           95
Gly Cys Gly Thr Gln Met Phe Phe Phe Val Phe Leu Gly Gly Ala Asp
          100          105          110
Cys Val Leu Leu Val Val Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys
          115          120          125
His Pro Leu Arg Tyr Arg Leu Ile Met Ser Trp Ser Leu Cys Val Glu
          130          135          140
Leu Leu Val Gly Ser Leu Val Leu Gly Phe Leu Leu Ser Leu Pro Leu
145          150          155          160
Thr Ile Leu Ile Phe His Leu Pro Phe Cys His Asn Asp Glu Ile Tyr
          165          170          175
His Phe Tyr Cys Asp Met Pro Ala Val Met Arg Leu Ala Cys Ala Asp
          180          185          190
Thr Arg Val His Lys Thr Ala Leu Tyr Ile Ile Ser Phe Ile Val Leu
          195          200          205
Ser Ile Pro Leu Ser Leu Ile Ser Ile Ser Tyr Val Phe Ile Val Val
          210          215          220
Ala Ile Leu Arg Ile Arg Ser Ala Glu Gly Arg Gln Gln Ala Tyr Ser
225          230          235          240
Thr Cys Ser Ser His Ile Leu Val Val Leu Leu Gln Tyr Gly Cys Thr
          245          250          255
Ser Phe Ile Tyr Leu Ser Pro Ser Ser Ser Tyr Ser Pro Glu Met Gly
          260          265          270
Arg Val Val Ser Val Ala Tyr Thr Phe Ile Thr Pro Ile Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Lys Glu Leu Lys Asp Ala Leu Arg Lys
          290          295          300
Ala Leu Arg Lys Phe
305

```

<210> 1916

<211> 329

<212> PRT

<213> Unknown (H38g834 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1916

```

Asp Ser Val Asp Gln Val Asn Asp Ser Leu Val Thr Glu Phe Val Leu
 1           5           10           15

```

Leu Gly Leu Ala Gln Ser Leu Glu Met Gln Phe Phe Leu Phe Leu Phe
 20 25 30
 Phe Ser Leu Phe Tyr Val Gly Ile Ile Leu Gly Asn Leu Phe Ile Val
 35 40 45
 Phe Thr Val Ile Phe Asp Pro His Leu His Ser Pro Met Tyr Ile Leu
 50 55 60
 Leu Ala Asn Leu Ser Leu Ile Asp Leu Ser Leu Ser Ser Thr Thr Val
 65 70 75 80
 Pro Arg Leu Ile Tyr Asp Leu Phe Thr Asp Cys Lys Val Ile Ser Phe
 85 90 95
 His Asn Cys Met Ile Gln Lys Phe Phe Ile His Val Thr Gly Gly Val
 100 105 110
 Glu Met Val Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile
 115 120 125
 Cys Lys Pro Leu His Tyr Pro Thr Ile Met Asn Pro Lys Met Cys Met
 130 135 140
 Phe Leu Val Ala Ala Ala Trp Val Ile Gly Val Ile His Ala Met Ser
 145 150 155 160
 Gln Phe Val Phe Val Ile Asn Leu Pro Phe Cys Gly Pro Asn Asn Val
 165 170 175
 Gly Ser Phe Tyr Cys Asp Phe Pro Arg Val Ile Lys Leu Ala Cys Met
 180 185 190
 Asp Thr Tyr Gly Leu Glu Phe Val Val Thr Ala Asn Ser Gly Phe Ile
 195 200 205
 Ser Met Gly Thr Phe Phe Phe Leu Ile Val Ser Tyr Ile Phe Ile Leu
 210 215 220
 Val Thr Val Gln Arg His Ser Ser Asn Asp Leu Ser Lys Ala Phe Phe
 225 230 235 240
 Thr Ser Xaa Ala His Ile Thr Val Val Val Leu Phe Phe Ala Pro Cys
 245 250 255
 Met Phe Leu Tyr Val Trp Pro Phe Pro Thr Lys Ser Leu Asp Lys Phe
 260 265 270
 Phe Ala Ile Met Asn Phe Val Val Thr Pro Val Leu Asn Pro Ala Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Asp Met Lys Phe Ala Met Arg Arg Leu Asn
 290 295 300
 Gln His Ile Leu Asn Ser Met Glu Met Thr Xaa His Ile Trp Leu Met
 305 310 315 320
 Arg Ala Gln Asp Lys Cys His Gly Pro
 325

<210> 1917

<211> 257

<212> PRT

<213> Unknown (H38g835 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(257)

<223> Xaa = Any Amino Acid

<400> 1917

Ser Met Tyr Phe Phe Leu Thr Asn Phe Ala Gly Leu Glu Ile Phe Tyr
 1 5 10 15
 Phe Phe Thr Ile Ala Pro Leu Thr Leu Ala Asn Val Leu Pro Met Gly
 20 25 30
 Arg Asn Leu Ile Ser Leu Pro Gly Cys Gly Gly Gln Met Phe Phe Phe
 35 40 45
 Ile Phe Leu Gly Arg Ala Asp Cys Ile Leu Leu Ala Val Met Ala Phe

50	55	60
Asp Trp Phe Val Ala	Ile Cys Cys Pro Leu	Cys Tyr Gly Leu Ile Met
65	70	75
Ser Trp Arg Leu Cys	Val Gln Leu Thr Leu	Gly Ser Leu Leu Leu Gly
85	90	95
Phe Phe Leu Ala Met	Gln Leu Thr Val Leu	Ile Phe Gln Leu Pro Leu
100	105	110
Cys Ser Ser Lys Glu	Ile Ser Thr Phe Tyr	Cys Asp Val Leu Pro Val
115	120	125
Met Arg Leu Ala Cys	Ala Asp Thr Trp Val	His Glu Ala Thr Met Ser
130	135	140
Met Val Ser Thr Thr	Phe Leu Thr Val Pro	Phe Leu Leu Ile Thr Leu
145	150	155
Ser Tyr Val Ser Ile	Met Ala Ala Ile Leu	Lys Ile Cys Ser Ala Glu
165	170	175
Gly Arg His Lys Ala	Phe Ser Thr Cys Ser	Ser His Leu Thr Val Val
180	185	190
Leu Leu Gln Asp Xaa	Cys Thr Arg Leu Ala	Phe Leu Cys Pro Ser Ser
195	200	205
Ser Tyr Tyr Pro Glu	Arg Gly Gln Ala Val	Ser Val Val Tyr Thr Phe
210	215	220
Ile Thr Pro Val Leu	Asn Pro Leu Ile Tyr	Ser Met Arg Asn Thr Glu
225	230	235
Leu Lys Asp Ala Leu	Lys Arg Ala Met Thr	Arg Val Pro Leu Leu Xaa
245	250	255
Thr		

<210> 1918

<211> 305

<212> PRT

<213> Unknown (H38g836 protein)

<220>

<223> Synthetic construct

<400> 1918

Met Val Thr Glu Phe	Ile Phe Leu Gly Leu	Ser Asp Ser Gln Glu Leu
1	5	10
Gln Thr Phe Leu Phe	Met Leu Phe Phe	Val Phe Tyr Gly Gly Ile Val
20	25	30
Phe Gly Asn Leu Leu	Ile Val Ile Thr	Val Val Ser Asp Ser His Leu
35	40	45
His Ser Pro Met Tyr	Phe Leu Leu Ala	Asn Leu Ser Leu Ile Asp Leu
50	55	60
Ser Leu Ser Ser Val	Thr Ala Pro Lys	Met Ile Thr Asp Phe Phe Ser
65	70	75
Gln Arg Lys Val Ile	Ser Phe Lys Gly	Cys Leu Val Gln Ile Phe Leu
85	90	95
Leu His Phe Phe Gly	Gly Ser Glu Met	Val Ile Leu Ile Ala Met Gly
100	105	110
Phe Asp Arg Tyr Ile	Ala Ile Cys Lys	Pro Leu His Tyr Thr Thr Ile
115	120	125
Met Cys Gly Asn Ala	Cys Val Gly Ile	Met Ala Val Ala Trp Gly Ile
130	135	140
Gly Phe Leu His Ser	Val Ser Gln Leu	Ala Phe Ala Val His Leu Pro
145	150	155
Phe Cys Gly Pro Asn	Glu Val Asp Ser	Phe Tyr Cys Asp Leu Pro Arg
165	170	175
Val Ile Lys Leu Ala	Cys Thr Asp Thr	Tyr Arg Leu Asp Ile Met Val
180	185	190

Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile
 195 200 205
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Cys Pro Leu Asp
 210 215 220
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
 225 230 235 240
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
 245 250 255
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
 260 265 270
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
 275 280 285
 Thr Ala Ile Arg Arg Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
 290 295 300
 Phe
 305

<210> 1919

<211> 318

<212> PRT

<213> Unknown (H38g837 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1919

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
 1 5 10 15
 Leu Ser Ser Ser Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe Ser
 20 25 30
 Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
 35 40 45
 Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
 50 55 60
 Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
 65 70 75 80
 Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
 85 90 95
 Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
 100 105 110
 Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
 115 120 125
 Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
 130 135 140
 Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
 145 150 155 160
 Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
 165 170 175
 Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
 180 185 190
 Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu
 195 200 205
 Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser
 210 215 220
 Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val
 225 230 235 240
 Gly Ile Leu Phe Phe Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro Leu

245								250				255			
Pro	Lys	Thr	Thr	His	Asp	Xaa	Tyr	Leu	Phe	Ile	Val	Pro	Leu	Leu	Ser
260								265				270			
Pro	Leu	Ser	Arg	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Asp	Met	Asn	Val	Ser
275								280				285			
Met	Glu	Arg	Leu	Gly	Lys	Trp	Ile	Ala	Gly	Ser	Ser	Arg	Met	Ser	Xaa
290								295				300			
Xaa	Met	Val	Leu	Ser	Arg	Val	Gln	Asp	Asp	Ser	Val	Ser	Pro		
305								310				315			

<210> 1920

<211> 328

<212> PRT

<213> Unknown (H38g838 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1) . . . (328)

<223> Xaa = Any Amino Acid

<400> 1920

Leu 1	Ser	Ile	Cys	Phe 5	Phe	Leu	Cys	Ile	Phe 10	Ser	Ala	Asp	Ile	Xaa 15	Ser
Met	Leu	Ala	Met	Glu	Gln	Asn	Asn	Gly 25	Thr	Glu	Val	Thr	Glu	Phe	Ile
Leu	Leu	Gly	Phe	Ala	Gly	Gln	His	Lys	Ser	Trp	His	Ile	Leu	Ser	Ile
Ala	Phe	Leu	Ala	Ile	Tyr	Val	Val	Thr	Pro	Val	Gly	Asn	Ile	Gly	Met
Ile	Leu	Leu	Ile	Lys	Ile	Asp	Ala	Ser	Leu	His	Ile	Pro	Met	Xaa	Ile
Phe	Leu	Gln	His	Leu	Ala	Phe	Val	Asp	Leu	Cys	Tyr	Thr	Ser	Ala	Ile
Thr	Pro	Lys	Met	Leu	Lys	Asn	Phe	Val	Glu	Thr	Lys	Lys	Ser	Ile	Ser
Cys	Ile	Gly	Cys	Met	Val	Gln	Leu	Leu	Val	Tyr	Gly	Thr	Phe	Ala	Thr
Ser	Asp	Cys	Tyr	Ile	Leu	Ala	Ala	Met	Ala	Val	Asp	Arg	Tyr	Val	Ala
Phe	Cys	Asn	Pro	Leu	His	Tyr	Pro	Gly	Val	Met	Ser	Gln	Arg	Leu	Cys
Ile	Lys	Leu	Leu	Val	Ser	Ser	Tyr	Val	Met	Gly	Phe	Leu	Asn	Ala	Ser
Ile	Asn	Ile	Ser	Phe	Thr	Phe	Ser	Leu	Asn	Phe	Cys	Lys	Ser	Lys	Thr
Ile	Asn	His	Phe	Phe	Cys	Asp	Glu	Pro	Pro	Ile	Ile	Ala	Leu	Pro	Cys
Ser	Asn	Ile	Asp	Leu	Asn	Ile	Met	Leu	Leu	Thr	Val	Phe	Val	Gly	Leu
Asn	Leu	Met	Cys	Thr	Val	Met	Val	Val	Ile	Ile	Ser	Cys	Ile	Tyr	Val
Leu	Val	Ala	Ile	Leu	Arg	Ile	Ser	Ser	Ala	Ala	Gly	Lys	Lys	Lys	Ser
Leu	Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Ala	Val	Thr	Ile	Phe	Tyr	Gly
Val	Leu	Ser	Tyr	Met	Tyr	Leu	Cys	His	Arg	Ile	Asn	Glu	Ser	Gln	Lys
Gln	Glu	Lys	Val	Ala	Ser	Val	Phe	Tyr	Gly	Ile	Ile	Pro	Met	Leu	

Asn Pro Leu Ile Tyr Ser Gln Arg Asn Gln Asp Val Ile Glu Ala Ile
 305 310 315 320
 Lys L u Thr Glu Lys Lys Tyr Phe
 325

<210> 1921
 <211> 338
 <212> PRT
 <213> Unknown (H38g839 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(338)
 <223> Xaa = Any Amino Acid

<400> 1921
 Met Ile Ser Phe Leu Val Pro Gly Leu Met Glu Glu Glu Asn Gln Arg
 1 5 10 15
 Gly Val Val His Phe His Phe His Phe Phe Ser Thr Asp Leu Val Val
 20 25 30
 Ala Ser Phe Ile Ile Val Ala Leu Met Leu His Leu Arg Ser Leu Val
 35 40 45
 Gly His Phe Thr Phe Gly Pro Thr Val Trp Gln Asp Pro Phe Leu His
 50 55 60
 Ile Pro Met Tyr Leu Phe Leu Phe Ser Leu Ala Leu Thr Met Leu Glu
 65 70 75 80
 Ile Gly Tyr Ser Thr Asn Ile Ser Pro Pro Thr Leu Ala Thr Val Leu
 85 90 95
 Tyr Met Gly Lys Met Leu Ile Ser Leu Pro Gly Tyr Gly Thr Gln Met
 100 105 110
 Leu Phe Val Ile Leu Leu Arg Gly Ser Glu Cys Val Leu Leu Ala Val
 115 120 125
 Met Ala Tyr Asp Arg Tyr Ile Thr Ile Cys His Pro Phe Asn Tyr Asn
 130 135 140
 Leu Ile Met Ser Gly Xaa Leu Cys Gly Gln Met Thr Leu Gly Ser Leu
 145 150 155 160
 Arg Leu Gly Phe Leu Leu Ser Leu Phe Leu Thr Met Leu Ile Xaa His
 165 170 175
 Pro Pro Phe Cys Gly Leu Asp Glu Thr Tyr His Phe Phe Cys Asp Met
 180 185 190
 Pro Thr Ala Ser Arg Leu Val Cys Ala Asp Thr Thr Val His Glu Ser
 195 200 205
 Ala Leu Xaa Leu Pro Cys Gly His His His His Pro Leu Pro Ser Ser
 210 215 220
 Leu Ile Cys Leu Pro Tyr Gly Cys Leu Ala Ala Thr Ile Leu Arg Met
 225 230 235 240
 His Ser Ala Lys Arg Lys His Xaa Ala Phe Ser Thr Ser Ser Ser His
 245 250 255
 Leu Ile Val Val Leu Leu Lys Tyr Trp Cys Cys Ile Leu Ile Cys Leu
 260 265 270
 Cys Pro Ser Ser Tyr Ser Pro Glu Glu Gly Trp Glu Val Ser Leu
 275 280 285
 Val His Met Phe Ile Leu Pro Val Trp Asn Pro Leu Ile Tyr Ser Val
 290 295 300
 Trp Asn Gln Asp Val Thr Asp Ala Val Glu Arg Leu Val Ala Arg Met
 305 310 315 320
 Ser Leu Val Leu Thr Ala Arg Asn Ile Pro Ser Xaa Lys Ile Phe Pro
 325 330 335
 Xaa Leu

<210> 1922
 <211> 329
 <212> PRT
 <213> Unknown (H38g840 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(329)
 <223> Xaa = Any Amino Acid

<400> 1922
 Asp Ser Val Asp Gln Val Asn Asp Ser Leu Val Thr Glu Phe Val Leu
 1 5 10 15
 Leu Gly Leu Ala Gln Ser Leu Glu Met Gln Phe Phe Leu Phe Leu Phe
 20 25 30
 Phe Ser Leu Phe Tyr Val Gly Ile Leu Gly Asn Leu Phe Ile Val
 35 40 45
 Phe Thr Val Ile Phe Asp Pro His Leu His Ser Pro Met Tyr Ile Leu
 50 55 60
 Leu Ala Asn Leu Ser Leu Ile Asp Leu Ser Leu Ser Ser Thr Thr Val
 65 70 75 80
 Pro Arg Leu Ile Tyr Asp Leu Phe Thr Asp Cys Lys Val Ile Ser Phe
 85 90 95
 His Asn Cys Met Ile Gln Lys Phe Phe Ile His Val Thr Gly Gly Val
 100 105 110
 Glu Met Val Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Thr Ala Ile
 115 120 125
 Cys Lys Pro Leu His Tyr Pro Thr Ile Met Asn Pro Lys Met Cys Met
 130 135 140
 Phe Leu Val Ala Ala Ala Trp Val Ile Gly Val Ile His Ala Met Ser
 145 150 155 160
 Gln Phe Val Phe Val Ile Asn Leu Pro Phe Cys Gly Pro Asn Asn Val
 165 170 175
 Gly Ser Phe Tyr Cys Asp Phe Pro Arg Val Ile Lys Leu Ala Cys Met
 180 185 190
 Asp Thr Tyr Gly Leu Glu Phe Val Val Thr Ala Asn Ser Gly Phe Ile
 195 200 205
 Ser Met Gly Thr Phe Phe Phe Leu Ile Val Ser Tyr Ile Phe Ile Leu
 210 215 220
 Val Thr Val Gln Arg His Ser Ser Asn Asp Leu Ser Lys Ala Phe Phe
 225 230 235 240
 Thr Ser Xaa Ala His Ile Thr Val Val Val Leu Phe Phe Ala Pro Cys
 245 250 255
 Met Phe Leu Tyr Val Trp Pro Phe Pro Thr Lys Ser Leu Asp Lys Phe
 260 265 270
 Phe Ala Ile Met Asn Phe Val Val Thr Pro Val Leu Asn Pro Ala Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Asp Met Lys Phe Ala Met Arg Arg Leu Asn
 290 295 300
 Gln His Ile Leu Asn Ser Met Glu Met Thr Xaa His Ile Trp Leu Met
 305 310 315 320
 Arg Ala Gln Asp Lys Cys His Gly Pro
 325

<210> 1923
 <211> 245
 <212> PRT

<213> Unknown (H38g841 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(245)

<223> Xaa = Any Amino Acid

<400> 1923

```

Met Gln Ser Glu His Leu Ala Glu Phe Ser Glu Phe Leu Ile Leu Ser
 1              5              10              15
Leu Ser Glu Ile Gln Asn Cys Ser Pro Phe Phe Gly Leu Phe Leu Ser
      20              25              30
Met Asn Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile
      35              40              45
Ser Ser Asp Ser His Leu His Lys Pro Met Tyr Phe Leu Leu Ser Lys
 50              55              60
Leu Ser Met Ala Ala Ile Cys Phe Val Phe Thr Met Ile Gln Lys Met
65              70              75              80
Met Val Asn Leu Arg Ala Gln Ser Lys Asp Ile Phe Thr Gln Pro Ser
      85              90              95
Gly Ser Pro Ile Pro Phe Xaa Met Cys Ser Leu Ile Arg Phe Leu Leu
      100             105             110
Ile Gln Gln Lys Ser Val Val Leu Ile Phe Glu Tyr Ser Arg Phe Xaa
      115             120             125
Phe Ser Tyr Leu Asn Leu Lys Met Xaa Thr Asn Tyr Ser Phe Val Xaa
      130             135             140
Ala Phe Gln Asn Asn Xaa Arg Gln Leu Cys Pro Phe Leu Asp Asn His
      145             150             155             160
His Thr Phe Phe Thr Leu Ile Asp Thr Gln Leu Leu Ile Ser His Gly
      165             170             175
Phe Ser Thr Gln Thr Thr Phe Ile Leu Ser Ser Tyr Ala Ser Gly Tyr
      180             185             190
Ala Thr Val Asp Ser Gln Cys Phe Ile Tyr Phe Leu Asn Met Met Ile
      195             200             205
Thr Ile Asn Leu Phe Val Arg Phe Lys Asn Ile Phe Met His Ser Ser
      210             215             220
Ile Ser Ile Asn Tyr Asn Tyr Tyr Phe Lys Lys Xaa Asn Lys Gly Gly
      225             230             235             240
Ile Tyr Glu Ile Tyr
              245

```

<210> 1924

<211> 305

<212> PRT

<213> Unknown (H38g842 protein)

<220>

<223> Synthetic construct

<400> 1924

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Glu Leu
 1              5              10              15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
      20              25              30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
      35              40              45
His Ser Pro Met Tyr Phe Leu Ala Asn Leu Ser Leu Ile Asp Leu
 50              55              60
Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser

```

```

65          70          75          80
Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
      85          90          95
Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
      100          105          110
Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile
      115          120          125
Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile
      130          135          140
Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Pro
      145          150          155
Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
      165          170          175
Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
      180          185          190
Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile
      195          200          205
Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp
      210          215          220
Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
      225          230          235
Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
      245          250          255
Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
      260          265          270
Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
      275          280          285
Thr Ala Ile Arg Arg Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
      290          295          300

```

Phe
305

<210> 1925

<211> 309

<212> PRT

<213> Unknown (H38g843 protein)

<220>

<223> Synthetic construct

<400> 1925

```

Met Ala Ala Gly Asn His Ser Thr Val Thr Glu Phe Ile Leu Lys Gly
1          5          10          15
Leu Thr Lys Arg Ala Asp Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
      20          25          30
Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu
      35          40          45
Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
      50          55          60
Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
      65          70          75          80
Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly
      85          90          95
Cys Met Ser Gln Leu Tyr Phe Phe Leu Val Phe Val Ile Ala Glu Cys
      100          105          110
Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu
      130          135          140
Val Ala Val Val Tyr Ala Ile Gly Leu Ile Gly Ser Thr Ile Glu Thr
      145          150          155          160

```

Gly Leu M t Leu Lys Leu Pro Tyr Cys Glu His Leu Ile Ser His Tyr
 165 170 175
 Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr
 180 185 190
 Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val
 195 200 205
 Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile
 210 215 220
 Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe
 245 250 255
 Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val
 260 265 270
 Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu
 290 295 300
 Arg Gly Lys Leu Phe
 305

<210> 1926

<211> 310

<212> PRT

<213> Unknown (H38g844 protein)

<220>

<223> Synthetic construct

<400> 1926

Met Ala Ala Lys Asn Ser Ser Val Thr Glu Phe Ile Leu Glu Gly Leu
 1 5 10 15
 Thr His Gln Pro Gly Leu Arg Ile Pro Leu Phe Phe Leu Phe Leu Gly
 20 25 30
 Phe Tyr Thr Val Thr Val Val Gly Asn Leu Gly Leu Ile Thr Leu Ile
 35 40 45
 Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn
 50 55 60
 Leu Ser Leu Ile Asp Phe Cys Phe Ser Thr Thr Ile Thr Pro Lys Met
 65 70 75 80
 Leu Met Ser Phe Val Ser Arg Lys Asn Ile Ile Ser Phe Thr Gly Cys
 85 90 95
 Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Val Ser Glu Ser Phe
 100 105 110
 Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115 120 125
 Leu Leu Tyr Thr Val Thr Met Ser Cys Gln Val Cys Leu Leu Leu Leu
 130 135 140
 Leu Gly Ala Tyr Gly Met Gly Phe Ala Gly Ala Met Ala His Thr Gly
 145 150 155 160
 Ser Ile Met Asn Leu Thr Phe Cys Ala Asp Asn Leu Val Asn His Phe
 165 170 175
 Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Ser Ser Tyr
 180 185 190
 Met Asn Glu Leu Val Val Phe Ile Val Val Ala Val Asp Val Gly Met
 195 200 205
 Pro Ile Val Thr Val Phe Ile Ser Tyr Ala Leu Ile Leu Ser Ser Ile
 210 215 220
 Leu His Asn Ser Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Ile Ile Val Val Ser Leu Phe Phe Gly Ser Gly Ala Phe

[illegible]

<210> 1927
<211> 157
<212> PRT
<213> Unknown (H38g845 protein)

<220>
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(157)
<223> Xaa = Any Amino Acid
```

<400> 1927																
Met	Gly	Glu	Ala	Arg	Asn	Arg	Thr	Val	Val	Gln	Glu	Phe	Ile	Leu	Glu	
1				5					10					15		
Gly	Phe	Pro	Ala	Val	Gln	His	Leu	Gly	Asn	Val	Leu	Phe	Leu	Val	His	
			20					25					30			
Leu	Leu	Ala	Tyr	Leu	Ala	Ser	Ile	Met	Ala	Asn	Met	Leu	Ile	Ile	Thr	
		35					40					45				
Ile	Thr	Trp	Ala	Asp	His	His	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu	
	50					55					60					
Ser	Ser	Phe	Ser	Phe	Cys	Glu	Cys	Cys	Phe	Ile	Thr	Thr	Val	Ile	Pro	
65					70					75					80	
Lys	Leu	Leu	Val	Ile	Leu	Leu	Ser	Gly	Arg	Ala	Lys	Ile	Pro	Leu	Ser	
				85					90					95		
Thr	Thr	Leu	Ser	His	Ala	Val	Pro	Phe	Ser	Phe	Leu	Tyr	Ser	Trp	Val	
			100					105					110			
Asn	Ser	Phe	Ser	Ser	Leu	Asn	Gly	Cys	Asp	Val	Pro	Leu	Asp	Xaa	Tyr	
		115					120					125				
Leu	Ala	Ile	Cys	Lys	Pro	Leu	His	Tyr	Ser	Thr	Ile	Met	Ser	Leu	Arg	
	130						135				140					
Thr	Ser	Phe	His	Lys	Val	Thr	Ala	Trp	Leu	Cys	Pro	Gly				
145					150					155						

<210> 1928
<211> 333
<212> PRT
<213> Unknown (H38g846 protein)

<220>
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(333)
<223> Xaa = Any Amino Acid
```

<400> 1928

Thr	Asp	Pro	Gln	Asn	Leu	Thr	Thr	Asp	Val	Ser	Ile	Phe	Leu	Val	Leu
1				5				10						15	
Glu	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Val	Leu	Ala	Gly	Leu	Phe
			20					25					30		

```

Leu Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
  35                               40                               45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
  50                               55                               60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro
  65                               70                               75                               80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Leu Ile Ser Tyr Ala
  85                               90                               95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
  100                              105                              110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
  115                              120                              125
Cys His Pro Leu Tyr Tyr Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
  130                              135                              140
Phe Leu Val Leu Leu Ser Cys Cys Leu Ser Leu Leu Asp Ser Gln Leu
  145                              150                              155                              160
His Asn Leu Ile Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile
  165                              170                              175
Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His His Ala Cys Cys
  180                              185                              190
Asp Thr Phe Thr Asn Asn Ile Val Met Tyr Phe Pro Ala Ala Ile Phe
  195                              200                              205
Gly Phe Leu Pro Thr Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val
  210                              215                              220
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Asn Tyr Lys Ala Leu
  225                              230                              235                              240
Ser Ala Cys Gly Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr
  245                              250                              255
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg Lys
  260                              265                              270
Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
  275                              280                              285
Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu Arg
  290                              295                              300
Arg Leu His Gly Arg Thr Val Xaa Ser Gln Tyr Leu Ile Ile Cys Ser
  305                              310                              315                              320
Ile Pro Phe Val Val Trp Val Xaa Lys Gly Ser Lys Val
  325                              330

```

<210> 1929

<211> 222

<212> PRT

<213> Unknown (H38g847 protein)

<220>

<223> Synthetic construct

<400> 1929

```

Ser Gln Leu Ser Leu Met Asp Leu Met Leu Ile Cys Thr Thr Leu Pro
  1                               5                               10                               15
Lys Met Ile Phe Ser Tyr Leu Ser Gly Lys Lys Ser Ile Ser Leu Ala
  20                               25                               30
Gly Cys Gly Thr Gln Ile Phe Phe Tyr Val Ser Leu Leu Gly Ala Glu
  35                               40                               45
Cys Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
  50                               55                               60
His Pro Leu Gln Tyr Thr Ile Leu Met Asn Pro Glu Leu Cys Val Phe
  65                               70                               75                               80
Met Thr Val Ala Ser Trp Thr Leu Gly Ser Leu Asp Gly Ile Ile Val
  85                               90                               95
Leu Ala Ala Val Leu Ser Phe Ser Tyr Cys Ser Ser Leu Glu Ile His

```

```

      100      105      110
His Phe Phe Cys Asp Val Ala Ala Leu Leu Pro Leu Ser Cys Thr Glu
      115      120      125
Thr Ser Ala Phe Glu Arg Leu Leu Val Ile Cys Cys Val Val Met Leu
      130      135      140
Ile Phe Pro Val Ser Val Ile Ile Leu Ser Tyr Ser His Val Leu Arg
145      150      155      160
Ala Val Ile His Met Gly Ser Gly Glu Ser Arg Arg Lys Ala Phe Thr
      165      170      175
Thr Cys Ser Ser His Pro Ser Val Val Gly Leu Tyr Tyr Gly Ala Ala
      180      185      190
Met Phe Met Tyr Met Arg Pro Ala Ser Lys His Thr Pro Asp Gln Asp
      195      200      205
Lys Met Val Ser Ala Phe Tyr Thr Asn Leu Thr Pro Met Leu
      210      215      220

```

<210> 1930

<211> 114

<212> PRT

<213> Unknown (H38g848 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(114)

<223> Xaa = Any Amino Acid

<400> 1930

```

Leu Ala Cys Ile Val Gly Xaa Lys Phe Ala Phe Ile Ile Ser Pro Asn
 1      5      10      15
His His Phe Met Ile Met Val Thr Phe Ile Leu Val Asn Ile Xaa Lys
      20      25      30
His Ser Ser Gly Asn Leu Ser Ser Ala Leu Ile Ile Leu Phe Ile Phe
      35      40      45
Ile Pro Val Val Ser Leu Phe Phe Thr Pro Cys Val Val Leu Tyr Val
      50      55      60
Trp Pro Thr Leu Pro Pro Ser Leu Asp Lys Asn Met Phe Ile Val Asp
65      70      75      80
Phe Val Val Asn Pro Val Leu Lys Pro Ala Thr Tyr Ile Leu Gln Asn
      85      90      95
Lys Asp Ile Lys Val Ala Leu Xaa Asn Leu His Glu Lys Arg Thr Tyr
      100      105      110
Ser Ser

```

<210> 1931

<211> 305

<212> PRT

<213> Unknown (H38g849 protein)

<220>

<223> Synthetic construct

<400> 1931

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Gly Leu
 1      5      10      15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
      20      25      30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
      35      40      45

```

His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu
 50 55 60
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser
 65 70 75 80
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
 85 90 95
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
 100 105 110
 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile
 115 120 125
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile
 130 135 140
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Pro
 145 150 155 160
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
 165 170 175
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
 180 185 190
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile
 195 200 205
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp
 210 215 220
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
 225 230 235 240
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
 245 250 255
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
 260 265 270
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
 275 280 285
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
 290 295 300
 Phe
 305

<210> 1932

<211> 223

<212> PRT

<213> Unknown (H38g850 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(223)

<223> Xaa = Any Amino Acid

<400> 1932

Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro
 1 5 10 15
 Lys Met Val Val Asp Ile Gln Ser His Ser Arg Ser Phe Ser Tyr Ala
 20 25 30
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 35 40 45
 Glu Thr Leu Leu Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile
 50 55 60
 Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
 65 70 75 80
 Phe Leu Leu Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Ala Gln
 85 90 95
 Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu

Ile	Pro	Asn	100	Phe	Leu	Cys	Asp	Pro	105	Ser	Pro	Leu	Pro	His	110	Leu	Ala	Cys
		115							120						125			
Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Met	Tyr	Phe	Pro	Ala	Ala	Ile			
		130					135					140						
Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Leu	Phe	Ser	Tyr	Tyr	Lys	Ile			
145					150					155					160			
Val	Ser	Ser	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly	Lys	Tyr	Lys	Ala			
			165						170					175				
Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Cys	Xaa	Phe	Tyr	Gly			
			180						185					190				
Thr	Gly	Val	Gly	Gly	Tyr	Leu	Gly	Ser	Asp	Val	Ser	Ser	Ser	Pro	Arg			
		195					200					205						
Lys	Ser	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met				
		210					215					220						

<210> 1933

<211> 329

<212> PRT

<213> Unknown (H38g851 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1933

Asp	Ser	Val	Asp	Gln	Val	Asn	Asp	Ser	Leu	Val	Thr	Glu	Phe	Val	Leu			
1				5					10					15				
Leu	Gly	Leu	Ala	Gln	Ser	Leu	Glu	Met	Gln	Phe	Phe	Leu	Phe	Leu	Phe			
			20					25					30					
Phe	Ser	Leu	Phe	Tyr	Val	Gly	Ile	Ile	Leu	Gly	Asn	Leu	Phe	Ile	Val			
		35				40					45							
Phe	Thr	Val	Ile	Phe	Asp	Pro	His	Leu	His	Ser	Pro	Met	Tyr	Ile	Leu			
		50				55					60							
Leu	Ala	Asn	Leu	Ser	Leu	Ile	Asp	Leu	Ser	Leu	Ser	Ser	Thr	Thr	Val			
65					70					75					80			
Pro	Arg	Leu	Ile	Tyr	Asp	Leu	Phe	Thr	Asp	Cys	Lys	Val	Ile	Ser	Phe			
				85					90					95				
His	Asn	Cys	Met	Ile	Gln	Lys	Phe	Phe	Ile	His	Val	Thr	Gly	Gly	Val			
		100						105					110					
Glu	Met	Val	Leu	Leu	Ile	Val	Met	Glu	Tyr	Asp	Arg	Tyr	Thr	Ala	Ile			
		115					120					125						
Cys	Lys	Pro	Leu	His	Tyr	Pro	Thr	Ile	Met	Asn	Pro	Lys	Met	Cys	Met			
		130					135					140						
Phe	Leu	Val	Ala	Ala	Ala	Trp	Val	Ile	Gly	Val	Ile	His	Ala	Met	Ser			
145					150					155					160			
Gln	Phe	Val	Phe	Val	Ile	Asn	Xaa	Pro	Phe	Cys	Gly	Pro	Asn	Asn	Val			
				165					170					175				
Gly	Ser	Phe	Tyr	Cys	Asp	Phe	Pro	Arg	Val	Ile	Lys	Leu	Ala	Cys	Met			
			180					185					190					
Asp	Thr	Tyr	Gly	Leu	Glu	Phe	Val	Val	Thr	Ala	Asn	Ser	Gly	Phe	Ile			
		195					200					205						
Ser	Met	Gly	Thr	Phe	Phe	Phe	Leu	Ile	Val	Ser	Tyr	Ile	Phe	Ile	Leu			
		210					215					220						
Val	Thr	Val	Gln	Arg	His	Ser	Ser	Asn	Asp	Leu	Ser	Lys	Ala	Phe	Phe			
225					230				235						240			
Thr	Ser	Xaa	Ala	His	Ile	Thr	Val	Val	Val	Leu	Phe	Phe	Ala	Pro	Cys			
				245					250						255			

Met Phe Leu Tyr Val Trp Pro Phe Pro Thr Lys Ser Leu Asp Lys Phe
 260 265 270
 Phe Ala Ile Met Asn Phe Val Val Thr Pro Val Leu Asn Pro Ala Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Asp Met Lys Phe Ala Met Arg Arg Leu Asn
 290 295 300
 Gln His Ile Leu Asn Ser Met Glu Thr Thr Xaa His Ile Trp Leu Met
 305 310 315 320
 Arg Ala Gln Asp Lys Cys His Gly Pro
 325

<210> 1934
 <211> 220
 <212> PRT
 <213> Unknown (H38g852 protein)

<220>
 <223> Synthetic construct

<400> 1934
 Ser Val Leu Ser Ile Ser Glu Thr Tyr Tyr Thr Val Ala Ile Asn Pro
 1 5 10 15
 Gln Met Leu Ser Gly Leu Leu Ser Pro Gln Gln Thr Ile Ser Ile Pro
 20 25 30
 Gly Cys Ala Ala Gln Leu Phe Phe Tyr Leu Thr Phe Gly Val Asn Lys
 35 40 45
 Cys Phe Leu Leu Thr Ala Met Gly Tyr Asp His Tyr Val Ala Ile Cys
 50 55 60
 Asn Pro Leu Gln Tyr Ser Val Ile Met Gly Lys Lys Ala Cys Ile Gln
 65 70 75 80
 Leu Val Ser Gly Ser Trp Asn Ile Gly Leu Ser Thr Ala Ile Ile Gln
 85 90 95
 Val Ser Ser Val Phe Ser Leu Pro Phe Cys Asp Ala Asn Leu Ile Ser
 100 105 110
 His Phe Phe Cys Asp Ile Arg Pro Ile Met Lys Leu Ala Cys Ala Asp
 115 120 125
 Thr Thr Ile Lys Glu Phe Ile Thr Leu Leu Ile Ser Leu Cys Val Leu
 130 135 140
 Val Leu Pro Met Val Leu Ile Phe Ile Ser Tyr Val Leu Ile Val Thr
 145 150 155 160
 Thr Ile Leu Lys Ile Ala Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala
 165 170 175
 Thr Cys Ala Ser His Leu Thr Val Val Ile Val His Tyr Gly Arg Thr
 180 185 190
 Ser Phe Ile Tyr Leu Lys Pro Lys Ser Gln Asn Ser Leu Gln Asp Arg
 195 200 205
 Leu Ile Ser Val Thr Tyr Thr Val Ile Thr Pro Leu
 210 215 220

<210> 1935
 <211> 313
 <212> PRT
 <213> Unknown (H38g853 protein)

<220>
 <223> Synthetic construct

<400> 1935
 Met Ser Thr Ser Asn His Thr Gln Phe His Pro Ser Ser Phe Leu Leu
 1 5 10 15
 Leu Gly Ile Pro Gly Leu Glu Asp Val His Ile Trp Ile Gly Val Pro

										20											25											30
Phe	Phe	Phe	Val	Tyr	Leu	Val	Ala	Leu	Leu	Gly	Asn	Thr	Ala	Leu	Leu																	
										35											40											45
Phe	Val	Ile	Gln	Thr	Glu	Gln	Ser	Leu	His	Glu	Pro	Met	Tyr	Tyr	Phe																	
										50											55											60
Leu	Ala	Met	Leu	Asp	Ser	Ile	Asp	Leu	Gly	Leu	Ser	Thr	Ala	Thr	Ile																	
										65											70											75
Pro	Lys	Met	Leu	Gly	Ile	Phe	Trp	Phe	Asn	Thr	Lys	Glu	Ile	Ser	Phe																	
										85											90											95
Gly	Gly	Cys	Leu	Ser	His	Met	Phe	Phe	Ile	His	Phe	Phe	Thr	Ala	Met																	
										100											105											110
Glu	Ser	Ile	Val	Leu	Val	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Ile	Ala	Ile																	
										115											120											125
Cys	Lys	Pro	Leu	Arg	Tyr	Thr	Met	Ile	Leu	Thr	Ser	Lys	Ile	Ile	Ser																	
										130											135											140
Leu	Ile	Ala	Gly	Ile	Ala	Val	Leu	Arg	Ser	Leu	Tyr	Met	Val	Val	Pro																	
										145											150											155
Leu	Val	Phe	Leu	Leu	Leu	Arg	Leu	Pro	Phe	Cys	Gly	His	Arg	Ile	Ile																	
										165											170											175
Pro	His	Thr	Tyr	Cys	Glu	His	Met	Gly	Ile	Ala	Arg	Leu	Ala	Cys	Ala																	
										180											185											190
Ser	Ile	Lys	Val	Asn	Ile	Arg	Phe	Gly	Leu	Gly	Asn	Ile	Ser	Leu	Leu																	
										195											200											205
Leu	Leu	Asp	Val	Ile	Leu	Ile	Ile	Leu	Ser	Tyr	Val	Arg	Ile	Leu	Tyr																	
										210											215											220
Ala	Val	Phe	Cys	Leu	Pro	Ser	Trp	Glu	Ala	Arg	Leu	Lys	Ala	Leu	Asn																	
										225											230											235
Thr	Cys	Gly	Ser	His	Ile	Gly	Val	Ile	Leu	Ala	Phe	Phe	Thr	Pro	Ala																	
										245											250											255
Phe	Phe	Ser	Phe	Leu	Thr	His	Arg	Phe	Gly	His	Asn	Ile	Pro	Gln	Tyr																	
										260											265											270
Ile	His	Ile	Leu	Ala	Asn	Leu	Tyr	Val	Val	Val	Pro	Pro	Ala	Leu																		
										275											280											285
Asn	Pro	Val	Ile	Tyr	Gly	Val	Arg	Thr	Lys	Gln	Ile	Arg	Glu	Arg	Val																	
										290											295											300
Leu	Arg	Ile	Phe	Leu	Lys	Thr	Asn	His																								
										305											310											

<210> 1936

<211> 295

<212> PRT

<213> Unknown (H38g854 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(295)

<223> Xaa = Any Amino Acid

<400> 1936

Tyr	Met	Ile	Thr	Ile	Leu	Trp	Glu	Ile	Ser	Lys	Pro	Val	Asn	Asn	Ile
1				5				10						15	
Phe	Leu	Thr	Leu	Ser	Val	Arg	Tyr	Gln	Met	Leu	Ile	Thr	Thr	Val	Ser
			20				25				30				
Xaa	Leu	Xaa	Met	Lys	Ser	Ile	Ile	Xaa	Ile	Tyr	Xaa	Ser	Phe	Ser	Glu
			35				40				45				
Tyr	Leu	Met	Ser	Xaa	Lys	Ile	Trp	Glu	His	Met	Xaa	Tyr	Cys	Ala	Cys
			50				55				60				
Ile	Asn	Met	Asp	Lys	Val	Ser	Glu	Val	Phe	Ser	Glu	His	Leu	Phe	Gly
65				70				75				80			

Ala Ala Glu Ile Ile Pro Leu Met Gly Met Val His Gly Cys Tyr Val
85 90 95
Thr Ile Cys Thr Ala Xaa Asn Ile Met Thr Gln Tyr Arg Cys Gly His
100 105 110
Leu Ala Gly Met Ala Cys Thr Gly Arg Phe Ile His Gly Thr Val Xaa
115 120 125
Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr Asn Ser Asn Val Thr Ile
130 135 140
Xaa Ile Ala His Phe Ile Cys Asp Leu Asn Thr Leu Leu Lys Leu Leu
145 150 155 160
Cys Ile Gly Ser His Asp Thr Leu Gly Leu Phe Val Ala Ala Asn Asp
165 170 175
Gly Phe Asn Cys Leu Leu Asn Ile Ile Phe Leu Met Val Ser Xaa Val
180 185 190
Ala Ile Leu Tyr Thr Leu Lys Ser His Ser Leu Glu Glu Arg Tyr Lys
195 200 205
Ala Leu Ser Thr Cys Val Ser His Thr Thr Val Ala Ile Xaa Phe Phe
210 215 220
Val Phe Cys Ile Leu Val Tyr Leu Cys Pro Val Thr Leu Leu Pro Val
225 230 235 240
Ser Lys Ala Val Ala Val Leu Tyr Thr Met Ile Thr Pro Thr Leu Asn
245 250 255
Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser Val Glu Lys
260 265 270
Leu Leu Gly Gln Lys Met Thr Xaa Arg Glu Lys Xaa Ser Lys His Lys
275 280 285
Met Ile Leu Leu Phe Gln Trp
290 295

<210> 1937

<211> 309

<212> PRT

<213> Unknown (H38g855 protein)

<220>

<223> Synthetic construct

<400> 1937

Met Glu Lys Lys Lys Asn Val Thr Glu Phe Ile Leu Ile Gly Leu Thr
1 5 10 15
Gln Asn Pro Ile Met Glu Lys Val Thr Phe Val Val Phe Leu Val Leu
20 25 30
Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Ile Val Val Thr Ile Thr
35 40 45
Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Thr His Leu
50 55 60
Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ala Pro Lys Leu Ile
65 70 75 80
Val Asp Ser Phe Gln Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met
85 90 95
Ala Gln Ala Tyr Ala Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu
100 105 110
Leu Thr Val Met Ala Cys Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu
115 120 125
Asn Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Ala
130 135 140
Val Ala Trp Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe
145 150 155 160
Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Gly His Phe Met
165 170 175
Cys Asp Leu Tyr Pro Leu Leu Lys Leu Val Cys Ile Asp Thr His Thr


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      180      185      190
Leu Gly Leu Phe Val Ala Val Asn Ser Gly Phe Ile Cys Leu Leu Asn
      195      200      205
Phe Leu Ile Leu Val Val Ser Tyr Val Ile Ile Leu Arg Ser Leu Lys
      210      215      220
Asn Asn Ser Leu Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ile Ser
      225      230      235      240
His Ile Ile Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
      245      250      255
Leu Arg Ser Val Thr Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe
      260      265      270
Tyr Thr Met Val Val Pro Met Leu Asn Pro Val Val Tyr Thr Leu Arg
      275      280      285
Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val
      290      295      300
Thr Ser Asp Asn Asp
305

```

<210> 1938

<211> 246

<212> PRT

<213> Unknown (H38g856 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(246)

<223> Xaa = Any Amino Acid

<400> 1938

```

Cys Ile Gln Gln His Xaa Ser Pro Leu Cys Leu Cys Met Phe Ser Phe
  1           5           10           15
Tyr Phe Asn Leu Tyr His Phe Phe Pro Lys Xaa Lys Tyr Leu His Ser
      20      25      30
Leu Arg Asp Ala Glu Ile Asn Xaa Leu Val Xaa Ser Lys Val Leu Ile
      35      40      45
Asn Gln Ile Tyr Thr Lys Ala Asn Trp Pro Phe His Gly Leu Xaa His
      50      55      60
Tyr Ala Gln Pro Leu His Thr Gln Thr Cys Ile Ser Phe Ser Asn Val
      65      70      75      80
Ile Xaa Cys Ser Thr Xaa Leu Phe Thr Gly His Phe Phe Leu Gly Gly
      85      90      95
Ser Gln Ile Phe Leu Leu Leu Val Met Ala Tyr Gly His Tyr Arg Ala
      100     105     110
Ile Cys Lys Ser Leu Gln Tyr Leu Val Val Met Lys Gln Trp Leu Cys
      115     120     125
Val Val Leu Leu Val Val Ser Trp Ala Gly Gly Phe Leu His Ile Val
      130     135     140
Ile Gln Leu Gly Leu Ile Tyr Gly Leu Pro Ser Tyr Asp Pro Asn Val
      145     150     155     160
Ile Gly His Phe Ile Cys Asp Met Asp Pro Leu Met Lys Leu Val Cys
      165     170     175
Asp Tyr Thr Leu Asn Arg Phe Ala Tyr Phe Ala Gly His Asp Xaa Ile
      180     185     190
Leu Gly Phe Met Tyr Phe Thr Tyr Ala Gln Thr Gly Leu Phe Pro Phe
      195     200     205
Gly Asp Ser Thr Ser Leu Phe Phe Cys His Phe Phe Pro Arg Gly Leu
      210     215     220
Gly Ser Ile Asn Leu Ala Ile His Ser Tyr Tyr Pro Cys Gly Ile Ser
      225     230     235     240

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Arg Asp Thr Glu Pro Thr
245

<210> 1939
<211> 262
<212> PRT
<213> Unknown (H38g857 protein)

<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(262)
<223> Xaa = Any Amino Acid

<400> 1939
Leu Ile Val Val Thr Val Thr Val Ser Glu Thr Leu Gly Ser Pro Met
1 5 10 15
Tyr Phe Phe Leu Ala Gly Leu Ser Phe Ile Asp Ile Ile Tyr Ser Ser
20 25 30
Ser Ile Ser His Arg Leu Ile Ser Asp Leu Phe Phe Gly Asn Asn Ser
35 40 45
Ile Ser Phe Pro Ser Cys Leu Ala Gln Leu Phe Thr Glu His Leu Phe
50 55 60
Gly Gly Ser Glu Val Phe Leu Leu Leu Val Met Ala Tyr Asp Leu His
65 70 75 80
Tyr Leu Val Ile Met Arg Gln Trp Val Cys Val Leu Leu Val Ala
85 90 95
Ser Trp Val Gly Gly Phe Leu His Ser Val Phe Gln Leu Ser Val Ile
100 105 110
Tyr Gly Leu Pro Phe Cys Asp Leu Asn Val Ile Asp His Phe Phe Cys
115 120 125
Asp Met His Pro Leu Leu Lys Leu Val Cys Thr Asp Thr His Val Ile
130 135 140
Gly Leu Leu Val Val Ala Asn Gly Gly Leu Gly Cys Thr Ile Val Phe
145 150 155 160
Leu Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu His Ser Leu Lys Asn
165 170 175
Leu Ser Gln Lys Gly Arg Xaa Lys Ala Leu Ser Thr Cys Ser Ser His
180 185 190
Ile Thr Val Val Val Phe Phe Phe Val Pro Cys Ile Phe Met Tyr Ala
195 200 205
Arg Pro Ala Arg Thr Phe Pro Ile Asp Lys Ser Val Ser Val Phe Tyr
210 215 220
Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
225 230 235 240
Ser Glu Met Thr Ser Ala Met Lys Lys Leu Trp Arg Arg Asp Phe Ile
245 250 255
Ser Ser Ser Thr Xaa Val
260

<210> 1940
<211> 309
<212> PRT
<213> Unknown (H38g858 protein)

<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(309)

<223> Xaa = Any Amino Acid

<400> 1940

```

M t Arg Gln Asn Asn Asn Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
 1           5           10           15
Gln Asp Leu Asp Val Gln Lys Ala Leu Phe Val Ile Phe Leu Leu Thr
      20           25           30
Tyr Leu Val Thr Val Val Gly Asn Leu Leu Ile Val Val Thr Ile Ile
      35           40           45
Ala Ser Pro Ser Leu Gly Ser Ser Met Tyr Phe Phe Leu Ala Cys Leu
      50           55           60
Ser Phe Ile Asp Ala Ala Tyr Ser Thr Thr Ile Ser Pro Lys Leu Ile
      65           70           75           80
Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met
      85           90           95
Gly Gln Leu Phe Ile Asp His Leu Asp Gly Gly Ala Glu Val Val Leu
      100          105          110
Leu Val Val Lys Ala Cys Asp His Val Asp Ile Trp Lys Pro Leu
      115          120          125
Arg Tyr Leu Thr Ile Met Asn Arg Gln Gly Xaa Met Arg Leu Leu Val
      130          135          140
Ala Val Val Thr Gly Gly Val Leu His Ser Leu Ser His Ile Val Ser
      145          150          155          160
Val Val Tyr Ser Leu Ala Tyr Cys Gly Pro Asn Val Ile Asp Tyr Phe
      165          170          175
Val Cys Asp Met Tyr Pro Leu Leu Glu Leu Val Cys Thr Asp Thr Tyr
      180          185          190
Phe Ile Gly Leu Thr Val Phe Val Asn Gly Gly Thr Ile Cys Ile Val
      195          200          205
Val Phe Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Ser Leu
      210          215          220
Lys Thr Tyr Ser Gln Glu Gly Arg His Lys Val Leu Phe Thr Cys Ser
      225          230          235          240
Ser His Ile Ile Val Phe Ala Leu Phe Phe Val Pro Cys Ile Phe Met
      245          250          255
Tyr Val Arg Pro Val Ser Asn Tyr Pro Phe Asp Lys Phe Leu Thr Val
      260          265          270
Phe Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu
      275          280          285
Arg Asn Ser Glu Met Arg Asn Ser Val Glu Thr Leu Leu Cys Lys Lys
      290          295          300
Leu Thr Val Leu Glu
      305

```

<210> 1941

<211> 305

<212> PRT

<213> Unknown (H38g859 protein)

<220>

<223> Synthetic construct

<400> 1941

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1           5           10           15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
      20           25           30
Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile
      35           40           45
Cys Asn Asp Ser His Leu His Thr Pro Met Tyr Phe Val Val Gly Asn
      50           55           60

```

Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
 65 70 75 80
 Leu Val Ile Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
 85 90 95
 Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Cys
 100 105 110
 Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro
 115 120 125
 Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val
 130 135 140
 Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys
 145 150 155 160
 Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe
 165 170 175
 Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly
 180 185 190
 Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys
 195 200 205
 Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val
 210 215 220
 Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr
 245 250 255
 Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile
 260 265 270
 Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu
 290 295 300
 Pro
 305

<210> 1942

<211> 316

<212> PRT

<213> Unknown (H38g860 protein)

<220>

<223> Synthetic construct

<400> 1942

Met Ile Cys Glu Asn His Thr Arg Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Thr Asn Asn Pro Glu Met Gln Val Ser Leu Phe Ile Phe Phe Leu
 20 25 30
 Ala Ile Tyr Thr Val Thr Leu Leu Gly Asn Phe Leu Ile Val Thr Val
 35 40 45
 Thr Ser Val Asp Leu Ala Leu Gln Thr Pro Met Tyr Phe Phe Leu Gln
 50 55 60
 Asn Leu Ser Leu Leu Glu Val Cys Phe Thr Leu Val Met Val Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Val Ser Pro Arg Lys Ile Ile Ser Phe Val Gly
 85 90 95
 Cys Gly Thr Gln Met Tyr Phe Phe Phe Phe Gly Ser Ser Glu Cys
 100 105 110
 Phe Leu Leu Ser Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
 115 120 125
 Pro Leu His Tyr Ser Val Ile Met Asn Arg Ser Leu Cys Leu Trp Met
 130 135 140
 Ala Ile Gly Ser Trp Met Ser Gly Val Pro Val Ser Met Leu Gln Thr

```

145          150          155          160
Ala Trp Met Met Ala Leu Pro Phe Cys Gly Pro Asn Ala Val Asp His
          165          170          175
Phe Phe Cys Asp Gly Pro Pro Val Leu Lys Leu Val Thr Val Asp Thr
          180          185          190
Thr Met Tyr Glu Met Gln Ala Leu Ala Ser Thr Leu Leu Phe Ile Met
          195          200          205
Phe Pro Phe Cys Leu Ile Leu Val Ser Tyr Thr Arg Ile Ile Ile Thr
          210          215          220
Ile Leu Arg Met Ser Ser Ala Thr Gly Arg Gln Lys Ala Phe Ser Thr
225          230          235          240
Cys Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ser
          245          250          255
Leu Thr Tyr Leu Arg Pro Lys Ser Asn Gln Ser Pro Glu Ser Lys Lys
          260          265          270
Leu Val Ser Leu Ser Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile
          275          280          285
Ile Tyr Gly Leu Arg Asn Asn Glu Val Lys Gly Ala Val Lys Arg Thr
          290          295          300
Ile Thr Gln Lys Val Leu Gln Lys Leu Asp Val Phe
305          310          315

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<210> 1943

<211> 309

<212> PRT

<213> Unknown (H38g861 protein)

<220>

<223> Synthetic construct

<400> 1943

```

Met Ala Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1          5          10          15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Ser Val Ile
          20          25          30
Tyr Ile Asn Ala Met Ile Gly Asn Val Leu Ile Val Val Thr Ile Thr
          35          40          45
Ala Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Ala Tyr Leu
          50          55          60
Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu Ile
65          70          75          80
Thr Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Phe Asn Gly Cys Met
          85          90          95
Thr Gln Val Phe Gly Glu His Phe Phe Arg Gly Val Glu Val Ile Leu
          100          105          110
Leu Thr Val Met Ala Tyr Asp His Tyr Val Ala Ile Cys Lys Pro Leu
          115          120          125
His Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly
          130          135          140
Val Ser Trp Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe
145          150          155          160
Ile Cys Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
          165          170          175
Cys Asp Leu Tyr Thr Leu Ile Asn Leu Ala Cys Thr Asn Thr His Thr
          180          185          190
Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
          195          200          205
Cys Leu Leu Leu Val Ser Cys Val Val Ile Leu Tyr Ser Leu Lys
          210          215          220
Thr His Ser Leu Glu Ala Arg His Glu Ala Leu Ser Thr Cys Val Ser
225          230          235          240

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His Ile Thr Val Val Ile Leu Ser Phe Ile Pro Cys Ile Phe Val Tyr
 245 250 255
 Met Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe
 260 265 270
 Tyr Thr Met Ile Thr Ser Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala
 290 295 300
 Ile Ser Ser Val Lys
 305

<210> 1944

<211> 164

<212> PRT

<213> Unknown (H38g862 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(164)

<223> Xaa = Any Amino Acid

<400> 1944

Trp Lys Asn His Phe Thr Ser Val Asn Cys Gly Phe Ala Ile Cys Arg
 1 5 10 15
 Ala Glu Cys Xaa Pro Xaa Pro Lys Ile Leu Ser Ile Ile Gly Leu Lys
 20 25 30
 Xaa Asn Ile Asn Glu Thr Leu Xaa Met Leu Asn Tyr Asn Thr Asn His
 35 40 45
 Met Val Ser Val Asp Val Leu Ile Val Pro Asn Ser Leu Ile Thr Leu
 50 55 60
 Ser Tyr Phe Phe Ile Val Ala Ala Ile Leu His Ile Arg Ser Ala Glu
 65 70 75 80
 Gly Arg His Lys Ala Phe Pro Thr Cys Ser Phe His Leu Val Val Ile
 85 90 95
 Leu Leu Gln His Asn Ala Thr Ser Leu Thr Tyr Leu Cys Pro Ser Ser
 100 105 110
 Ile Phe Ser Tyr Glu Arg Gly Lys Val Val Ser Thr Val Tyr Thr Cys
 115 120 125
 Ile Thr Pro Val Pro Asn Pro Leu Ile Cys Ser Met Arg Lys Lys Glu
 130 135 140
 Leu Lys His Ala Leu Lys Lys Lys Glu Glu Ile Ala Arg Phe Leu Leu
 145 150 155 160
 Leu Arg Thr His

<210> 1945

<211> 318

<212> PRT

<213> Unknown (H38g863 protein)

<220>

<223> Synthetic construct

<400> 1945

Met Phe Ser Ser Glu Pro Thr Ile Asp Gly Asn Gln Ser Leu Cys Ala
 1 5 10 15
 Lys Phe Thr Phe Val Ala Phe Ser Ser Ile Glu Glu Leu Gln Leu Val
 20 25 30
 Leu Phe Ile Val Phe Leu Ile Ile Tyr Leu Cys Thr Ile Gly Gly Asn

```

      35              40              45
Ile Ile Ile Ile Ser Leu Ile Trp Ile Thr Pro Ala Leu His Thr Pro
  50              55              60
Met Tyr Phe Phe Leu Val Asn Leu Ser Phe Leu Glu Met Cys Tyr Thr
  65              70              75              80
Thr Ser Val Val Pro Leu Leu Val His Leu Leu Val Glu Thr Lys Thr
      85              90              95
Ile Ser Val Gly Gly Cys Ala Thr Gln Met Tyr Ile Phe Ala Ile Leu
      100              105              110
Gly Leu Thr Glu Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Phe
      115              120              125
Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Leu Phe Met Gly Pro Arg
      130              135              140
Val Cys Leu Lys Leu Ala Ala Ala Ser Trp Phe Thr Gly Val Val Val
      145              150              155              160
Glu Ser Ala Gln Ile Thr Leu Ile Phe Thr Leu Pro Phe Cys Gly Thr
      165              170              175
Gly Lys Ile Pro Thr Leu Phe Cys Asp Ile Met Pro Val Leu Lys Leu
      180              185              190
Ala Cys Ile Asp Thr Ser Gln Ile Glu Ile Val Met Phe Ser Leu Ser
      195              200              205
Val Leu Phe Ile Val Ser Pro Cys Phe Leu Ile Leu Cys Ser His Met
      210              215              220
His Ile Pro Val Thr Ile Leu Arg Ile Pro Ser Ala Ala Gly Arg His
      225              230              235              240
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Leu Val Val Ser Leu Phe
      245              250              255
Tyr Gly Thr Ala Leu Phe Thr Tyr Leu Gln Pro Lys Thr Ala His Thr
      260              265              270
Pro Glu Thr Asp Lys Ala Thr Ala Leu Met Tyr Thr Met Val Thr Pro
      275              280              285
Ala Leu Asn Pro Val Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu
      290              295              300
Ala Phe Gln Arg Ile Thr Gln Arg Asn Ser Leu Arg Gln Thr
      305              310              315

```

<210> 1946

<211> 291

<212> PRT

<213> Unknown (H38g864 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(291)

<223> Xaa = Any Amino Acid

<400> 1946

```

Ser Met Tyr Leu Val Thr Met Leu Arg Asn Leu Phe Ile Ile Leu Ala
  1              5              10              15
Gly Ser Ser Asp Pro His Phe His Thr Pro Met Tyr Phe Phe Leu Ser
      20              25              30
Asn Leu Ser Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro Lys
      35              40              45
Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly
      50              55              60
Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu Asp
      65              70              75              80
Met Leu Leu Thr Leu Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
      85              90              95

```

Ile Cys His Pro Leu His Tyr Arg Val Ile Met Asn Pro His Leu Cys
 100 105 110
 Val Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Asp Ser Gln
 115 120 125
 Leu His Ser Trp Ile Val Leu His Asn Ser Pro Phe Gln Glu Cys Gly
 130 135 140
 Asn Leu Xaa Phe Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala
 145 150 155 160
 Cys Ser Asp Ser Ile Ile Asn Asn Ile Leu Cys Ile Leu Asp Ile Pro
 165 170 175
 Ile Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys
 180 185 190
 Ile Val Ser Ser Ile Pro Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys
 195 200 205
 Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr
 210 215 220
 Glu Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Ser Ser Pro
 225 230 235 240
 Arg Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Ile Pro Met
 245 250 255
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile His Ser Ala
 260 265 270
 Leu Trp Arg Leu Arg Ser Arg Thr Val Lys Ser His Asp Leu Phe His
 275 280 285
 Pro Phe Ser
 290

<210> 1947

<211> 327

<212> PRT

<213> Unknown (H38g865 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1947

Met Asp Val Ser Ile Phe Leu Leu Leu Gly Thr Thr Glu Asp Pro Glu
 1 5 10 15
 Arg Gln Pro Val Leu Thr Gly Leu Phe Leu Ser Met Cys Leu Val Thr
 20 25 30
 Val Leu Gly Lys Leu Leu Ile Met Leu Ala Phe Ser Pro Asp Ser His
 35 40 45
 Leu His Thr His Met Tyr Phe Phe Leu Ser Asn Leu Ser Leu Pro Asp
 50 55 60
 Ile Gly Phe Thr Ser Thr Ile Val Pro Lys Met Ile Ala Asp Ile Gln
 65 70 75 80
 Ser His Ser Arg Val Ile Ser Tyr Ala Gly Arg Leu Thr Gln Met Ser
 85 90 95
 Leu Phe Ala Ile Phe Gly Gly Met Glu Glu Asp Met Leu Leu Ser Val
 100 105 110
 Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Tyr His Ser
 115 120 125
 Ala Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Leu Leu Phe Phe
 130 135 140
 Phe Phe Leu Ser Leu Leu Asp Thr Gln Leu His Asn Leu Ile Ala Leu
 145 150 155 160
 Gln Met Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Asp

										165			170				175			
Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	Cys	Cys	Asp	Thr	Phe	Thr	Asn	Asn					
				180			185			190										
Ile	Ile	Val	Tyr	Phe	Pro	Ala	Val	Ile	Phe	Val	Phe	Leu	Pro	Ile	Ser					
				195			200			205										
Gly	Thr	Leu	Phe	Ser	Tyr	Lys	Thr	Val	Ser	Ser	Ile	Leu	Arg	Val	Ser					
				210			215			220										
Ser	Ser	Gly	Gly	Lys	Tyr	Lys	Thr	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu					
				225			230			235			240							
Ser	Val	Ile	Cys	Xaa	Phe	Tyr	Gly	Thr	Gly	Val	Gly	Gly	Tyr	Leu	Ser					
				245			250			255										
Ser	Asp	Val	Ser	Ser	Ser	Leu	Arg	Lys	Ala	Ala	Val	Ala	Ser	Val	Met					
				260			265			270										
Tyr	Lys	Met	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg					
				275			280			285										
Asn	Arg	Asp	Met	Lys	Ser	Val	Leu	Arg	Arg	Pro	His	Gly	Ser	Thr	Val					
				290			295			300										
Xaa	Ser	Gln	Tyr	Leu	Leu	Ile	Cys	Ser	Ile	Pro	Phe	Val	Gly	Trp	Val					
				305			310			315			320							
Lys	Lys	Gly	Ser	Lys	Val	Lys														
				325																

<210> 1948

<211> 254

<212> PRT

<213> Unknown (H38g866 protein)

<220>

<223> Synthetic construct

<400> 1948

Met	Gly	Asp	Lys	Gly	Thr	Gly	Asn	His	Ser	Asp	Val	Thr	Asp	Phe	Ile		
1				5				10				15					
Leu	Glu	Gly	Phe	Arg	Val	Arg	Pro	Glu	Phe	Tyr	Ile	Leu	Leu	Phe	Phe		
				20			25			30							
Leu	Phe	Leu	Leu	Ile	Tyr	Ser	Met	Val	Leu	Leu	Gly	Asn	Ile	Ser	Val		
				35			40			45							
Met	Thr	Ile	Ile	Val	Thr	Asp	Ser	Gln	Leu	Asn	Thr	Pro	Met	Tyr	Phe		
				50			55			60							
Phe	Leu	Gly	Asn	Leu	Ser	Phe	Ile	Asp	Val	Ser	Tyr	Ser	Thr	Val	Ile		
				65			70			75			80				
Ala	Pro	Lys	Ala	Met	Ala	His	Phe	Leu	Ser	Glu	Lys	Lys	Thr	Val	Ser		
				85			90			95							
Phe	Ala	Gly	Cys	Val	Ala	Gln	Leu	Phe	Leu	Phe	Ala	Leu	Phe	Ile	Val		
				100			105			110							
Thr	Glu	Gly	Phe	Val	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Phe	Ser	Ala		
				115			120			125							
Ile	Cys	Asn	Pro	Leu	Leu	His	Ser	Val	His	Met	Ser	Arg	Arg	Leu	Cys		
				130			135			140							
Thr	Gln	Leu	Val	Ala	Gly	Ser	Tyr	Phe	Cys	Gly	Trp	Ala	Ser	Ser	Ile		
				145			150			155			160				
Leu	Gln	Val	Ser	Val	Thr	Phe	Ser	Val	Ser	Phe	Cys	Ala	Ser	Arg	Val		
				165			170			175							
Ile	Ala	His	Phe	Tyr	Cys	Asp	Ser	Tyr	Gln	Ile	Glu	Lys	Ile	Ser	Cys		
				180			185			190							
Ser	Asn	Leu	Phe	Val	Asn	Lys	Met	Val	Ser	Leu	Ser	Leu	Ser	Val	Ile		
				195			200			205							
Ile	Ile	Leu	Pro	Thr	Ile	Val	Val	Ile	Ile	Val	Ser	Tyr	Leu	Tyr	Ile		
				210			215			220							
Val	Ser	Ser	Val	Leu	Lys	Ile	Pro	Ser	Ser	Glu	Gly	Arg	Lys	Lys	Asp		
				225			230			235			240				

Phe Ser Thr Cys Ser Ser His Arg Gly Val Val Ser Leu Leu
245 250

<210> 1949

<211> 335

<212> PRT

<213> Unknown (H38g867 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1949

Tyr	Thr	Asp	Pro	Gln	Asn	Leu	Thr	Asp	Ala	Ser	Lys	Tyr	Leu	Leu	Leu
1				5					10					15	
Glu	Leu	Ser	Glu	Asp	Pro	Lys	Leu	Gln	Leu	Ala	Leu	Ser	Gly	Arg	Glu
			20					25					30		
Pro	Cys	Thr	Cys	Thr	Xaa	Ser	Leu	Val	Leu	Glu	Asn	Leu	Leu	Ile	Ile
			35				40					45			
Leu	Ala	Val	Ser	Ser	Asp	Phe	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe
	50					55					60				
Leu	Ser	Asn	Leu	Ser	Leu	Ala	Asp	Ile	Gly	Phe	Thr	Ser	Asn	Thr	Val
65					70					75					80
Pro	Lys	Met	Ile	Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr
				85					90					95	
Ala	Gly	Cys	Leu	Thr	Gln	Met	Ser	Leu	Phe	Ala	Val	Phe	Gly	Gly	Met
			100					105					110		
Glu	Glu	Asn	Met	Leu	Leu	Ser	Val	Arg	Ala	Tyr	Asp	Arg	Phe	Val	Ala
		115					120					125			
Ile	Cys	His	Pro	Leu	Tyr	Tyr	Ser	Ala	Ile	Met	Asn	Pro	Cys	Phe	Cys
	130					135						140			
Gly	Phe	Leu	Val	Leu	Phe	Phe	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ser	Gln
145					150					155					160
Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Ile	Lys	Asp	Val	Glu
				165					170					175	
Ile	Pro	Asn	Phe	Trp	Asp	Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	Cys	
		180					185					190			
Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Val	Met	Tyr	Phe	Leu	Ala	Ala	Ile
		195					200					205			
Phe	Gly	Phe	Leu	Pro	Ile	Ser	Arg	Ile	Ile	Phe	Ser	Tyr	Tyr	Lys	Ile
	210					215						220			
Val	Ser	Ser	Met	Leu	Ser	Val	Ser	Ser	Ser	Gly	Gly	Lys	Tyr	Lys	Ala
225					230					235					240
Phe	Ser	Thr	Cys	Gly	Ser	Pro	Leu	Ser	Val	Val	Cys	Leu	Phe	Tyr	Gly
				245					250					255	
Lys	Val	Val	Gly	Gly	Tyr	Leu	Ser	Ser	Asp	Val	Ser	Ser	Ser	Pro	Arg
			260						265					270	
Lys	Gly	Ala	Val	Ala	Ser	Met	Met	Tyr	Thr	Val	Ile	Thr	Pro	Met	Leu
		275					280					285			
Asn	Pro	Phe	Ile	Tyr	Arg	Leu	Arg	Asn	Arg	Asp	Ile	Lys	Arg	Val	Leu
	290					295					300				
Trp	Trp	Leu	His	Gly	Arg	Thr	Val	Xaa	Ser	His	Tyr	Phe	Ile	Ile	Cys
305					310					315					320
Ser	Ile	Pro	Phe	Val	Val	Trp	Val	Lys	Lys	Gly	Ser	Lys	Val	Lys	
				325					330					335	

<210> 1950

<211> 317

<212> PRT
 <213> Unknown (H38g868 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(317)
 <223> Xaa = Any Amino Acid

<400> 1950
 Thr Gly Val Xaa Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Glu
 1 5 10 15
 Leu Gln Pro Ala Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu
 20 25 30
 Val Thr Val Leu Arg Asn Leu Phe Ser Ile Leu Ala Val Ser Ser Asp
 35 40 45
 Cys Pro Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp
 50 55 60
 Pro Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met Ile Val Asp
 65 70 75 80
 Thr Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr Gln
 85 90 95
 Met Ser Phe Leu Leu Val Ala Cys Ile Glu Gly Met Leu Leu Thr
 100 105 110
 Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro Leu His Tyr
 115 120 125
 Pro Val Ile Val Asn Pro His Leu Cys Val Phe Phe Val Leu Val Ser
 130 135 140
 Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu
 145 150 155 160
 Gln Leu Thr Ile Ile Lys Asn Val Glu Ile Ser Asn Leu Val Cys Asp
 165 170 175
 Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Asn
 180 185 190
 Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly Phe Leu Pro Ile Ser
 195 200 205
 Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile Leu Arg Ile
 210 215 220
 Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Cys His
 225 230 235 240
 Leu Ala Val Val Cys Trp Phe Tyr Gly Thr Gly Ile Gly Met Tyr Leu
 245 250 255
 Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val Ala Ser Val
 260 265 270
 Met Tyr Ala Val Val Thr Pro Met Leu Asn Leu Phe Ile Cys Ser Leu
 275 280 285
 Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg Arg Leu Gly Ser Arg Ala
 290 295 300
 Phe Glu Ser Pro Xaa Ser Val Pro Ser Phe Phe Leu Cys
 305 310 315

<210> 1951
 <211> 313
 <212> PRT
 <213> Unknown (H38g869 protein)

<220>
 <223> Synthetic construct

<400> 1951

```

Met Gly Asp Arg Gly Thr Ser Asn His Ser Glu Met Thr Asp Phe Ile
 1      5      10      15
Leu Ala Gly Phe Arg Val Arg Pro Glu Leu His Ile Leu Leu Phe Leu
 20      25      30
Leu Phe Leu Phe Val Tyr Ala Met Ile Leu Leu Gly Asn Val Gly Met
 35      40      45
Met Thr Ile Ile Met Thr Asp Pro Arg Leu Asn Thr Pro Met Tyr Phe
 50      55      60
Phe Leu Gly Asn Leu Ser Phe Ile Asp Leu Phe Tyr Ser Ser Val Ile
 65      70      75      80
Glu Pro Lys Ala Met Ile Asn Phe Trp Ser Glu Asn Lys Ser Ile Ser
 85      90      95
Phe Ala Gly Cys Val Ala Gln Leu Phe Leu Phe Ala Leu Leu Ile Val
 100     105     110
Thr Glu Gly Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Phe Ile Ala
 115     120     125
Ile Cys Asn Pro Leu Leu Tyr Ser Val Gln Met Ser Thr Arg Leu Cys
 130     135     140
Thr Gln Leu Val Ala Gly Ser Tyr Phe Cys Gly Cys Ile Ser Ser Val
 145     150     155     160
Ile Gln Thr Ser Met Thr Phe Thr Leu Ser Phe Cys Ala Ser Arg Ala
 165     170     175
Val Asp His Phe Tyr Cys Asp Ser Arg Pro Leu Gln Arg Leu Ser Cys
 180     185     190
Ser Asp Leu Phe Ile His Arg Met Ile Ser Phe Ser Leu Ser Cys Ile
 195     200     205
Ile Ile Leu Pro Thr Ile Ile Val Ile Ile Val Ser Tyr Met Tyr Ile
 210     215     220
Val Ser Thr Val Leu Lys Ile His Ser Thr Glu Gly His Lys Lys Ala
 225     230     235     240
Phe Ser Thr Cys Ser Ser His Leu Gly Val Val Ser Val Leu Tyr Gly
 245     250     255
Ala Val Phe Phe Met Tyr Leu Thr Pro Asp Arg Phe Pro Glu Leu Ser
 260     265     270
Lys Val Ala Ser Leu Cys Tyr Ser Leu Val Thr Pro Met Leu Asn Pro
 275     280     285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Gln Glu Ala Leu Lys Lys
 290     295     300
Phe Leu Glu Lys Lys Asn Ile Ile Leu
305      310

```

<210> 1952

<211> 277

<212> PRT

<213> Unknown (H38g870 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(277)

<223> Xaa = Any Amino Acid

<400> 1952

```

His Ser Phe Leu Arg Tyr Ile Phe Ala Lys Leu Thr Gly Glu Pro Glu
 1      5      10      15
Leu Gln Pro Ser Leu Tyr Ser Val Phe Trp Ser Pro Xaa Leu Gly Xaa
 20      25      30
Pro His His Thr Ser Met Tyr Pro Leu His Thr Ser Met Tyr Leu Tyr
 35      40      45
Ile Phe Ser Phe Ser Phe Ile Gly Phe Phe Tyr Ser Ser Val Ile Ser

```

```

      50      55      60
Pro Gln Met Thr Ile Ser Phe Val Thr Glu Lys Asn Ile Ile Thr Tyr
65      70      75      80
Val Thr Ser Asn Thr Gln Pro Phe Pro Leu Cys Phe Phe Val Ile Ser
      85      90      95
Asp Tyr Ser Ile Phe Ile Pro Leu Ala Leu Asp His Tyr Glu Ala Met
      100      105      110
Thr Leu Pro Val Ser Phe Ile Ser Phe Ile Ser Val Asp Gly Ser Xaa
      115      120      125
Val Ile Glu Phe Ala Asp Ala Val Val His Gln Gly Ser Met Asp Gln
      130      135      140
Phe Leu Phe Cys Asp His Ser Cys Met Ser Leu Asn Leu Cys Asn Ile
145      150      155      160
Gly Pro Leu Gln Ala Ala Xaa Ile Ser Thr Tyr Val Ser Lys Gln Val
      165      170      175
Asp Leu Tyr Ser Xaa Glu Pro Ala Val Tyr His Ala Val Leu Ser Phe
      180      185      190
Ser Tyr Phe Val Phe Ile Leu Phe Asn Ile Phe His Xaa Pro Ser Gly
      195      200      205
Pro Asn Leu Gln Pro Asp Ser Ile Asn Leu Phe Ile Ser Phe Phe Gly
      210      215      220
Leu Gly Thr Phe Met Tyr Leu Arg Ser Pro Glu Ala Met Gly Xaa Cys
225      230      235      240
Lys Phe Thr Val Ser Phe Thr Lys Met Gly Pro Val Met Asn Gly Leu
      245      250      255
Phe Asn Thr Leu Arg Asn Lys Thr Ile Xaa Leu Ala Ala Met Lys Pro
      260      265      270
Leu Ser Phe Ser Ser
      275

```

<210> 1953

<211> 335

<212> PRT

<213> Unknown (H38g871 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1953

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
1      5      10      15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
      20      25      30
Leu Ser Met Cys Leu Val Thr Val Leu Glu Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Arg Glu
      100      105      110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile
      115      120      125
Cys His Pro Pro Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly
      130      135      140

```

Phe Leu Asp Leu Leu Ser Leu Phe Phe Phe Phe Phe Phe Phe Ser
 145 150 155 160
 Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met
 165 170 175
 Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Cys
 180 185 190
 Cys Asp Thr Phe Thr Arg Asn Ile Asn Met Tyr Phe Pro Ala Ala Val
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Ile
 210 215 220
 Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Thr Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
 245 250 255
 Thr Gly Val Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg
 260 265 270
 Lys Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
 275 280 285
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Ser Val Leu
 290 295 300
 Arg Arg Pro His Ser Ser Ala Val Xaa Ser Gln Tyr Leu Leu Ile Cys
 305 310 315 320
 Ser Ile Pro Phe Val Gly Trp Val Lys Lys Gly Ser Lys Val Lys
 325 330 335

<210> 1954

<211> 342

<212> PRT

<213> Unknown (H38g872 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(342)

<223> Xaa = Any Amino Acid

<400> 1954

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65 70 75 80
 Lys Met Ser Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100 105 110
 Lys Arg His Ala Pro Glu Val Met Ala Tyr Asp Leu Phe Val Pro Ile
 115 120 125
 Cys His Leu Leu Tyr Arg Ser Thr Ile Leu Asn Pro Phe Val Arg Gly
 130 135 140
 Phe Leu Asn Leu Leu Ser Leu Phe Val Gly Phe Phe Phe Phe Ser Leu
 145 150 155 160
 Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr
 165 170 175
 Tyr Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln

```

      180      185      190
Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Asn Asn Met
      195      200      205
Tyr Phe Pro Ala Ala Val Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu
      210      215      220
Phe Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser
      225      230      235      240
Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val
      245      250      255
Val Cys Xaa Phe Tyr Gly Ala Gly Val Gly Gly Tyr Leu Gly Ser Asp
      260      265      270
Val Ser Ser Ser Pro Arg Lys Gly Ala Val Ala Ser Val Thr Tyr Tyr
      275      280      285
Thr Val Val Thr Pro Met Leu Asn Ser Phe Ile Tyr Ser Leu Arg Asn
      290      295      300
Gly Asp Ile Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Xaa
      305      310      315      320
Ser Gln Tyr Val Leu Ile Cys Ser Ile Pro Phe Val Gly Trp Val Asn
      325      330      335
Lys Asp Ser Lys Val Lys
      340

```

<210> 1955

<211> 348

<212> PRT

<213> Unknown (H38g873 protein)

<220>

<223> Synthetic construct

<400> 1955

```

Met Asp Leu Gly Asn Ser Gly Asn Asp Ser Val Val Thr Lys Phe Val
  1          5          10          15
Leu Leu Gly Leu Thr Glu Thr Ala Ala Leu Gln Pro Ile Leu Phe Val
      20      25      30
Ile Phe Leu Leu Ala Tyr Val Thr Thr Ile Gly Gly Thr Leu Ser Ile
      35      40      45
Leu Ala Ala Ile Leu Met Glu Thr Lys Leu His Ser Pro Met Tyr Phe
      50      55      60
Phe Leu Gly Asn Leu Ser Leu Pro Asp Val Gly Cys Val Ser Val Thr
      65      70      75      80
Val Pro Ala Met Leu Ser His Phe Ile Ser Asn Asp Arg Ser Ile Pro
      85      90      95
Tyr Lys Ala Cys Leu Ser Glu Leu Phe Phe His Leu Leu Ala Gly
      100      105      110
Ala Asp Cys Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Leu Ala
      115      120      125
Ile Cys Gln Ser Leu Thr Tyr Ser Ser Arg Met Ser Trp Gly Ile Gln
      130      135      140
Gln Ala Leu Val Gly Met Ser Trp Val Phe Ser Phe Thr Asn Ala Leu
      145      150      155      160
Thr Gln Thr Val Ala Leu Ser Pro Leu Asn Phe Cys Gly Pro Asn Val
      165      170      175
Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Pro Phe Gln Leu Ser Cys
      180      185      190
Ala Ser Val His Leu Asn Gly Gln Leu Leu Phe Val Ala Ala Ala Phe
      195      200      205
Met Gly Val Ala Pro Leu Val Leu Ile Thr Val Ser Tyr Ala His Val
      210      215      220
Ala Ala Ala Val Leu Arg Ile Arg Ser Ala Glu Gly Lys Lys Lys Ala
      225      230      235      240

```

Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
 245 250 255
 Thr Gly Val Phe Ser Tyr Thr Arg Leu Gly Ser Val Glu Ser Ser Asp
 260 265 270
 Lys Asp Lys Gly Ile Gly Ile Leu Asn Thr Val Ile Ser Pro Met Leu
 275 280 285
 Asn Pro Leu Ile Tyr Trp Thr Ser Leu Leu Asp Val Gly Cys Ile Ser
 290 295 300
 His Cys Ser Ser Asp Ala Gly Val Ser Pro Gly Pro Pro Val Gln Ser
 305 310 315 320
 Ser Leu Cys Cys Leu Gln Phe Thr Ala Leu Leu Ser Pro Pro Pro Gly
 325 330 335
 Trp Gly Gly Leu Ser Pro Leu Asn Ser His Gly Leu
 340 345

<210> 1956

<211> 230

<212> PRT

<213> Unknown (H38g874 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(230)

<223> Xaa = Any Amino Acid

<400> 1956

Met Leu Ile Pro Ser Ser Thr Arg Lys Met Ala Ala Glu Ser His Ser
 1 5 10 15
 Thr Val Thr Glu Phe Ile Leu Arg Lys Lys Pro Ala Arg Ala Pro Ala
 20 25 30
 Pro Pro Leu Leu Gly Ile Cys Leu Lys Thr Val Val Gly Ala Leu Ile
 35 40 45
 Leu Ile Thr Leu Val Phe Leu Asn Ser Gln Leu His Pro Pro Met Tyr
 50 55 60
 Tyr Val Ile Arg Asn Leu Ser Phe Met Asp His Cys Asn Cys Ser Ile
 65 70 75 80
 Ser Thr Pro Lys Ile Leu Val Lys Phe Val Leu Glu Lys Thr Ile Ile
 85 90 95
 Ser Tyr Glu Asp Gly Met Ser Gln Leu Cys Ser Ala Ser Cys Tyr Ile
 100 105 110
 Leu Ser Trp Pro Ser Val Thr Cys Gly Pro Ala Thr Ala Val Ile Thr
 115 120 125
 Phe His Gln Val Ser Ser Leu Leu Val Val Val Val Tyr Tyr Met Glu
 130 135 140
 Leu Thr Gly Thr Thr Ile Glu Phe Cys Leu Val Leu Lys Xaa Tyr Xaa
 145 150 155 160
 Cys Glu Leu Phe Ile Ser His Tyr Phe Cys Ser Cys Thr Ser Ile Tyr
 165 170 175
 Asp Ile Asp Arg Thr Ile Phe Phe Phe Thr Xaa Cys Asn Ile Val Val
 180 185 190
 Thr Arg Leu Thr Val Val Ser Tyr Ser Phe Leu Ser Ser Ile Leu His
 195 200 205
 Ile Ser Phe Thr Lys Gly Lys Leu Trp Val Phe Pro Val Gly Leu Thr
 210 215 220
 His Ser Cys Cys Cys Leu
 225 230

<210> 1957

<211> 331

<212> PRT

<213> Unknown (H38g875 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1957

```

His Thr Glu Pro Arg Asn Leu Thr Ser Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Leu Leu Ser
      20           25           30
Leu Ser Leu Ser Met His Leu Val Met Val Leu Arg Asn Leu Leu Asn
      35           40           45
Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Thr Tyr Phe
      50           55           60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
      65           70           75           80
Val Pro Asn Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85           90           95
His Ala Asp Cys Leu Thr Gln Ile Ser Phe Leu Leu Leu Phe Ala Cys
      100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Thr Tyr Asp Cys Phe Val Ala
      115          120          125
Ile Cys Cys Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
      145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
      165          170          175
Ile Ser Asn Ser Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
      180          185          190
Ser Asp Ser Val Ile Asn Ser Ile Phe Met His Phe His Asn Thr Met
      195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Val Ser Tyr Tyr Lys Ile
      210          215          220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
      225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
      245          250          255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Leu Ser Pro Pro Pro Arg
      260          265          270
Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
      275          280          285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
      290          295          300
Trp Arg Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro
      305          310          315          320
Phe Ser Cys Val Gly Lys Gly Asn His Ile Lys
      325          330

```

<210> 1958

<211> 322

<212> PRT

<213> Unknown (H38g876 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1958

```

His Arg Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Leu Ala Val Arg Ser Asp Ser Pro Leu His Thr Pro Ile Tyr Phe
          50           55           60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
          65           70           75           80
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
          85           90           95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
          100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
          115          120          125
Ile Cys His Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
          145          150          155          160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Phe Ala Cys
          180          185          190
Ser Asp Ser Ile Ile Asn Ser Ile Phe Ile Tyr Phe His Ser Thr Met
          195          200          205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
          210          215          220
Ile Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
          225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
          245          250          255
Thr Asp Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
          260          265          270
Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
          275          280          285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
          290          295          300
Trp Gly Leu His Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro
          305          310          315          320
Phe Ser

```

<210> 1959

<211> 315

<212> PRT

<213> Unknown (H38g877 protein)

<220>

<223> Synthetic construct

<400> 1959

```

Met Gln Pro Glu Ser Gly Ala Asn Gly Thr Val Ile Ala Glu Phe Ile
 1           5           10           15
Leu Leu Gly Leu Leu Glu Ala Pro Gly Leu Gln Pro Val Val Phe Val

```

<210> 1960
<211> 323
<212> PRT
<213> Unknown (H38g878 protein)

<220>
<223> Synthetic construct

<400> 1960															
Met	Thr	Asp	Tyr	Asn	Glu	Pro	Met	Glu	Pro	Met	Glu	Asp	Lys	Asn	Gln
1				5					10					15	
Thr	Val	Val	Thr	Glu	Phe	Leu	Leu	Leu	Gly	Leu	Thr	Asp	His	Pro	Tyr
			20					25					30		
Gln	Lys	Ile	Val	Leu	Phe	Phe	Met	Phe	Leu	Phe	Val	Tyr	Leu	Ile	Thr
	35						40					45			
Leu	Gly	Gly	Asn	Leu	Gly	Met	Ile	Thr	Leu	Ile	Trp	Ile	Asp	Pro	Arg
	50					55					60				
Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Arg	His	Leu	Ser	Phe	Val	Asp
65					70					75					80
Ile	Cys	Ser	Ser	Ser	Ser	Val	Val	Pro	Lys	Met	Leu	Cys	Asn	Ile	Phe
				85					90				95		
Ala	Glu	Lys	Lys	Asp	Ile	Thr	Phe	Leu	Gly	Cys	Ala	Ala	Gln	Met	Trp
			100					105					110		

Phe Phe Gly Leu Phe Glu Ala Ala Glu Cys Phe Leu Leu Ala Ala Met
 115 120 125
 Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Thr Leu
 130 135 140
 Ile Met Ser Gln Gln Val Cys Met Gln Leu Val Val Gly Pro Tyr Ala
 145 150 155 160
 Met Ala Leu Ile Ser Thr Met Thr His Thr Ile Phe Thr Phe Cys Leu
 165 170 175
 Pro Phe Cys Gly Ser Asn Ile Ile Asn His Phe Phe Cys Asp Ile Phe
 180 185 190
 Pro Leu Leu Ser Leu Ala Cys Ala Asp Thr Trp Val Asn Lys Phe Val
 195 200 205
 Leu Phe Val Leu Ala Gly Ala Ile Gly Val Leu Ser Gly Leu Ile Ile
 210 215 220
 Met Val Ser Tyr Ile Cys Ile Leu Met Thr Ile Leu Lys Ile Gln Thr
 225 230 235 240
 Ala Asp Gly Lys Gln Lys Ala Phe Phe Thr Cys Phe Ser His Leu Ala
 245 250 255
 Ala Val Ser Ile Leu Tyr Gly Thr Leu Phe Leu Ile Tyr Val Arg Pro
 260 265 270
 Ser Ser Ser Ser Ser Leu Gly Ile Tyr Lys Val Ile Ser Leu Phe Tyr
 275 280 285
 Thr Val Val Ile Pro Met Val Asn Pro Leu Ile Tyr Ser Leu Arg Asn
 290 295 300
 Lys Glu Val Lys Asp Ala Phe Arg Arg Lys Ile Glu Arg Lys Lys Phe
 305 310 315 320
 Ile Ile Gly

<210> 1961

<211> 229

<212> PRT

<213> Unknown (H38g879 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(229)

<223> Xaa = Any Amino Acid

<400> 1961

Phe Phe Ser Leu Asp Leu Ile Arg Ser Gln Ala Asn Thr Met Ser Lys
 1 5 10 15
 Lys His Trp Thr Ala Ile Ala Glu Phe Ile Pro Leu Gly Pro Thr Asp
 20 25 30
 Gln Ala Glu Leu Gln Leu Val Leu Phe Phe Phe Thr Phe Leu Val Ile
 35 40 45
 Tyr Leu Ile Met Val Met Gly Asn Leu Ser Met Ile Leu Ile Ile Arg
 50 55 60
 Ser Asp Xaa Lys Leu His Ile Pro Met Tyr Phe Phe Leu Ser His Leu
 65 70 75 80
 Ser Phe Ala Val Leu Cys Tyr Thr Leu Asn Val Thr Pro Gln Ile Leu
 85 90 95
 Val Asn Phe Leu Ser Lys Arg Lys Thr Ile Phe Phe Ile Gly Cys Val
 100 105 110
 Ser Val Leu Xaa Phe Tyr Phe Phe Ile Val Leu Ile Ile Arg Asp Tyr
 115 120 125
 His Met Leu Thr Val Met Ala Asn Asp Cys Tyr Met Ala Ile Cys Lys
 130 135 140
 Pro Leu Leu Tyr Gly Ser Lys Met Ser Arg Phe Val Cys Leu Ser Leu

```

145          150          155          160
Ala Ser Val Ser Xaa Ile Tyr Gly Phe Ala Asn Tyr Leu Ala Gln Thr
          165          170          175
Ile Arg Met Leu Leu Leu Ser Phe Xaa Gly Ser Asn Glu Ile Asn His
          180          185          190
Phe Asp Cys Ala Asp Pro Pro Leu Leu Val Leu Pro Cys Ala Gly Thr
          195          200          205
Cys Val Lys Xaa Ile Ile Met Leu Met Glu Pro His Cys Leu Leu Lys
          210          215          220
Pro Gly Tyr Ile Leu
225

```

<210> 1962

<211> 286

<212> PRT

<213> Unknown (H38g880 protein)

<220>

<223> Synthetic construct

<400> 1962

```

Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val
 1          5          10          15
Ser Ser Asp Ser His Pro His Thr Pro Met Tyr Phe Phe Leu Ser Asn
          20          25          30
Leu Cys Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met
          35          40          45
Ile Val Asp Met Gly Ser His Ser Arg Val Ile Ser Tyr Gly Gly Cys
          50          55          60
Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile Val Asp Met
          65          70          75          80
Phe Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys Arg Pro
          85          90          95
Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe Phe Val
          100          105          110
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp
          115          120          125
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
          130          135          140
Val Cys Glu Pro Ser Gln Leu Leu Lys Leu Ala Ser Tyr Asp Ser Val
          145          150          155          160
Ile Asn Ser Ile Phe Ile Tyr Phe Asp Asn Thr Met Phe Gly Phe Leu
          165          170          175
Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser Ile
          180          185          190
Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Ala Cys
          195          200          205
Gly Cys His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
          210          215          220
Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly Met Val
          225          230          235          240
Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile
          245          250          255
Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Val Cys
          260          265          270
Asn Lys Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser
          275          280          285

```

<210> 1963

<211> 325

<212> PRT

<213> Unknown (H38g881 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1963

```

Met Ala Asn Glu Asn Tyr Thr Lys Val Thr Xaa Phe Ile Phe Thr Gly
 1           5           10           15
Leu Asn Tyr Asn Pro Gln Leu Arg Val Phe Leu Phe Leu Leu Phe Leu
      20           25           30
Thr Thr Phe Tyr Val Ile Asn Val Thr Gly Asn Leu Gly Met Ile Val
 35           40           45
Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 50           55           60
Ser His Leu Ser Phe Val Asp Thr Cys Phe Ser Ser Val Val Ser Pro
 65           70           75           80
Lys Met Leu Thr Asp Phe Phe Val Lys Arg Lys Ala Ile Ser Phe Leu
      85           90           95
Gly Cys Ala Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Ala Ala Asp
      100           105           110
Cys Phe Leu Leu Glu Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys
      115           120           125
Asn Pro Leu Leu Tyr Ser Val Ala Met Ser Gln Arg Leu Cys Ile Gln
      130           135           140
Leu Val Val Gly Pro Tyr Val Ile Gly Leu Met Asn Thr Met Thr His
 145           150           155           160
Thr Thr Asn Ala Phe Cys Leu Pro Phe Cys Gly Pro Asn Val Ile Asn
      165           170           175
Pro Phe Phe Cys Asp Met Ser Pro Leu Leu Ser Leu Val Cys Ala Asp
      180           185           190
Thr Arg Leu Asn Lys Leu Ala Val Phe Ile Val Ala Gly Ala Val Gly
      195           200           205
Val Phe Ser Gly Leu Thr Ile Leu Ile Ser Tyr Ile Tyr Ile Leu Met
      210           215           220
Ala Ile Leu Arg Ile Arg Ser Ala Asp Gly Arg Cys Lys Thr Phe Ser
 225           230           235           240
Thr Cys Ser Ser His Leu Thr Ala Val Phe Ile Ser Tyr Gly Thr Leu
      245           250           255
Phe Phe Ile Tyr Val His Pro Ser Ala Thr Phe Ser Leu Asp Leu Asn
      260           265           270
Lys Val Val Ser Val Phe Tyr Thr Ala Val Ile Pro Met Leu Asn Pro
      275           280           285
Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ile His Arg
      290           295           300
Thr Val Thr Gln Arg Lys Phe Cys Lys Ala Xaa Ile Leu Ile Gln Lys
 305           310           315           320
Glu Leu Gly Arg Lys
      325

```

<210> 1964

<211> 314

<212> PRT

<213> Unknown (H38g882 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1964

```

Met Glu Thr Glu Asn Asn Thr Thr Val Thr Glu Phe Ile Ile Leu Gly
 1              5              10              15
Leu Thr Asp Asn Pro Met Leu Cys Ala Ile Phe Phe Val Phe Phe Leu
      20              25              30
Ala Val Tyr Ile Val Thr Ile Pro Gly Asn Ile Ser Ile Ile Leu Leu
      35              40              45
Ile Gln Ser Ser Pro Gln Leu His Thr Leu Met Tyr Leu Phe Leu Ser
      50              55              60
His Leu Ala Ser Val Asp Ile Gly Tyr Ser Ile Ser Val Thr Pro Ile
      65              70              75              80
Ile Leu Ile Asn Phe Leu Arg Glu Lys Thr Thr Ile Pro Val Thr Gly
      85              90              95
Cys Ile Ala Gln Leu Gly Ser Asp Val Met Phe Gly Thr Thr Glu Cys
      100             105             110
Phe Leu Leu Asp His Tyr Val Ala Ile Cys Ser Pro Leu Leu Tyr Ser
      115             120             125
Ile Gln Met Pro Pro Val Val Cys Phe Leu Leu Leu Gly Ala Ser Tyr
      130             135             140
Leu Gly Gly Cys Leu Asn Ala Ser Ser Phe Thr Gly Cys Leu Met Asn
      145             150             155             160
Leu Ser Phe Cys Gly Pro Asn Lys Ile Asn His Phe Phe Cys Asp Leu
      165             170             175
Phe Pro Leu Leu Lys Leu Ser Cys Gly His Val Tyr Ile Ala Glu Ile
      180             185             190
Ser Pro Ala Ile Ser Ser Ala Ser Val Leu Ile Ser Thr Leu Phe Thr
      195             200             205
Ile Ile Val Ser Tyr Ile Tyr Ile Leu His Ser Ile Leu Lys Val Cys
      210             215             220
Ser Thr Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser His Leu
      225             230             235             240
Thr Ala Val Thr Leu Phe Tyr Gly Thr Ile Leu Phe Val Tyr Val Met
      245             250             255
Pro Lys Ser Ser Tyr Ser Ala Asp Gln Val Lys Val Ala Phe Val Ile
      260             265             270
Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg
      275             280             285
Asn Lys Glu Val Lys Glu Ala Met Arg Lys Leu Met Ala Arg Thr His
      290             295             300
Trp Phe Ser Xaa Ile Lys Ser Val Xaa Ser
      305             310

```

<210> 1965

<211> 202

<212> PRT

<213> Unknown (H38g883 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(202)

<223> Xaa = Any Amino Acid

<400> 1965

```

Ile Phe Ala Ile Leu Thr Thr Ile Asp Cys Cys Val Phe Val Trp Glu
 1              5              10              15

```

Phe Leu Glu Cys Thr Val Phe Val Asn Lys Arg Ala Cys Ala Gln Leu
 20 25 30
 Ala Cys Gly Ala Phe Cys Ile Gly Leu Ile Met Thr Val Val Xaa Ile
 35 40 45
 Thr Thr Val Ser Gln Arg Tyr Lys Arg Ser Thr Tyr Ala Ile Val Asp
 50 55 60
 Cys Phe Leu Phe Asp Thr Leu Leu Val Met Lys Leu Ser Cys Ile Asp
 65 70 75 80
 Asn Thr Ile Tyr Glu Ile Ile Gln Tyr Phe Ile His His Thr Cys Val
 85 90 95
 Gln Val Ser Met Gly Leu Val Cys Ile Ser Tyr Ile Asp Ile Pro Val
 100 105 110
 Thr Ser Ile Val Leu Arg Ile Ser Xaa Ser Glu Val Phe Ala Thr Cys
 115 120 125
 Val Pro Gln Pro Pro Pro His His Gly His Cys Leu Tyr Val Cys Ala
 130 135 140
 Cys Thr Ala Tyr Leu Lys His Lys Pro Met Asn Ser Ile Glu Lys Gly
 145 150 155 160
 Leu Leu Xaa Glu Thr Tyr Ile Ile Ile Ile His Ser Ala Ser Gly Pro
 165 170 175
 Val Val Tyr Thr Leu Arg Tyr Met Glu Ala Lys Asp Thr Met Tyr Arg
 180 185 190
 Ala Val Asp Arg Asn Ile Ser Xaa Gln Ile
 195 200

<210> 1966

<211> 315

<212> PRT

<213> Unknown (H38g884 protein)

<220>

<223> Synthetic construct

<400> 1966

Met Glu Pro Glu Ala Gly Thr Asn Arg Thr Ala Val Ala Glu Phe Ile
 1 5 10 15
 Leu Leu Gly Leu Val Gln Thr Glu Glu Met Gln Pro Val Val Phe Val
 20 25 30
 Leu Leu Leu Phe Ala Tyr Leu Val Thr Thr Gly Gly Asn Leu Ser Ile
 35 40 45
 Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ala Pro Met Tyr Phe
 50 55 60
 Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Thr Val Thr
 65 70 75 80
 Val Pro Ala Met Leu Gly Arg Leu Leu Ser His Lys Ser Thr Ile Ser
 85 90 95
 Tyr Asp Ala Cys Leu Ser Gln Leu Phe Phe Phe His Leu Leu Ala Gly
 100 105 110
 Met Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala
 115 120 125
 Ile Cys Gln Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
 130 135 140
 Arg Met Leu Val Ala Ala Ser Leu Ala Cys Ala Phe Thr Asn Ala Leu
 145 150 155 160
 Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu
 165 170 175
 Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
 180 185 190
 Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Ala Val Gly Phe Ile
 195 200 205
 Met Ala Gly Thr Pro Leu Val Leu Ile Ile Thr Ala Tyr Ser His Val

210 215 220
 Ala Ala Val Leu Arg Ile Arg Ser Val Glu Gly Arg Lys Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe Phe Gly
 245 250 255
 Arg Gly Ile Phe Asn Tyr Met Arg Leu Gly Ser Glu Glu Ala Ser Asp
 260 265 270
 Lys Asp Lys Gly Val Gly Val Phe Asn Thr Val Ile Asn Pro Met Leu
 275 280 285
 Asn Pro Leu Ile Tyr Ser Leu Arg Asn Pro Asp Val Gln Gly Ala Leu
 290 295 300
 Trp Gln Ile Phe Leu Gly Arg Arg Ser Leu Thr
 305 310 315

<210> 1967
 <211> 309
 <212> PRT
 <213> Unknown (H38g885 protein)

<220>
 <223> Synthetic construct

<400> 1967
 Met Lys Arg Lys Asn Phe Thr Glu Val Ser Glu Phe Ile Phe Leu Gly
 1 5 10 15
 Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu
 20 25 30
 Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile
 35 40 45
 Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg
 65 70 75 80
 Met Leu Leu Ser Leu Ile Phe His Asn Gln Pro Ile Ser Leu Ala Gly
 85 90 95
 Cys Ala Thr Gln Met Phe Phe Phe Val Ile Leu Ala Thr Asn Asn Cys
 100 105 110
 Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu Arg Tyr Thr Val Ile Met Ser Lys Gly Leu Cys Ala Gln Leu
 130 135 140
 Val Cys Gly Ser Phe Gly Ile Gly Leu Thr Met Ala Val Leu His Val
 145 150 155 160
 Thr Ala Met Phe Asn Leu Pro Phe Cys Gly Thr Val Val Asp His Phe
 165 170 175
 Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr
 180 185 190
 Ile Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Phe Val
 195 200 205
 Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Val Ile Ser Ser Ile
 210 215 220
 Leu Gln Ile Ala Ser Ala Glu Gly Arg Lys Lys Thr Phe Ala Thr Cys
 225 230 235 240
 Val Ser His Leu Thr Val Val Ile Val His Cys Gly Cys Ala Ser Ile
 245 250 255
 Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Ile Glu Lys Asp Leu Val
 260 265 270
 Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Val Val
 290 295 300

Gly Arg Asn Ile Ser
305

<210> 1968

<211> 320

<212> PRT

<213> Unknown (H38g886 protein)

<220>

<223> Synthetic construct

<400> 1968

```

Met Leu Gln Arg Val Gly Glu Met Asp Gly Gly Asn Gln Ser Glu Gly
 1           5           10           15
Ser Glu Phe Leu Leu Gly Ile Ser Glu Ser Pro Glu Gln Gln Gln
      20           25           30
Met Leu Phe Trp Met Phe Leu Val Arg Tyr Leu Val Thr Val Leu Gly
 35           40           45
Asn Val Leu Ile Ile Leu Ala Ile Ser Ser Asp Ser Arg Leu His Thr
 50           55           60
Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser Phe Thr Asp Leu Phe Phe
 65           70           75           80
Val Thr Asn Thr Ile Pro Lys Met Leu Val Asn Leu Gln Ser Gln Asn
      85           90           95
Lys Ala Ile Ser Tyr Thr Gly Cys Leu Thr Gln Leu Tyr Phe Leu Val
      100           105           110
Ser Leu Val Ala Leu Asp Asn Leu Asn Leu Ala Val Met Ala Tyr Asp
      115           120           125
Arg Tyr Val Ala Ile Cys Arg Pro Leu His Tyr Val Thr Ala Met Ile
      130           135           140
Pro Gly Leu Cys Ile Leu Leu Leu Ser Leu Cys Trp Val Phe Ser Ala
      145           150           155           160
Leu Tyr Gly Leu Ile His Ile Leu Leu Met Thr Arg Val Thr Phe Cys
      165           170           175
Gly Ser Gln Lys Ile His Tyr Leu Phe Cys Glu Met Tyr Phe Leu Leu
      180           185           190
Arg Leu Ala Cys Ser Asn Ile His Val Asn His Thr Val Leu Val Ala
      195           200           205
Thr Gly Cys Phe Ile Phe Leu Ile Pro Leu Gly Phe Met Ile Thr Ser
      210           215           220
Tyr Ala Arg Ile Val Arg Ala Ile Leu Gln Ile Pro Ser Ala Thr Gly
      225           230           235           240
Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Ser
      245           250           255
Leu Phe Tyr Gly Thr Leu Gly Met Val Tyr Leu Gln Pro Leu Gln Thr
      260           265           270
Tyr Ser Met Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr
      275           280           285
Pro Met Ile Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met His
      290           295           300
Gly Ala Leu Gly Arg Leu Arg Gln Gly Lys Ala Phe Gln Lys Leu Thr
      305           310           315           320

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<210> 1969

<211> 276

<212> PRT

<213> Unknown (H38g887 protein)

<220>

<223> Synthetic construct

<400> 1969

```

Met Arg Arg Lys Asn Leu Thr Glu Val Thr Glu Phe Val Phe Leu Gly
 1           5           10           15
Phe Ser Arg Phe His Lys His His Ile Thr Leu Phe Val Val Phe Leu
 20           25           30
Ile Leu Tyr Thr Leu Thr Val Ala Gly Asn Ala Ile Ile Met Thr Ile
 35           40           45
Ile Cys Ile Asp Arg His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50           55           60
Met Leu Ala Ser Ser Lys Thr Val Tyr Thr Leu Phe Ile Ile Pro Gln
 65           70           75           80
Met Leu Ser Ser Phe Val Thr Gln Thr Gln Pro Ile Ser Leu Ala Gly
 85           90           95
Cys Thr Thr Gln Thr Phe Phe Phe Val Thr Leu Ala Ile Asn Asn Cys
 100          105          110
Phe Leu Leu Thr Val Met Gly Tyr Asp His Tyr Met Ala Ile Cys Asn
 115          120          125
Pro Leu Arg Tyr Arg Val Ile Thr Ser Lys Lys Val Cys Val Gln Leu
 130          135          140
Val Cys Gly Ala Phe Ser Ile Gly Leu Ala Met Ala Ala Val Gln Val
 145          150          155          160
Thr Ser Ile Phe Thr Leu Pro Phe Cys His Thr Val Val Gly His Phe
 165          170          175
Phe Cys Asp Ile Leu Pro Val Met Lys Leu Ser Cys Ile Asn Thr Thr
 180          185          190
Ile Asn Glu Ile Ile Asn Phe Val Val Arg Leu Phe Val Ile Leu Val
 195          200          205
Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Val
 210          215          220
Leu Lys Ile Ala Ser Ala Glu Gly Trp Lys Lys Thr Phe Ala Thr Cys
 225          230          235          240
Ala Phe His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile
 245          250          255
Ala Tyr Leu Met Pro Lys Ser Glu Asn Ser Ile Glu Gln Asp Leu Leu
 260          265          270
Leu Ser Val Thr
 275

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<210> 1970

<211> 312

<212> PRT

<213> Unknown (H38g888 protein)

<220>

<223> Synthetic construct

<400> 1970

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1           5           10           15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20           25           30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
 35           40           45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50           55           60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65           70           75           80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85           90           95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
 100          105          110

```

Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
 145 150 155 160
 Phe Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
 165 170 175
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr
 180 185 190
 His Ile Ile His Thr Ala Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Thr Leu Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
 210 215 220
 Ile Leu Gln Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
 245 250 255
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu
 290 295 300
 Trp Arg Pro Phe Gln Arg Pro Lys
 305 310

<210> 1971

<211> 299

<212> PRT

<213> Unknown (H38g889 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(299)

<223> Xaa = Any Amino Acid

<400> 1971

Met Ala Asp Gly Asn Tyr Lys Arg Ile Thr Glu Phe Ile Phe Val Gly
 1 5 10 15
 Leu Arg Tyr His Leu Gln Leu Gln Val Phe Leu Phe Leu Pro Phe Leu
 20 25 30
 Pro Phe Tyr Leu Ile Thr Met Thr Glu Asn Leu Gly Met Met Val Arg
 35 40 45
 Ile Trp Leu Asp Ser Cys Phe His Thr Pro Met Tyr Phe Val Leu Ser
 50 55 60
 Tyr Leu Ser Phe Val Asp Ile Cys Phe Ser Ser Val Val Gly His Lys
 65 70 75 80
 Leu Leu Thr Asp Leu Phe Ala Val Arg Lys Ala Ile Ser Phe Leu Gly
 85 90 95
 Cys Pro Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Val Ile Glu Tyr
 100 105 110
 Leu Leu Leu Ala Ser Met Ala Tyr Asp Asn Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Val Ala Met Xaa Xaa Arg Leu Cys Ile Gln Leu
 130 135 140
 Val Val Val Arg Tyr Ala Ala Asp Phe Phe Asn Thr Ile Thr His Thr
 145 150 155 160
 Thr Ala Ala Phe His Phe Pro Phe Phe His Ser Asn Ile Ile Asn His

165 170 175
 Phe Phe Cys Asp Met Ser Leu Leu Leu Ser Leu Val Cys Ala Asp Ala
 180 185 190
 Arg Ile Asn Lys Leu Leu Val Phe Ile Val Ala Gly Ala Val Leu Val
 195 200 205
 Val Ser Ser Leu Thr Ile Ile Ile Ser Tyr Phe Tyr Ile Leu Thr Asp
 210 215 220
 Ile Leu Arg Ile Cys Ser Ala Asn Gly Lys Asn Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Ala Val Ser Ile Phe Tyr Gly Ser Leu Phe
 245 250 255
 Phe Ser Tyr Val Arg Pro Gly Ala Thr Phe Tyr Pro Glu Leu Asn Lys
 260 265 270
 Ile Val Leu Val Phe Cys Ile Ile Pro Met Leu Lys Pro Leu Ile Tyr
 275 280 285
 Ser Leu Ile Asn Lys Glu Val Ser Xaa Pro Leu
 290 295

<210> 1972

<211> 311

<212> PRT

<213> Unknown (H38g890 protein)

<220>

<223> Synthetic construct

<400> 1972

Met Glu Lys Ile Asn Asn Val Thr Glu Phe Ile Phe Trp Gly Leu Ser
 1 5 10 15
 Gln Ser Pro Glu Ile Glu Lys Val Cys Phe Val Val Phe Ser Phe Phe
 20 25 30
 Tyr Ile Ile Ile Leu Leu Gly Asn Leu Leu Ile Met Leu Thr Val Cys
 35 40 45
 Leu Ser Asn Leu Phe Lys Ser Pro Met Tyr Phe Phe Leu Ser Phe Leu
 50 55 60
 Ser Phe Val Asp Ile Cys Tyr Ser Ser Val Thr Ala Pro Lys Met Ile
 65 70 75 80
 Val Asp Leu Leu Ala Lys Asp Lys Thr Ile Ser Tyr Val Gly Cys Met
 85 90 95
 Leu Gln Leu Leu Gly Val His Phe Phe Gly Cys Thr Glu Ile Phe Ile
 100 105 110
 Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Met Thr Ile Met Asn Arg Glu Thr Cys Asn Lys Met Leu Leu
 130 135 140
 Gly Thr Trp Val Gly Gly Phe Leu His Ser Ile Ile Gln Val Ala Leu
 145 150 155 160
 Val Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp His Tyr Phe
 165 170 175
 Cys Asp Val His Pro Val Leu Lys Leu Ala Cys Thr Glu Thr Tyr Ile
 180 185 190
 Val Gly Val Val Val Thr Ala Asn Ser Gly Thr Ile Ala Leu Gly Ser
 195 200 205
 Phe Val Ile Leu Leu Ile Ser Tyr Ser Ile Ile Leu Val Ser Leu Arg
 210 215 220
 Lys Gln Ser Ala Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys Gly Ser
 225 230 235 240
 His Ile Ala Met Val Val Ile Phe Phe Gly Pro Cys Thr Phe Met Tyr
 245 250 255
 Met Arg Pro Asp Thr Thr Phe Ser Glu Asp Lys Met Val Ala Val Phe
 260 265 270

Tyr Thr Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Glu Val Lys Asn Ala Met Lys Lys Leu Trp Gly Arg Asn Val
 290 295 300
 Phe Leu Glu Ala Lys Gly Lys
 305 310

<210> 1973

<211> 318

<212> PRT

<213> Unknown (H38g891 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1973

Met Asp Tyr Arg Asn Gln Thr Leu Val Thr Glu Phe Phe Ser Val Gly
 1 5 10 15
 Leu Thr Asn Leu Phe Gln His Lys Ile Ala Leu Phe Leu Val Phe Leu
 20 25 30
 Phe Val Tyr Leu Val Thr Val Pro Gly Asn Leu Gly Met Ile Thr Leu
 35 40 45
 Ile Trp Met Asp Ser Arg Leu Gln Thr Pro Lys Tyr Phe Ser Leu Cys
 50 55 60
 His Leu Ser Phe Val Asp Val Cys Ser Ser Ser Ala Ile Gly Pro Lys
 65 70 75 80
 Met Leu Thr Asp Ile Phe Val Glu Lys Lys Val Ile Ser Phe Gly Cys
 85 90 95
 Val Ala Gln Leu Trp Phe Phe Gly His Phe Val Val Thr Glu Cys Phe
 100 105 110
 Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Met Ala Ile Tyr Lys Pro
 115 120 125
 Leu Leu Tyr Thr Leu Ile Met Ser Gln Gln Val Cys Val Gln Leu Val
 130 135 140
 Val Gly Pro Tyr Ala Val Gly Leu Ile Ser Thr Met Thr His Met Thr
 145 150 155 160
 Phe Thr Phe Arg Leu Leu Tyr Cys Gly Pro Asn Ile Ile Asn His Phe
 165 170 175
 Phe Cys Asp Leu Leu Pro Val Leu Ser Leu Ala Tyr Ala Asp Thr His
 180 185 190
 Ile Asn Lys Cys Leu Leu Phe Ile Leu Val Gly Ala Leu Gly Val Leu
 195 200 205
 Ser Gly Val Ile Ile Leu Val Ser Tyr Ile Tyr Ile Val Ile Ala Ile
 210 215 220
 Leu Arg Ile Arg Ser Ala Asp Ala Arg Arg Lys Asp Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Met Ala Val Ser Ile Leu Tyr Gly Thr Leu Phe Phe
 245 250 255
 Ile Cys Val Cys Pro Ser Ser Ser Phe Ser Ile Asn Ile Asn Lys Val
 260 265 270
 Val Ser Leu Phe Tyr Thr Ala Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ser Phe Ser Lys Lys Phe
 290 295 300
 Glu Arg Lys Lys Phe Leu Ile Gly Arg Xaa Thr Arg Ile Pro
 305 310 315

<210> 1974
 <211> 310
 <212> PRT
 <213> Unknown (H38g892 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(310)
 <223> Xaa = Any Amino Acid

<400> 1974
 Met Val Asn Phe Thr His Val Ser Glu Phe Val Leu Leu Gly Phe Gln
 1 5 10 15
 Gly Gly Pro Gly Met Gln Ala Met Leu Phe Leu Ile Phe Leu Ile Leu
 20 25 30
 Tyr Gly Ile Ala Val Val Gly Asn Leu Gly Met Ile Val Ile Ile Trp
 35 40 45
 Val Asp Ala His Leu His Thr Pro Met Tyr Ala Phe Leu Gln Ser Leu
 50 55 60
 Ser Leu Leu Asp Ile Cys Tyr Ser Ser Thr Ile Ala Pro Arg Ala Leu
 65 70 75 80
 Ala Asn Ser Met Gln Glu Asp His Thr Ile Ser Phe Gly Gly Cys Ala
 85 90 95
 Ala Gln Phe Phe Phe Leu Ser Leu Phe Gly Ile Thr Glu Ala Phe Leu
 100 105 110
 Leu Ala Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu
 115 120 125
 Leu Tyr Ser Val Ser Met Ser His Gln Val Cys Val Leu Leu Ile Ser
 130 135 140
 Gly Ser Tyr Leu Trp Gly Val Val Asn Ala Ile Ala Gln Thr Thr Met
 145 150 155 160
 Thr Phe Arg Leu Pro Phe Cys Gly Ser Asn Glu Ile Asn Asp Phe Phe
 165 170 175
 Cys Asp Val Pro Pro Leu Leu Ser Leu Ser Cys Ser Asp Thr Phe Ile
 180 185 190
 Asn Gln Leu Val Leu Leu Gly Leu Cys Gly Ser Ile Ile Val Ser Thr
 195 200 205
 Phe Leu Ile Val Leu Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu
 210 215 220
 Arg Ile Pro Thr Met Gln Gly Arg Xaa Lys Ala Phe Ser Thr Cys Ala
 225 230 235 240
 Ser His Leu Thr Gly Val Cys Leu Phe Phe Gly Thr Val Phe Phe Met
 245 250 255
 Tyr Ala Gln Pro Ser Ala Ile Phe Phe Met Glu Gln Ser Lys Ile Val
 260 265 270
 Ser Ile Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Glu Val Lys Gln Ala Leu Arg Arg Ser Met Gln
 290 295 300
 Lys Leu Ser Leu Xaa Ser
 305 310

<210> 1975
 <211> 309
 <212> PRT
 <213> Unknown (H38g893 protein)

<220>
 <223> Synthetic construct

<400> 1975
 Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
 20 25 30
 Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
 35 40 45
 Ile Cys Ser Asp Val Arg Leu His Asn Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ala Asn His Leu Leu Gly Ser Lys Ser Ile Ser Phe Gly Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Met Ile Ala Leu Gly Asn Thr Asp Ser
 100 105 110
 Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser His
 115 120 125
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
 130 135 140
 Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
 145 150 155 160
 Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
 165 170 175
 Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
 180 185 190
 His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val
 195 200 205
 Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
 210 215 220
 Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly
 245 250 255
 Thr Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
 260 265 270
 Thr Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
 275 280 285
 Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Arg Lys Leu Phe Asn
 290 295 300
 Lys Arg Ile Ser Ser
 305

<210> 1976

<211> 309

<212> PRT

<213> Unknown (H38g894 protein)

<220>

<223> Synthetic construct

<400> 1976

Met Lys Lys Glu Asn Gln Ser Phe Asn Leu Asp Phe Ile Leu Leu Gly
 1 5 10 15
 Val Thr Ser Gln Gln Glu Gln Asn Asn Val Phe Phe Val Ile Phe Leu
 20 25 30
 Cys Ile Tyr Pro Ile Thr Leu Thr Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile Cys Ala Asp Ile Arg Leu His Asn Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Ile Ile Phe Ser Ser Val Thr Ile Pro Lys


```

65          70          75          80
Val Leu Ala Asn His Leu Leu Gly Ser Lys Phe Ile Ser Phe Gly Gly
          85          90          95
Cys Leu Met Gln Met Tyr Phe Met Ile Ala Leu Ala Lys Ala Asp Ser
          100          105          110
Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Cys
          115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Leu Leu
          130          135          140
Ile Ala Gly Ser Trp Val Ile Gly Asn Thr Ser Ala Leu Pro His Thr
145          150          155          160
Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
          165          170          175
Phe Tyr Cys Asp Ile Met Pro Leu Leu Lys Leu Ser Cys Ser Asp Val
          180          185          190
His Phe Asn Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Leu
          195          200          205
Pro Leu Leu Cys Ile Ile Val Ser Tyr Val Gln Val Phe Ser Thr Val
          210          215          220
Phe Gln Val Pro Ser Thr Lys Ser Leu Phe Lys Ala Phe Cys Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Phe Leu Tyr Tyr Gly Thr Thr Met Gly
          245          250          255
Met Tyr Phe Arg Pro Leu Thr Ser Tyr Ser Pro Lys Asp Ala Val Ile
          260          265          270
Thr Val Met Tyr Val Ala Val Thr Pro Ala Leu Asn Pro Phe Ile Tyr
          275          280          285
Ser Leu Arg Asn Trp Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Ser
          290          295          300
Lys Arg Ile Ser Ser
305

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<210> 1977

<211> 329

<212> PRT

<213> Unknown (H38g895 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1977

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Ala Leu Leu Phe His Ser Tyr Lys His Pro Thr Gln Arg Arg Met Thr
1          5          10          15
Val Lys Ser His Ser Ile Val Thr Glu Phe Ser Leu Arg Gly Leu Thr
          20          25          30
Lys Gln Pro Asp Leu Gln Leu Phe His Phe Leu Ile Phe Leu Asp Ile
          35          40          45
His Met Val Thr Met Val Gly Asn Leu Gly Met Ile Thr Leu Ile Cys
          50          55          60
Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Phe Ser Asn Leu
65          70          75          80
Ser Leu Leu Asp Leu Cys Tyr Ser Ser Ile Thr Asn Pro Lys Met Leu
          85          90          95
Val Asn Phe Val Leu Lys Lys Ser Ile Ile Ser Tyr Ala Gly Tyr Met
          100          105          110
Ser Xaa Phe Tyr Phe Phe Leu Val Phe Val Ile Ala Arg Cys Tyr Met
          115          120          125

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Leu Met Val Lys Ala Cys Asp His Tyr Val Ala Ile Cys Cys Pro Leu
 130                135                140
Leu Cys Asn Val Ile Met Ser His Val Thr Cys Ser Leu Met Val Ala
145                150                155                160
Val Val Tyr Thr Met Gly Leu Val Val Ser Thr Ile Glu Thr Gly Leu
                165                170                175
Ile Leu Lys Leu Pro Tyr Cys Glu Leu Leu Thr Ser Arg Cys Phe Cys
                180                185                190
Asp Ile Leu Pro Leu Met Lys Leu Ser Xaa Ser Ser Ala Tyr Asp Val
                195                200                205
Glu Met Ala Val Phe Phe Phe Ala Arg Phe Asn Leu Arg Ile Met Ile
                210                215                220
Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Phe Ser Ile Leu His
225                230                235                240
Ile Ser Thr Thr Glu Gly Arg Ser Lys Val Phe Ser Thr Cys Ser Phe
                245                250                255
His Leu Ala Ala Ile Gly Met Phe His Gly Xaa Thr Ala Phe Arg Tyr
                260                265                270
Leu Lys Pro Ala Ile Thr Ser Ser Leu Ala Gln Glu Asn Val Ala Ser
                275                280                285
Val Phe Tyr Thr Thr Val Ile Tyr Val Pro Asn Pro Leu Met Tyr Ser
                290                295                300
Leu Lys Asn Lys Asp Val Lys Ala Ala Met Gln Lys Thr Leu Arg Ser
305                310                315                320
Lys Phe Cys Cys Arg Cys Asn Tyr Leu
                325

```

<210> 1978

<211> 316

<212> PRT

<213> Unknown (H38g896 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1978

```

Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu Leu Trp
 1                5                10                15
Gly Leu Ser Asp Gln Pro Gln Gln His Ile Phe Phe Leu Leu Phe
                20                25                30
Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile Val Leu
                35                40                45
Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu
                50                55                60
Ala Ser Leu Ser Cys Ala Asp Ile Phe Ser Thr Thr Thr Val Pro
65                70                75                80
Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser Tyr Ala
                85                90                95
Gly Cys Leu Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly Asp Met Asp
                100                105                110
Ile Phe Leu Pro Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
                115                120                125
His Leu Leu His Tyr Met Met Ile Met Ser Leu His Arg Cys Ala Phe
                130                135                140
Leu Val Thr Ala Cys Trp Thr Leu Thr Ser Leu Leu Ala Met Thr Arg
145                150                155                160
Thr Phe Leu Ile Phe Arg Leu Ser Leu Cys Ser Xaa Ile Leu Pro Gly

```

<400> 1979															
Asp	Thr	Asp	Pro	Gln	Ser	Leu	Thr	Asp	Val	Ser	Ile	Phe	Leu	Leu	Leu
1				5					10					15	
Lys	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Val	Val	Ala	Gly	Leu	Phe	
			20					25					30		
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu
		35					40						45		
Ala	Val	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu
		50				55					60				
Ser	Asn	Leu	Ser	Leu	Ala	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro
65					70					75					80
Lys	Met	Ile	Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala
				85					90					95	
Gly	Cys	Leu	Thr	Gln	Met	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Met	Glu
			100					105					110		
Glu	Asn	Met	Leu	Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile
		115					120						125		
Cys	His	Pro	Leu	Tyr	Cys	Ser	Ala	Ile	Phe	Asn	Pro	Cys	Phe	Cys	Gly
		130				135					140				
Phe	Leu	Asp	Leu	Leu	Ser	Phe	Ile	Phe	Phe	Phe	Leu	Ser	Leu	Ser	Asp
145					150					155					160
Ser	Gln	Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Lys	Asp
				165					170					175	
Val	Glu	Ile	Pro	Asn	Phe	Phe	Trp	Glu	Pro	Ser	Gln	Leu	Ser	His	Leu
			180					185						190	
Ala	Cys	Cys	Asp	Thr	Phe	Thr	Arg	Asn	Ile	Met	Tyr	Phe	Pro	Ala	Ala
		195					200					205			
Ile	Phe	Gly	Phe	Leu	Pro	Ile	Leu	Gly	Thr	Leu	Phe	Ser	Tyr	Cys	Lys
		210				215					220				

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Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
225          230          235          240
Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr
          245          250          255
Gly Thr Gly Ile Gly Gly Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro
          260          265          270
Arg Lys Gly Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met
          275          280          285
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Ser Val
          290          295          300
Leu Arg Arg Pro His Gly Ser Thr Val Xaa Ser Gln His Leu Leu Ile
305          310          315          320
Cys Ser Ile Pro Phe Val Gly Trp Phe Lys Lys Gly Ala Lys Val Lys
          325          330          335

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<210> 1980

<211> 309

<212> PRT

<213> Unknown (H38g898 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(309)

<223> Xaa = Any Amino Acid

<400> 1980

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Met Arg Gln Asn Asn Ile Thr Glu Phe Val Leu Leu Gly Phe Ser
1          5          10          15
Gln Asp Leu Asp Val Gln Lys Ala Leu Phe Val Ile Phe Leu Thr
          20          25          30
Tyr Leu Val Thr Val Val Gly Asn Leu Leu Ile Val Val Thr Ile Ile
          35          40          45
Thr Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Cys Leu
          50          55          60
Ser Phe Ile Asp Ala Ala Tyr Ser Thr Thr Ile Ser Pro Lys Leu Ile
65          70          75          80
Val Asp Leu Leu Cys Asp Lys Lys Thr Ile Ser Phe Pro Ala Cys Met
          85          90          95
Gly Gln Leu Phe Ile Tyr His Leu Phe Gly Gly Ser Glu Val Phe Leu
          100          105          110
Leu Val Val Met Ala Cys Asp His Tyr Val Ala Ile Cys Lys Pro Leu
          115          120          125
His Tyr Leu Thr Ile Met Asn Arg Gln Val Xaa Ile Leu Leu Val
          130          135          140
Val Val Val Thr Gly Gly Phe Leu His Ser Val Phe Gln Ile Val Val
145          150          155          160
Val Tyr Ser Leu Ala Phe Cys Gly Pro Asn Val Ile Asp Tyr Phe Val
          165          170          175
Cys Asp Met Tyr Pro Leu Leu Glu Leu Val Cys Thr Asp Thr Tyr Phe
          180          185          190
Ile Gly Leu Thr Val Phe Val Asn Gly Gly Thr Ile Cys Ile Val Val
          195          200          205
Phe Thr Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Ser Leu Lys
          210          215          220
Thr Tyr Ser Gln Glu Gly Arg His Lys Val Leu Phe Thr Cys Ser Ser
225          230          235          240
His Ile Ile Val Phe Ala Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
          245          250          255
Val Arg Pro Val Ser Asn Tyr Pro Phe Asp Lys Phe Leu Thr Val Phe

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260 265 270
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ser Glu Met Arg Asn Ser Val Glu Thr Leu Leu Cys Lys Ser Xaa
 290 295 300
 Leu Tyr Xaa Ser Lys
 305

<210> 1981
 <211> 313
 <212> PRT
 <213> Unknown (H38g899 protein)

<220>
 <223> Synthetic construct

<400> 1981
 Met Glu Arg Ile Asn Ser Thr Leu Leu Thr Ala Phe Ile Leu Thr Gly
 1 5 10 15
 Ile Pro Tyr Pro Leu Arg Leu Arg Thr Leu Phe Phe Val Phe Phe Phe
 20 25 30
 Leu Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Ile Thr
 35 40 45
 Val Trp Ala Asp Pro Arg Leu His Ala Arg Pro Met Tyr Ile Phe Leu
 50 55 60
 Gly Val Leu Ser Val Ile Asp Met Ser Ile Ser Ser Ile Ile Val Pro
 65 70 75 80
 Arg Leu Met Met Asn Phe Thr Leu Gly Val Lys Pro Ile Pro Phe Gly
 85 90 95
 Gly Cys Val Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly Ser Thr Gln
 100 105 110
 Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys
 115 120 125
 Gln Pro Leu Arg Tyr Pro Val Leu Met Thr Ala Lys Leu Ser Ala Leu
 130 135 140
 Leu Val Ala Gly Ala Trp Met Ala Gly Ser Ile His Gly Ala Leu Gln
 145 150 155 160
 Ala Ile Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp
 165 170 175
 Tyr Phe Phe Cys Asp Ile Pro Ala Val Leu Arg Leu Ala Cys Ala Asp
 180 185 190
 Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile Gly Val Val Val
 195 200 205
 Ala Ser Cys Phe Ser Leu Ile Leu Leu Ser Tyr Ile Gln Ile Ile Gln
 210 215 220
 Ala Ile Leu Arg Ile His Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Ala His Val Thr Val Val Thr Val Tyr Tyr Val Pro Cys
 245 250 255
 Ala Phe Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu Asp Gly Ala
 260 265 270
 Ala Ala Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile
 275 280 285
 Tyr Thr Leu Arg Asn Gln Glu Val Lys Leu Ala Leu Lys Arg Met Leu
 290 295 300
 Arg Ser Pro Arg Thr Pro Ser Glu Val
 305 310

<210> 1982
 <211> 318
 <212> PRT

<213> Unknown (H38g900 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1982

```

Met Gly Lys Thr Lys Asn Thr Ser Leu Asp Thr Val Val Arg Asp Phe
 1           5           10           15
Ile Leu Leu Gly Leu Ser His Pro Pro Asn Ile Arg Ser Leu Leu Phe
      20           25           30
Leu Val Phe Phe Val Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu
 35           40           45
Ile Leu Leu Thr Val Trp Ala Asp Pro Lys Leu Arg Ala Arg Pro Met
 50           55           60
Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser
 65           70           75           80
Val Ile Val Pro Xaa Ile Ile Leu Asn Phe Thr Pro Ala Asn Lys Ala
      85           90           95
Ile Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu
 100           105           110
Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr
 115           120           125
Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg
 130           135           140
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His
 145           150           155           160
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
      165           170           175
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
 180           185           190
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile
 195           200           205
Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
 210           215           220
Asn Ile Val Asn Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg
 225           230           235           240
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
      245           250           255
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Gly Pro
 260           265           270
Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
 275           280           285
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu
 290           295           300
Lys Arg Ile Thr Ala Gly Gln Gly Thr Glu Xaa Lys Xaa Val
 305           310           315

```

<210> 1983

<211> 310

<212> PRT

<213> Unknown (H38g901 protein)

<220>

<223> Synthetic construct

<400> 1983

Met Gly Lys Thr Lys Asn Thr Ser Leu Asp Ala Val Val Thr Asp Phe

```

1           5           10           15
Ile Leu Leu Gly Leu Ser His Pro Pro Asn Leu Arg Ser Leu Leu Phe
      20           25           30
Leu Val Phe Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu
      35           40           45
Ile Leu Leu Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met
      50           55           60
Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser
      65           70           75           80
Val Thr Val Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala
      85           90           95
Ile Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu
      100          105          110
Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr
      115          120          125
Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg
      130          135          140
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His
      145          150          155          160
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
      165          170          175
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu
      180          185          190
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val
      195          200          205
Arg Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
      210          215          220
Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg
      225          230          235          240
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
      245          250          255
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro
      260          265          270
Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
      275          280          285
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu
      290          295          300
Lys Arg Ile Thr Ala Gly
      305          310

```

<210> 1984

<211> 300

<212> PRT

<213> Unknown (H38g902 protein)

<220>

<223> Synthetic construct

<400> 1984

```

Met Phe Ile Leu Thr Gly Phe Thr Asp Asp Phe Glu Leu Gln Val Phe
1           5           10           15
Leu Phe Leu Leu Phe Phe Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn
      20           25           30
Leu Gly Leu Val Val Leu Val Ile Glu Asp Ser Trp Leu His Asn Pro
      35           40           45
Met Tyr Tyr Phe Leu Ser Val Leu Ser Phe Leu Asp Ala Cys Tyr Ser
      50           55           60
Thr Val Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys
      65           70           75           80
Ser Ile Ser Phe Ile Gly Cys Ala Thr Gln Met Leu Leu Phe Val Thr
      85           90           95

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Phe Gly Thr Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp His
      100      105      110
Tyr Val Ala Ile Tyr Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro
      115      120      125
Arg Val Tyr Val Pro Leu Ile Thr Ala Ser Tyr Val Ala Gly Ile Leu
      130      135      140
His Ala Thr Ile His Ile Val Ala Thr Phe Ser Leu Ser Phe Cys Gly
      145      150      155      160
Ser Asn Glu Ile Arg His Val Phe Cys Asp Met Pro Pro Leu Leu Ala
      165      170      175
Ile Ser Cys Ser Asp Thr His Thr Asn Gln Leu Leu Leu Phe Tyr Phe
      180      185      190
Val Gly Ser Ile Glu Ile Val Thr Ile Leu Ile Val Leu Ile Ser Cys
      195      200      205
Asp Phe Ile Leu Leu Ser Ile Leu Lys Met His Ser Ala Lys Gly Arg
      210      215      220
Gln Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Gly Val Thr Ile
      225      230      235      240
Tyr His Gly Thr Ile Leu Val Ser Tyr Met Arg Pro Ser Ser Ser Tyr
      245      250      255
Ala Ser Asp His Asp Ile Ile Val Ser Ile Phe Tyr Thr Ile Val Ile
      260      265      270
Pro Lys Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
      275      280      285
Lys Ala Val Lys Lys Met Leu Lys Leu Val Tyr Lys
      290      295      300

```

<210> 1985

<211> 324

<212> PRT

<213> Unknown (H38g903 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1985

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His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
  1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20      25      30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35      40      45
Ile Leu Ala Val Arg Ser Glu Ser Pro Leu His Thr Thr Met Tyr Phe
      50      55      60
Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
      65      70      75      80
Val Pro Lys Met Ile Val Asp Met Gln Trp Tyr Ser Lys Val Ile Ser
      85      90      95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100      105      110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
      115      120      125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130      135      140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
      145      150      155      160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu

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      165      170      175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
      180      185      190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Gly Ser Thr Met
      195      200      205
Phe Gly Ph Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
      210      215      220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
      225      230      235      240
Phe Ser Thr Tyr Gly Ser His Leu Ala Val Phe Cys Xaa Phe Asp Gly
      245      250      255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg
      260      265      270
Asn Gly Val Val Val Ser Val Lys Xaa Ala Val Val Thr Pro Met Pro
      275      280      285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
      290      295      300
Arg Arg Leu Pro Asn Lys Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
      305      310      315      320
Phe Phe Trp Cys

```

<210> 1986
 <211> 335
 <212> PRT
 <213> Unknown (H38g904 protein)

<220>
 <223> Synthetic construct

 <221> VARIANT
 <222> (1)...(335)
 <223> Xaa = Any Amino Acid

```

<400> 1986
Asp Thr Asp Pro Gln Ser Ile Thr Asp Val Ser Ile Phe Leu Leu Leu
 1      5      10      15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
      20      25      30
Leu Ser Met Cys Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
      65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Lys Val Ile Tyr Ala Gly
      85      90      95
Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Lys
      100      105      110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Pro Ile Cys
      115      120      125
His Pro Leu Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe
      130      135      140
Leu Asn Leu Leu Ser Phe Phe Phe Phe Leu Ser Leu Leu Asp Ser Gln
      145      150      155      160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
      165      170      175
Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys
      180      185      190
Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala Val
      195      200      205

```

Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Met
 210 215 220
 Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
 245 250 255
 Thr Gly Val Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg
 260 265 270
 Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
 275 280 285
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
 290 295 300
 Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile Cys
 305 310 315 320
 Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys
 325 330 335

<210> 1987

<211> 310

<212> PRT

<213> Unknown (H38g905 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1987

Met Glu Asn Arg Lys Asn Val Thr Xaa Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Gln Asn Pro Glu Gly Gln Lys Val Leu Phe Val Thr Phe Leu Leu Ile
 20 25 30
 Tyr Ile Val Thr Ile Met Gly Asn Leu Leu Ile Met Val Thr Ile Met
 35 40 45
 Ala Ser Gln Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Ser Leu
 50 55 60
 Ser Phe Ile His Thr Val Tyr Tyr Thr Ala Ile Ala Pro Lys Met Ile
 65 70 75 80
 Val Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Gln Gly Cys Met
 85 90 95
 Ala Gln Leu Phe Met Asp His Leu Phe Ala Gly Ala Glu Val Ile Leu
 100 105 110
 Leu Val Val Met Ala Tyr Asp Gln Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Leu Ile Ile Met Asn Arg Arg Val Cys Val Leu Met Leu Leu
 130 135 140
 Val Ala Trp Ile Gly Gly Phe Leu His Ser Leu Val Gln Phe Leu Phe
 145 150 155 160
 Ile Tyr Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp Asn Phe Leu
 165 170 175
 Cys Asp Leu Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asn Thr Tyr Val
 180 185 190
 Thr Gly Leu Ser Met Ile Ala Asn Gly Gly Ala Ile Cys Thr Val Thr
 195 200 205
 Phe Phe Pro Leu Leu Leu Ser Tyr Gly Val Ile Leu Pro Ser Leu Lys
 210 215 220
 Thr Gln Ser Leu Glu Gly Lys Cys Lys Ala Phe Tyr Thr Cys Ala Ser
 225 230 235 240
 His Ile Thr Val Ile Thr Leu Phe Phe Val Pro Cys Ile Phe Leu Leu

245 250 255
 Ala Arg Pro Asn Ser Thr Phe Pro Ile Asp Lys Ser Met Thr Val Val
 260 265 270
 Leu Thr Cys Ile Thr Pro Met Leu Lys Pro Leu Ile Tyr Ala Leu Arg
 275 280 285
 Asn Ala Glu Met Lys Ser Ala Met Arg Lys Leu Trp Ser Glu Lys Val
 290 295 300
 Ser Leu Ala Gly Lys Gly
 305 310

<210> 1988

<211> 308

<212> PRT

<213> Unknown (H38g906 protein)

<220>

<223> Synthetic construct

<400> 1988

His Met Pro Pro Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Gln Asn Pro His Leu Gln Lys Ile Leu Phe Ile Val Phe Leu Phe Ile
 20 25 30
 Phe Leu Phe Thr Met Leu Ala Asn Leu Phe Ile Val Ile Thr Ile Ser
 35 40 45
 Cys Ser Pro Thr Leu Ser Ser Pro Met Tyr Phe Phe Leu Thr Tyr Leu
 50 55 60
 Ser Phe Ile Asp Ala Ser Tyr Thr Ser Val Thr Thr Pro Lys Met Ile
 65 70 75 80
 Thr Asp Leu Leu Tyr Gln Arg Arg Thr Ile Ser Leu Ala Gly Cys Leu
 85 90 95
 Thr Gln Leu Phe Val Glu His Leu Leu Gly Gly Ser Glu Ile Ile Leu
 100 105 110
 Leu Ile Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Thr Ile Met Gln Gln Gly Ile Cys His Leu Leu Val Val
 130 135 140
 Ile Ala Trp Ile Gly Gly Ile Leu His Ala Thr Val Gln Ile Leu Phe
 145 150 155 160
 Met Thr Asp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
 165 170 175
 Cys Asp Leu Phe Pro Leu Leu Lys Leu Ala Cys Arg Asp Thr Tyr Arg
 180 185 190
 Leu Gly Met Leu Val Ala Ala Asn Ser Gly Ala Met Cys Leu Leu Ile
 195 200 205
 Phe Ser Leu Leu Val Ile Ser Tyr Ile Val Ile Leu Ser Ser Leu Lys
 210 215 220
 Ser Tyr Ser Ser Glu Gly Gln His Lys Ala Leu Ser Thr Cys Gly Ser
 225 230 235 240
 His Phe Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Thr Tyr
 245 250 255
 Met His Pro Val Val Thr Tyr Ser Val Asp Lys Leu Val Thr Val Phe
 260 265 270
 Phe Ala Ile Leu Thr Pro Met Leu Asn Pro Ile Ile Tyr Thr Val Arg
 275 280 285
 Asn Thr Glu Val Lys Asn Ala Val Arg Ser Leu Leu Arg Lys Arg Val
 290 295 300
 Thr Val Tyr Ala
 305

<210> 1989

<211> 166
 <212> PRT
 <213> Unknown (H38g907 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(166)
 <223> Xaa = Any Amino Acid

<400> 1989
 Met Tyr Thr Thr Leu Leu Met Ala Arg Leu Cys Leu Cys Ala Asp Asn
 1 5 10 15
 Val Ile Pro His Ser Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala
 20 25 30
 Leu Ser Asp Thr Arg Val Asn Glu Xaa Val Ile Phe Ile Met Gly Gly
 35 40 45
 Leu Ile Leu Val Ile Pro Ser Ile Leu Ile Leu Gly Ser Tyr Ala Arg
 50 55 60
 Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Cys Ile Cys Lys
 65 70 75 80
 Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
 85 90 95
 Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr
 100 105 110
 Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met
 115 120 125
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala
 130 135 140
 Leu Ser Arg Val Ile His Gln Lys Lys Thr Phe Phe Ser Leu Xaa Xaa
 145 150 155 160
 Xaa His Leu Glu Leu Leu
 165

<210> 1990
 <211> 333
 <212> PRT
 <213> Unknown (H38g908 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(333)
 <223> Xaa = Any Amino Acid

<400> 1990
 Met Gly Pro Lys Asn Leu Thr Arg Val Leu Glu Phe Phe Leu Leu His
 1 5 10 15
 Phe Leu Asp Asp Leu Glu Leu Gln Pro Phe Leu Ser Gly Cys Pro Xaa
 20 25 30
 Thr Met His Leu Val Thr Val Leu Ala Asn Leu Leu Thr Ser Phe Xaa
 35 40 45
 Leu Ser Ala Leu Pro His Leu His Asn Pro Met Asn Phe Asn Leu Ser
 50 55 60
 Leu Ala Asp Ile Gly Phe Thr Pro Ala Thr Ile Ser Lys Ile Thr Val
 65 70 75 80
 Asp Leu Gln Thr His Ser Arg Ile Ile Leu Tyr Met Ser Cys Leu Lys
 85 90 95
 Xaa Met Ser Phe Lys Ile Ile Phe Gly Cys Leu His Asn Leu Leu Met

```

      100      105      110
Thr Val Met Ala Tyr Asp Pro Phe Val Ala Thr Cys His Leu Leu Tyr
      115      120      125
Tyr Thr Val Ile Arg Asn Pro His Leu Cys Gly Leu Leu Leu Leu Val
      130      135      140
Ser Leu Phe Ser Leu Ser Phe Phe Phe Leu Ile Ser Leu Leu Glu Thr
145      150      155      160
Gln Leu Tyr Ser Leu Met Val Ser Gln Val Leu Cys Met Gln Asp Val
      165      170      175
Asp Ile Pro His Phe Phe Cys Asp Pro Ser Gln Phe Leu His Leu Ser
      180      185      190
Cys Ser Asp Thr Ala Thr Asn Asn Thr Leu Met His Phe Ile Gly Ala
      195      200      205
Ile Phe Cys Gly Pro Phe Ser Gly Ile Leu Tyr Cys Tyr Thr Gln Ile
      210      215      220
Met Phe Ser Ile Leu Ile Thr Leu Xaa Asn Val Gly Ser Ile Lys Gln
225      230      235      240
Thr Phe Ser Thr His Arg Ser His Leu Ser Val Val Cys Leu Phe Tyr
      245      250      255
Gly Thr Gly Leu Gly Val Tyr Leu Ser Leu Ala Gly Ser Pro Ser Pro
      260      265      270
Arg Thr Gly Val Val Ala Ser Met Val Tyr Thr Thr Val Thr Leu Met
      275      280      285
Leu Asn Pro Val Ile His Ser Leu Arg Asn Arg Asp Ile Lys Asn Thr
      290      295      300
Trp Trp Trp Leu Leu Ser Ile Thr Ala Trp Tyr Gln Tyr Leu Cys Tyr
305      310      315      320
Pro Leu Trp Ser Val Val Arg Lys Asn Ser Lys Leu Lys
      325      330

```

<210> 1991

<211> 308

<212> PRT

<213> Unknown (H38g909 protein)

<220>

<223> Synthetic construct

<400> 1991

```

Met Gly Thr Ser Asn Asn Glu Thr Glu Phe Ile Leu Leu Gly Ile Thr
1      5      10      15
Lys Asn Pro Glu Leu Arg Lys Ile Phe Ser Ala Leu Phe Leu Ala Met
      20      25      30
Tyr Val Thr Thr Val Leu Gly Asn Leu Phe Ile Val Val Thr Leu Ala
      35      40      45
Ala Ser Trp Ser Leu Arg Ser Pro Met Tyr Phe Ser Leu Thr Ser Leu
      50      55      60
Ser Leu Met Gly Ala Thr Tyr Ser Ser Ile Thr Ala Pro Lys Met Thr
65      70      75      80
Val Asp Ser Leu Arg Ser Thr Thr Ile Ser Leu Glu Gly Cys Met Thr
      85      90      95
Gln Leu Phe Ala Glu His Phe Ser Asp Gly Val Ala Ile Ile Leu Leu
      100      105      110
Thr Val Met Val Cys Asp Cys Tyr Glu Ala Ile Ser Lys Pro Leu His
      115      120      125
Asp Thr Thr Ile Met Ser Pro Arg Val Cys Cys Leu Leu Val Val Glu
      130      135      140
Ala Trp Val Gly Gly Leu Thr His Ala Thr Ile Gln Leu Phe Phe Phe
145      150      155      160
Leu Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile
      165      170      175

```

Cys Asp Leu Phe Pro Leu Leu Lys Leu Ala Tyr Met Asp Thr His Met
 180 185 190
 Leu Gly Leu Leu Val Ile Leu Asn Ser Gly Val Met Cys Met Ala Ile
 195 200 205
 Phe Leu Ile Leu Ile Ala Ser Tyr Ile Val Thr Leu Tyr Ser Leu Lys
 210 215 220
 Ser Cys Ser Ser Val Gly Arg Arg Asn Thr Leu Ser Thr Cys Gly Ser
 225 230 235 240
 His His Thr Val Val Ile Leu Phe Phe Val Glu Cys Ile Phe Leu Tyr
 245 250 255
 Ile Arg Pro Val Val Thr Tyr Pro Ile Asp Lys Asp Met Ala Ile Ser
 260 265 270
 Phe Thr Ile Val Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Gly Ile Lys Val Lys Asn Ala Ile Arg Lys Met Trp Met Lys Gln Gly
 290 295 300
 Thr Leu Gly Gly
 305

<210> 1992

<211> 318

<212> PRT

<213> Unknown (H38g910 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1992

Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Val Asp Gly Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys Leu
 20 25 30
 Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala Leu
 35 40 45
 Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu Gly
 50 55 60
 His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro Arg
 65 70 75 80
 Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln Ala
 85 90 95
 Cys Leu Ala Glu Met Tyr Phe Phe Val Thr Leu Gly Ile Thr Glu Ser
 100 105 110
 Tyr Leu Met Ala Ala Met Ser Xaa Arg Ala Arg Arg Val Pro Ala
 115 120 125
 Pro Leu Tyr Gly Ala Leu Val Thr Pro Ser Ala Cys Ala Ser Leu Val
 130 135 140
 Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His Thr Leu
 145 150 155 160
 Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg Pro Phe
 165 170 175
 Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp Thr Ser
 180 185 190
 Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val Leu Ala
 195 200 205
 Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val Ala Val
 210 215 220
 Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly Ala His

225 230 235 240
 Leu Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser Val Leu Ser Val
 245 250 255
 Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr Asp Arg Leu Ala
 260 265 270
 Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn Pro Phe Ile Asn
 275 280 285
 Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Arg Gly Leu Arg
 290 295 300
 Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala Asn Leu Ala
 305 310 315

<210> 1993

<211> 311

<212> PRT

<213> Unknown (H38g911 protein)

<220>

<223> Synthetic construct

<400> 1993

Met Lys Gly Ala Asn Leu Ser Gln Gly Met Glu Phe Glu Leu Leu Gly
 1 5 10 15
 Leu Thr Thr Asp Pro Gln Leu Gln Arg Leu Leu Phe Val Val Phe Leu
 20 25 30
 Gly Met Tyr Thr Ala Thr Leu Leu Gly Asn Leu Val Met Phe Leu Leu
 35 40 45
 Ile His Val Ser Ala Thr Leu His Thr Pro Met Tyr Ser Leu Leu Lys
 50 55 60
 Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Thr Val Val Pro Gln
 65 70 75 80
 Thr Leu Val Asn Phe Leu Ala Lys Arg Lys Val Ile Ser Tyr Phe Gly
 85 90 95
 Cys Met Thr Gln Met Phe Phe Tyr Ala Gly Phe Ala Thr Ser Glu Cys
 100 105 110
 Tyr Leu Ile Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Thr Ile Met Ser Pro Glu Val Cys Ala Ser Leu
 130 135 140
 Ile Val Gly Ser Tyr Ser Ala Gly Phe Leu Asn Ser Leu Ile His Thr
 145 150 155 160
 Gly Cys Ile Phe Ser Leu Lys Phe Cys Gly Ala His Val Val Thr His
 165 170 175
 Phe Phe Cys Asp Gly Pro Pro Ile Leu Ser Leu Ser Cys Val Asp Thr
 180 185 190
 Ser Leu Cys Glu Ile Leu Leu Phe Ile Phe Ala Gly Phe Asn Leu Leu
 195 200 205
 Ser Cys Thr Leu Thr Ile Leu Ile Ser Tyr Phe Leu Ile Leu Asn Thr
 210 215 220
 Ile Leu Lys Met Ser Ser Ala Gln Gly Arg Phe Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ala Ile Cys Leu Phe Phe Gly Thr Thr Leu
 245 250 255
 Phe Met Tyr Leu Arg Pro Arg Ser Ser Tyr Ser Leu Thr Gln Asp Arg
 260 265 270
 Thr Val Ala Val Ile Tyr Thr Val Val Ile Pro Val Leu Asn Pro Leu
 275 280 285
 Met Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ile Lys Val
 290 295 300
 Trp Gly Arg Lys Thr Met Glu
 305 310

<210> 1994
 <211> 316
 <212> PRT
 <213> Unknown (H38g912 protein)

<220>
 <223> Synthetic construct

<400> 1994

```

Met Gln Asn Gln Ser Phe Val Thr Glu Phe Val Leu Leu Gly Leu Ser
 1           5           10           15
Gln Asn Pro Asn Val Gln Glu Ile Val Phe Val Val Phe Leu Phe Val
      20           25           30
Tyr Ile Ala Thr Val Gly Gly Asn Met Leu Ile Val Val Thr Ile Leu
      35           40           45
Ser Ser Pro Ala Leu Leu Val Ser Pro Met Tyr Phe Phe Leu Gly Phe
      50           55           60
Leu Ser Phe Leu Asp Ala Cys Phe Ser Ser Val Ile Thr Pro Lys Met
      65           70           75           80
Ile Val Asp Ser Leu Tyr Val Thr Lys Thr Ile Ser Phe Glu Gly Cys
      85           90           95
Met Met Gln Leu Phe Ala Glu His Phe Phe Ala Gly Val Glu Val Ile
      100          105          110
Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro
      115          120          125
Leu His Tyr Ser Ser Ile Met Asn Arg Arg Leu Cys Gly Ile Leu Met
      130          135          140
Gly Val Ala Trp Thr Gly Gly Leu Leu His Ser Met Ile Gln Ile Leu
      145          150          155          160
Phe Thr Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe
      165          170          175
Met Cys Asp Leu Tyr Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr His
      180          185          190
Ile Phe Gly Leu Met Val Val Ile Asn Ser Gly Phe Ile Cys Ile Ile
      195          200          205
Asn Phe Ser Leu Leu Leu Val Ser Tyr Ala Val Ile Leu Leu Ser Leu
      210          215          220
Arg Thr His Ser Ser Glu Gly Arg Trp Lys Ala Leu Ser Thr Cys Gly
      225          230          235          240
Ser His Ile Ala Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Val
      245          250          255
Tyr Thr Arg Pro Pro Ser Ala Phe Ser Leu Asp Lys Met Ala Ala Ile
      260          265          270
Phe Tyr Ile Ile Leu Asn Pro Leu Leu Asn Pro Leu Ile Tyr Thr Phe
      275          280          285
Arg Asn Lys Glu Val Lys Gln Ala Met Arg Arg Ile Trp Asn Arg Leu
      290          295          300
Met Val Val Ser Asp Glu Lys Glu Asn Ile Lys Leu
      305          310          315

```

<210> 1995
 <211> 310
 <212> PRT
 <213> Unknown (H38g913 protein)

<220>
 <223> Synthetic construct

<400> 1995

```

Met Gln Leu Asn Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr

```



```

1           5           10           15
Gln Asp Pro Phe Trp Lys Lys Ile Val Phe Val Ile Phe Leu Arg Leu
20           25           30
Tyr Leu Gly Thr Leu Leu Gly Asn Leu Leu Ile Ile Ile Ser Val Lys
35           40           45
Ala Ser Gln Ala Leu Lys Asn Pro Met Phe Phe Phe Leu Phe Tyr Leu
50           55           60
Ser Leu Ser Asp Thr Cys Leu Ser Thr Ser Ile Ala Pro Arg Met Ile
65           70           75           80
Val Asp Ala Leu Leu Lys Lys Thr Thr Ile Ser Phe Ser Glu Cys Met
85           90           95
Ile Gln Val Phe Ser Ser His Val Phe Gly Cys Leu Glu Ile Phe Ile
100          105          110
Leu Ile Leu Thr Ala Val Asp Arg Tyr Val Asp Ile Cys Lys Pro Leu
115          120          125
His Tyr Met Thr Ile Ile Ser Gln Trp Val Cys Gly Val Leu Met Ala
130          135          140
Val Ala Trp Val Gly Ser Cys Val His Ser Leu Val Gln Ile Phe Leu
145          150          155          160
Ala Leu Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Cys Phe
165          170          175
Cys Asp Leu Gln Pro Leu Leu Lys Gln Ala Cys Ser Glu Thr Tyr Val
180          185          190
Val Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ala Val Ser
195          200          205
Tyr Val Met Leu Ile Phe Ser Tyr Val Ile Phe Leu His Ser Leu Arg
210          215          220
Asn His Ser Ala Glu Val Ile Lys Lys Ala Leu Ser Thr Cys Val Ser
225          230          235          240
His Ile Ile Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Met Tyr
245          250          255
Thr Cys Pro Ala Thr Val Phe Pro Met Asp Lys Met Ile Ala Val Phe
260          265          270
Tyr Thr Val Gly Thr Ser Phe Leu Asn Pro Val Ile Tyr Thr Leu Lys
275          280          285
Asn Thr Glu Val Lys Ser Ala Met Arg Lys Leu Trp Ser Lys Lys Leu
290          295          300
Ile Thr Asp Asp Lys Arg
305          310

```

<210> 1996

<211> 321

<212> PRT

<213> Unknown (H38g914 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1996

```

Met Glu Thr Thr Asn His Ser Ala Val Thr Glu Phe Phe Leu Val Gly
1           5           10           15
Leu Ser Gln Tyr Pro Glu Leu Gln Leu Phe Leu Phe Leu Cys Leu
20           25           30
Ile Met Tyr Met Ile Ile Leu Leu Gly Asn Ser Phe Leu Ile Ile Ile
35           40           45
Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
50           55           60

```

```

Asn Leu Ser Phe Leu Gly Ile Cys Tyr Thr Ser Ser Ser Ile Pro Pro
65          70          75          80
Met Leu Ile Ile Phe Val Ser Glu Arg Lys Ser Ile Ser Phe Ile Gly
          85          90          95
Cys Ala Leu Gln Met Val Val Ser Leu Gly Leu Gly Ser Ile Glu Cys
          100         105         110
Ile Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115         120         125
Pro Leu Arg Tyr Ser Ile Ile Met Asn Arg Val Leu Tyr Val Gln Met
          130         135         140
Ala Ala Trp Ser Trp Ile Ile Gly Cys Leu Thr Ser Leu Leu Arg Thr
145         150         155         160
Val Leu Thr Met Met Leu Pro Phe Cys Gly Asn Asn Ile Ile Asp His
          165         170         175
Leu Thr Cys Glu Ile Leu Ala Leu Leu Lys Val Ile Cys Ser Asp Ile
          180         185         190
Ser Ile Asn Val Phe Ile Met Thr Val Ser Ser Ile Val Leu Leu Val
          195         200         205
Ile Leu Leu Ile Phe Ile Ser Tyr Val Phe Ile Leu Ser Ser Ile Leu
          210         215         220
Arg Ile Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Phe Thr Cys Ser
225         230         235         240
Ala His Leu Thr Val Val Ile Leu Phe Tyr Gly Ser Val Leu Phe Met
          245         250         255
His Met Lys Pro Lys Ser Lys Phe Thr Thr Ala Ser Asp Glu Ile Ile
          260         265         270
Gly Leu Ser Tyr Glu Val Ile Thr Pro Met Asn Pro Ile Ile Tyr Ser
          275         280         285
Leu Arg Asn Lys Glu Ile Lys Glu Ala Val Lys Lys Ile Leu Ser Arg
          290         295         300
His Val His Leu Trp Lys Ile Xaa Lys Ala Leu Arg His Val Thr Phe
305         310         315         320
Ser

```

<210> 1997

<211> 177

<212> PRT

<213> Unknown (H38g915 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(177)

<223> Xaa = Any Amino Acid

<400> 1997

```

Ala Val Xaa Trp Ile Ser Ala Glu Phe Ala Leu Pro Met Tyr Phe Phe
1          5          10         15
Leu Lys Asn Leu Ser Val Leu Asp Leu Cys Tyr Ile Ser Val Thr Val
          20         25         30
Pro Lys Ser Ile Arg Asn Ser Leu Thr Arg Arg Ser Ser Ile Ser Tyr
          35         40         45
Leu Gly Cys Val Ala Gln Ala Tyr Phe Phe Ser Ala Phe Ala Ser Ala
          50         55         60
Glu Leu Ala Phe Leu Thr Val Met Ser Tyr Asp Arg Tyr Val Ala Ile
65         70         75         80
Cys His Pro Leu Gln Tyr Arg Ala Val Met Thr Ser Gly Gly Cys Tyr
          85         90         95
Gln Met Ala Val Thr Thr Trp Leu Ser Cys Phe Ser Tyr Ala Ala Val

```

100 105 110
 His Thr Gly Asn Met Phe Arg Glu His Val Cys Arg Ser Asn Val Ile
 115 120 125
 His Gln Phe Phe Arg Asp Ile Pro Gln Val Leu Ala Leu Val Ser Xaa
 130 135 140
 Glu Val Phe Phe Val Glu Leu Xaa Pro Ser Pro Glu Pro Gln Cys Leu
 145 150 155 160
 Asp Leu Gly Cys Phe Ile Pro Met Met Ile Ser Asn Phe Pro Asn Leu
 165 170 175
 Leu

<210> 1998
 <211> 191
 <212> PRT
 <213> Unknown (H38g916 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(191)
 <223> Xaa = Any Amino Acid

<400> 1998
 Val Xaa Trp Ile Ser Ala Glu Phe Ala Leu Pro Met Tyr Leu Phe Leu
 1 5 10 15
 Ser Asp Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro
 20 25 30
 Gln Met Leu Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu
 35 40 45
 Gly Cys Ser Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu
 50 55 60
 Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys
 65 70 75 80
 Gln Pro Leu His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln
 85 90 95
 Leu Ala Ser Val Ala Trp Val Met Ser Leu Val Gln Ser Ile Val Gln
 100 105 110
 Thr Ser Ser Thr Leu His Leu Pro Phe Cys Pro His Gln Gln Ile Asp
 115 120 125
 Asp Phe Leu Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Xaa Gly Asp
 130 135 140
 Thr Ser Tyr Asn Glu Ile Gln Leu Thr Val Ser Ser Val Ile Leu Val
 145 150 155 160
 Asp Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Gly Ala Thr Ala Gln
 165 170 175
 Ala Gly Leu Arg Ile Asn Phe Ala Lys Ala Trp Lys Lys Gly Leu
 180 185 190

<210> 1999
 <211> 134
 <212> PRT
 <213> Unknown (H38g921 protein)

<220>
 <223> Synthetic construct

<400> 1999
 Cys Tyr Pro Leu Gln Leu Arg Lys Pro Phe Met Ser Ser Leu Ala Leu
 1 5 10 15

Gln Ala Gln Ala Trp Pro Trp Val Pro Gly Ser Gly Gly Phe Val Ala
 20 25 30
 Ile Ala Val Pro Thr Ser Pro Ser Ser Ser Gly Leu Ser Phe Cys Gly
 35 40 45
 Pro Pro Val Ala Ile Asn His Phe Leu Ser Cys Asp Ile Ala Pro Leu
 50 55 60
 Ile Ala Leu Ala Cys Thr Gln His Thr Gly Ser Glu Ser Phe Val Ala
 65 70 75 80
 Phe Val Ile Ala Val Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu
 85 90 95
 Val Ser His Met Cys Thr Ser Ser Ser Thr Ile Leu Arg Ile Pro Ser
 100 105 110
 Ala Ser Gly Arg Lys Gln Ser Leu Ser Pro Arg Ala Pro Arg His Leu
 115 120 125
 Thr Val Val Leu Ile Leu
 130

<210> 2000

<211> 196

<212> PRT

<213> Unknown (H38g924 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(196)

<223> Xaa = Any Amino Acid

<400> 2000

Thr Pro Pro Met Tyr Phe Leu Phe Leu Gly Glu Ala Glu Cys Phe Leu
 1 5 10 15
 Leu Ala Thr Met Glu Tyr Asp Arg Tyr Glu Asp Ile Cys Ser Pro Leu
 20 25 30
 Asn Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Gly
 35 40 45
 Asp Ser Trp Val Pro Ser Phe Pro Glu Ala Thr Glu Gln Ala Thr Met
 50 55 60
 Ala Leu Arg Phe Pro Phe Xaa Gly Thr Asn Lys Val Asn His Leu Phe
 65 70 75 80
 Leu Arg Gln Pro Ala Val Leu Lys Ala Gly Leu Met Gln Asp Thr Ala
 85 90 95
 Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Ala Met Asn
 100 105 110
 Pro Cys Leu Leu Ile Leu Ser Ser Tyr Thr Arg Ile Gly Ala Ala Ile
 115 120 125
 Pro Gln Glu Pro Ile Lys Leu Lys Gly Lys Gln Xaa Arg Pro Phe Ser
 130 135 140
 Thr Cys Ser Xaa His Leu Pro Trp Trp Pro Leu Phe Ser Asn Ile Ile
 145 150 155 160
 Ile Xaa Ala Ser Thr Tyr Phe Leu Gly Leu Lys Ser Asn Lys Phe Phe
 165 170 175
 Trp Arg Gly Lys Lys Val Val Phe Ile Tyr Thr Thr Leu Val Glu Thr
 180 185 190
 Pro Xaa Trp Asn
 195

<210> 2001

<211> 128

<212> PRT

<213> Unknown (H38g925 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(128)

<223> Xaa = Any Amino Acid

<400> 2001

```

His Cys Met Phe Leu Ala His Gly Ser Pro Leu Pro Pro Thr Gln Leu
 1           5           10           15
Pro Ile Xaa Phe Cys Asp Tyr Ile Ser His Arg Tyr Leu Thr Cys His
      20           25           30
Leu Ser Leu Pro Asn Ser Phe Ser Ser Phe Pro Tyr Gln Xaa Ile
      35           40           45
Leu Pro Leu Ser Leu Leu Ala Gln Ala Arg Asn Pro Gly Ile Ile Phe
      50           55           60
Phe Leu Pro Thr Phe Asn Ala Leu Xaa Ser Pro Val His Ser Thr Ser
65           70           75           80
Xaa Arg Leu Ser Leu Ser Thr Tyr Tyr Tyr Ala Ser Gln Glu Thr Ile
      85           90           95
Ser Pro Arg Phe Asp Ser Thr Ala Val Ala Ser Tyr Leu Ile Phe Leu
      100          105          110
His Leu Leu Trp Pro Ile Phe Asn Pro Phe Ile Tyr Cys Leu Arg Asn
      115          120          125

```

<210> 2002

<211> 192

<212> PRT

<213> Unknown (H38g926 protein)

<220>

<223> Synthetic construct

<400> 2002

```

Phe Phe Leu Thr Leu Ala Gly Ala Glu Ala Leu Leu Leu Thr Ser Met
 1           5           10           15
Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His Tyr Leu Ile
      20           25           30
Arg Met Arg Lys Arg Val Cys Ala Leu Met Ile Thr Gly Ser Trp Met
      35           40           45
Ile Gly Ser Ile Asn Ser Cys Ala His Thr Val Tyr Ala Leu Arg Ile
      50           55           60
Pro Tyr Cys Lys Ser Arg Ala Ile Asn His Phe Phe Cys Asp Val Pro
65           70           75           80
Ala Met Leu Thr Leu Ala Cys Thr Asp Thr Trp Val Tyr Glu Cys Thr
      85           90           95
Val Phe Leu Ser Thr Thr Ile Phe Leu Val Phe Pro Phe Ile Cys Ile
      100          105          110
Ala Cys Ser Tyr Gly Arg Ile Leu Leu Ala Val Tyr His Met His Ser
      115          120          125
Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys Ser Thr His Leu Thr
130          135          140
Val Val Thr Phe Tyr Tyr Ala Pro Phe Ala Tyr Thr Tyr Leu Arg Pro
145          150          155          160
Lys Ser Leu Arg Ser Pro Thr Glu Asp Lys Val Leu Ala Val Phe Phe
      165          170          175
Phe Ile Ser Ser Phe Ser Ser Asn Pro Phe Met Tyr Thr Leu Arg Asn
      180          185          190

```

<210> 2003

<211> 158
 <212> PRT
 <213> Unknown (H38g927 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(158)
 <223> Xaa = Any Amino Acid

<400> 2003
 Pro Met Tyr Phe Phe Leu Ser Met Leu Ser Ile Ser Glu Thr Cys Tyr
 1 5 10 15
 Met Val Ala Ile Thr Pro His Met Leu Ser Arg Leu Leu Asn Pro His
 20 25 30
 Xaa Leu Ile Val Met Gln Gly Cys Val Thr Gln Leu Phe Tyr Val Thr
 35 40 45
 Phe Gly Ile Asn Asn Cys Phe Leu Leu Ile Ala Met Gly Tyr Asp Cys
 50 55 60
 Tyr Val Val Phe Cys Asn Pro Leu Arg Tyr Ser Xaa Val Arg Gly Leu
 65 70 75 80
 Cys Val Xaa Leu Gly Ser Gly Ser Leu Arg Ile Gly Leu Gly Met Ala
 85 90 95
 Ile Val Gln Val Thr Ser Met Phe Gly Leu Pro Phe Cys Asp Asp Phe
 100 105 110
 Val Ile Ser His Phe Phe Cys Asp Val Arg Pro Leu Leu Lys Leu Ala
 115 120 125
 Cys Thr Asp Thr Thr Val Asn Glu Ile Ile Asn Phe Val Val Ser Val
 130 135 140
 Cys Val Leu Val Leu His Ile Ala Leu Ile Phe Ile Ser Tyr
 145 150 155

<210> 2004
 <211> 192
 <212> PRT
 <213> Unknown (H38g928 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(192)
 <223> Xaa = Any Amino Acid

<400> 2004
 Leu Leu Ala Thr Lys Ala Tyr Asp Xaa Tyr Val Pro Ile Arg His Pro
 1 5 10 15
 Phe Pro Tyr Pro Thr Arg Met Ser Pro Ala Met Cys Ala Ala Leu Val
 20 25 30
 Gly Met Ala Trp Leu Val Ser His Gly Asn Ser Leu Leu Tyr Ile Leu
 35 40 45
 Leu Met Ala Arg Leu Ser Phe Leu Cys Phe Pro Thr Lys Cys Thr His
 50 55 60
 Phe Phe Cys Asp Pro Pro Ser Leu Ser Xaa Arg Leu Ser Cys Ser Asp
 65 70 75 80
 Asn His Thr Ser Lys Leu Leu Ile Phe Thr Lys Gly Ala Ala Val Val
 85 90 95
 Val Thr Pro Leu Leu Leu Ile Leu Ala Ser Leu Trp Asp His Asn Lys
 100 105 110
 Leu Thr Val Leu Gln Leu Pro Ser Thr Ser Gly Arg Leu Arg Asp Leu

```

      115              120              125
Xaa Pro Thr Cys Gly Ser His Leu Asp Val Val Ser Leu Phe Tyr Arg
    130              135              140
Thr Val Ile Ala Val Tyr Phe Gln Ala Thr Ser Ser Thr Arg Ala Glu
    145              150              155              160
Trp Asp Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu
      165              170              175
Asn Pro Ile Ile Tyr Ser Leu Thr Xaa Pro Arg Gly Arg Thr Leu Arg
    180              185              190

```

<210> 2005
 <211> 176
 <212> PRT
 <213> Unknown (H38g929 protein)

<220>
 <223> Synthetic construct

```

<400> 2005
Arg Val Pro Pro Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Val Phe
  1              5              10              15
Asp Met Gly Phe Ser Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu
      20              25              30
Met Gly Leu Gly Arg Leu Ile Ser Tyr Lys Asp Cys Val Cys Gln Leu
    35              40              45
Phe Phe Phe His Phe Leu Gly Ser Ile Glu Cys Phe Leu Phe Thr Val
    50              55              60
Met Ala Tyr Asp Arg Phe Thr Ala Ile Cys Tyr Pro Leu Arg Tyr Thr
    65              70              75              80
Val Ile Met Asn Pro Arg Ile Cys Val Ala Leu Ala Val Gly Thr Trp
      85              90              95
Leu Leu Gly Cys Ile His Ser Ser Ile Leu Thr Ser Leu Thr Phe Thr
    100              105              110
Leu Pro His Cys Gly Pro Asn Glu Val Asp His Phe Phe Cys Asp Ile
    115              120              125
Pro Ala Leu Leu Pro Leu Ala Cys Ala Asp Thr Ser Leu Ala Gln Arg
    130              135              140
Val Ser Phe Thr Asn Val Gly Leu Ile Ser Ala Gly Cys Phe Leu Leu
    145              150              155              160
Asn Leu Leu Ser Tyr Thr Arg Ile Thr Asn Ile Tyr Leu Lys His Ser
      165              170              175

```

<210> 2006
 <211> 44
 <212> PRT
 <213> Unknown (H38g930 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(44)
 <223> Xaa = Any Amino Acid

```

<400> 2006
Cys Ile Lys Leu Gly Thr Glu Leu Gly Ser Thr Ser Asn Gly Arg Gln
  1              5              10              15
Cys Ala Gly Ile Arg Pro Ser Tyr Val Phe Thr Leu His Leu Xaa Ala
      20              25              30
Asn Val Asn Pro Phe Ile Tyr Thr Leu Ser Asn Lys
    35              40

```

<210> 2007
 <211> 187
 <212> PRT
 <213> Unknown (H38g931 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(187)
 <223> Xaa = Any Amino Acid

<400> 2007
 Val Xaa Trp Ile Ser Ala Glu Phe Ala Leu Pro Met Tyr Leu Leu Leu
 1 5 10 15
 Ser Gln Leu Ser Leu Met Asp Leu Met Tyr Ile Ser Thr Thr Val Pro
 20 25 30
 Lys Met Ala Tyr Asn Phe Leu Ser Gly Gln Lys Gly Ile Ser Phe Leu
 35 40 45
 Gly Cys Gly Val Gln Ser Phe Phe Leu Thr Met Ala Cys Ser Glu
 50 55 60
 Gly Leu Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys
 65 70 75 80
 His Ser Leu Tyr Tyr Pro Ile Arg Met Ser Lys Met Met Cys Val Lys
 85 90 95
 Met Ile Gly Gly Ser Trp Thr Leu Gly Ser Ile Asn Ser Leu Ala His
 100 105 110
 Thr Val Phe Ala Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asp
 115 120 125
 His Phe Phe Cys Asp Val Pro Ala Met Leu Leu Leu Ser Cys Thr Asp
 130 135 140
 Thr Trp Val Tyr Glu Tyr Met Val Leu Xaa Gly Gln Ser Leu Phe Leu
 145 150 155 160
 Leu Leu Pro Phe Ile Gly Ile Thr Ser Ser Glu Gly Arg Val Leu Ile
 165 170 175
 Ala Gly Tyr Ile Met His Ser Lys Glu Gly Arg
 180 185

<210> 2008
 <211> 62
 <212> PRT
 <213> Unknown (H38g934 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(62)
 <223> Xaa = Any Amino Acid

<400> 2008
 Gly Gly Asn Arg Lys Lys Arg Glu Lys Glu Gly Arg Lys Lys Arg Lys
 1 5 10 15
 Val Arg Lys Lys Thr Gly Xaa Gly Arg Xaa Glu Val Gly Leu Leu Lys
 20 25 30
 Gly Ser Asn Ile Val Met Tyr Met Ala Pro Lys Tyr Arg His Pro Glu
 35 40 45
 Glu Gln Gln Lys Val Leu Phe Leu Phe Tyr Ser Ser Phe Asn
 50 55 60

<210> 2009
 <211> 103
 <212> PRT
 <213> Homo sapien (1000494-1-1-323)

<400> 2009

```

Pro Tyr Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Val Thr
1          5          10          15
Asp Thr Ser Cys Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val
          20          25          30
Ile Ala Thr Pro Phe Val Cys Ile Leu Ala Pro Tyr Ala Arg Ile Leu
          35          40          45
Val Ala Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe
          50          55          60
Ser Ala Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr
65          70          75          80
Thr Ile Gly Val Tyr Leu Cys Arg Ser Ser Val Leu Thr Thr Ala Lys
          85          90          95
Glu Lys Ala Ser Ala Val Met
          100

```

<210> 2010
 <211> 314
 <212> PRT
 <213> Homo sapien (1336040-1-1-945)

<400> 2010

```

Met Glu Phe Thr Asp Arg Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu
1          5          10          15
Leu Gly Phe Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Met
          20          25          30
Phe Leu Thr Leu Tyr Ala Ile Ile Leu Ile Gly Asn Ile Gly Leu Met
          35          40          45
Leu Leu Ile Arg Ile Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe
          50          55          60
Leu Ser Asn Leu Ser Phe Val Asp Leu Cys Tyr Phe Ser Asp Ile Val
65          70          75          80
Pro Lys Met Leu Val Asn Phe Leu Ser Glu Asn Lys Ser Ile Ser Tyr
          85          90          95
Tyr Gly Cys Ala Leu Gln Phe Tyr Phe Phe Cys Thr Phe Ala Asp Thr
          100          105          110
Glu Ser Phe Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Asn Pro Leu Leu Tyr Thr Val Val Met Ser Arg Gly Ile Cys Met
          130          135          140
Arg Leu Ile Val Leu Ser Tyr Leu Gly Gly Asn Met Ser Ser Leu Val
145          150          155          160
His Thr Ser Phe Ala Phe Ile Leu Lys Tyr Cys Asp Lys Asn Val Ile
          165          170          175
Asn His Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Thr
          180          185          190
Asp Thr Thr Ile Asn Glu Trp Leu Leu Ser Thr Tyr Gly Ser Ser Val
          195          200          205
Glu Ile Ile Cys Phe Ile Ile Ile Ile Ser Tyr Phe Phe Ile Leu
          210          215          220
Leu Ser Val Leu Lys Ile Arg Ser Phe Ser Gly Arg Lys Lys Thr Phe
225          230          235          240
Ser Thr Cys Ala Ser His Leu Thr Ser Val Thr Ile Tyr Gln Gly Thr
          245          250          255
Leu Leu Phe Ile Tyr Ser Arg Pro Ser Tyr Leu Tyr Ser Pro Asn Thr
          260          265          270

```

Asp Lys Ile Ile Ser Val Phe Tyr Thr Ile Phe Ile Pro Val Leu Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ala Glu
 290 295 300
 Lys Val Leu Arg Ser Lys Val Asp Ser Ser
 305 310

<210> 2011

<211> 317

<212> PRT

<213> Homo sapien (1336042-1-1-954)

<400> 2011

Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu
 20 25 30
 Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
 35 40 45
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
 65 70 75 80
 Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
 85 90 95
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
 115 120 125
 Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
 130 135 140
 Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr
 145 150 155 160
 Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His
 165 170 175
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
 180 185 190
 Ser Ser Asn Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met
 195 200 205
 Thr Pro Leu Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
 210 215 220
 Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile
 245 250 255
 Phe Thr Tyr Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys
 260 265 270
 Leu Phe Ser Val Phe Tyr Ala Ile Leu Thr Pro Met Leu Asn Pro Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu
 290 295 300
 Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr
 305 310 315

<210> 2012

<211> 318

<212> PRT

<213> Homo sapien (1369835-1-20155-22741)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2012

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
 1          5          10          15
Leu Ser Ser Ser Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe Ser
      20          25          30
Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
      35          40          45
Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
      50          55          60
Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
      65          70          75          80
Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
      85          90          95
Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
      100          105          110
Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
      115          120          125
Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
      130          135          140
Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
      145          150          155          160
Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
      165          170          175
Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
      180          185          190
Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu
      195          200          205
Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser
      210          215          220
Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val
      225          230          235          240
Gly Ile Leu Phe Phe Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro Leu
      245          250          255
Pro Lys Thr Thr His Asp Xaa Tyr Leu Phe Ile Val Pro Leu Leu Ser
      260          265          270
Pro Leu Ser Arg Ile Tyr Thr Leu Arg Asn Lys Asp Met Asn Val Ser
      275          280          285
Met Glu Arg Leu Gly Lys Trp Ile Ala Gly Ser Ser Arg Met Ser Xaa
      290          295          300
Xaa Met Val Leu Ser Arg Val Gln Asp Asp Ser Val Ser Pro
      305          310          315

```

<210> 2013

<211> 319

<212> PRT

<213> Homo sapien (1857946-1-1-1049)

<220>

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 2013

```

Phe Ser Ser Val Asn Asn Ser Cys Pro Arg Asn Val Arg Pro Val Leu
 1          5          10          15
Ser Val Trp Ala Met Tyr Leu Val Met Ile Gly Ser Ile Val Met Thr
      20          25          30
Met Leu Gly Asn Met Ile Val Met Ile Ser Ile Ala His Phe Lys Gln

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```

      35              40              45
Leu His Ser Pro Thr Asn Phe Leu Ile Leu Ser Met Ala Ile Thr Asp
  50              55              60
Phe Leu Leu Ser Cys Val Val Met Pro Phe Ser Val Ile Thr Ser Ile
  65              70              75              80
Glu Ser Cys Trp Tyr Phe Gly Asp Leu Phe Cys Lys Val His Ser Cys
      85              90              95
Cys Asp Ile Ile Leu Cys Thr Thr Ser Ile Phe His Leu Cys Phe Ile
      100              105              110
Ser Val Asp Arg Tyr Asp Ala Val Xaa Asp Pro Leu Gln Tyr Val Thr
      115              120              125
Arg Ile Thr Ile Pro Val Ile Glu Leu Phe Leu Leu Ile Ser Trp Ser
      130              135              140
Ile Pro Ile Leu Phe Ala Phe Gly Leu Val Phe Ser Lys Leu Asn Ile
      145              150              155              160
Ile Gly Ala Glu Glu Phe Val Ala Ala Ile Asp Cys Thr Gly Leu Cys
      165              170              175
Val Leu Ile Phe Asn Lys Pro Gly Gly Val Leu Ala Ser Phe Ile Ala
      180              185              190
Phe Phe Leu Pro Gly Thr Thr Thr Val Gly Ile Tyr Ile His Ile Phe
      195              200              205
Thr Val Ala Arg Lys His Ala Met Gln Ile Gly Thr Gly Ser Arg Thr
      210              215              220
Lys Gln Ala Gly Ser Glu Ser Lys Lys Lys Trp His Pro Leu Lys Arg
      225              230              235              240
Glu Ser Lys Ala Thr Arg Thr Leu Gly Ile Val Met Gly Val Phe Val
      245              250              255
Leu Cys Trp Leu Pro Phe Phe Val Leu Thr Ile Thr Asp Pro Phe Ile
      260              265              270
Asn Phe Thr Thr Leu Glu Asp Leu Tyr Asn Val Phe Leu Trp Leu Gly
      275              280              285
Tyr Phe Asn Ser Ala Phe Asn Ser Ile Leu Tyr Gly Met Leu Tyr Pro
      290              295              300
Trp Phe Arg Lys Ala Leu Arg Met Ile Val Thr Gly Met Ile Phe
      305              310              315

```

<210> 2014

<211> 134

<212> PRT

<213> Homo sapien (2358019-1-250070-250529)

<220>

<221> VARIANT

<222> (1)...(134)

<223> Xaa = Any Amino Acid

<400> 2014

```

Leu Leu Phe Leu Met Phe Phe Ile Thr Ser Leu Gly His Lys Phe His
  1              5              10              15
Leu Ile Ser Phe Pro Phe Ser Gln Gln Thr Thr Xaa Gln Lys Tyr Phe
      20              25              30
Ile Ile Phe Glu Val Xaa Leu Cys Xaa Xaa His Thr Leu Thr Ala Leu
      35              40              45
Ile Tyr Cys Xaa Met Ser Leu Phe Xaa Gly Ile Asp Leu Phe Val Gly
      50              55              60
Tyr Asn Pro Cys Ser Pro Arg Val Leu Phe Leu Phe Leu Gly Arg Gly
      65              70              75              80
Pro Ser Gly Phe Ser Leu Glu Ser Leu Ser Phe Tyr Arg Thr Ser Phe
      85              90              95
Thr Trp Gln His Leu His Leu Lys Phe Tyr Cys Pro Ser Xaa Gly Xaa
      100              105              110

```

Leu Leu Lys Ser Phe Leu Ser Ala Ile Trp Leu Leu Phe Ser Thr Tyr
 115 120 125
 Phe Leu Arg Val Leu Ser
 130

<210> 2015
 <211> 127
 <212> PRT
 <213> Homo sapien (2447218-1-32642-33129)

<220>
 <221> VARIANT
 <222> (1)...(127)
 <223> Xaa = Any Amino Acid

<400> 2015
 Asn Leu Leu Pro Val Trp Thr Pro Gly Ser Arg Val Pro Ser Xaa Ser
 1 5 10 15
 Gln Ile Ser Val Ser Glu Lys Gln Gly Met Ser Phe Pro Lys Lys Leu
 20 25 30
 Phe Gln Asn His Lys Leu Phe Leu Phe Ala Gly Met Asn Val Phe
 35 40 45
 Leu Gln Thr Val Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro
 50 55 60
 Leu His Tyr Arg Val Ile Met Asn Pro Gly Ile Phe Gly Leu Trp Val
 65 70 75 80
 Leu Val Ser Trp Ser Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Arg
 85 90 95
 Met Val Leu Gln Leu Ser Phe Cys Thr Asn Leu Glu Ile Pro His Ile
 100 105 110
 Phe Phe Cys Glu Leu Asn Gln Leu Ile Leu Leu Ala Cys Ser Asn
 115 120 125

<210> 2016
 <211> 216
 <212> PRT
 <213> Homo sapien (2921627-1-1-649)

<400> 2016
 Leu Ile Asp Met Met Tyr Ile Ser Thr Ile Val Pro Lys Met Leu Val
 1 5 10 15
 Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly Cys Thr Ala
 20 25 30
 Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe Phe Leu Leu
 35 40 45
 Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
 50 55 60
 Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile Ile Ala Gly
 65 70 75 80
 Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr Pro Ile Thr
 85 90 95
 Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His Phe Phe Cys
 100 105 110
 Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Ala Leu Tyr
 115 120 125
 Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu Ile Pro Phe
 130 135 140
 Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr Val Gln Cys
 145 150 155 160
 Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys Ser Ser
 165 170 175

His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr Thr Tyr
 180 185 190
 Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys Val Leu Ser
 195 200 205
 Val Phe Tyr Thr Ile Leu Thr Pro
 210 215

<210> 2017

<211> 216

<212> PRT

<213> Homo sapien (2921629-1-1-649)

<400> 2017

Phe Val Asp Met Gly Leu Thr Ser Ser Thr Val Thr Lys Met Leu Val
 1 5 10 15
 Asn Ile Gln Thr Arg His His Thr Ile Thr Tyr Thr Gly Cys Leu Thr
 20 25 30
 Gln Met Tyr Phe Phe Leu Met Phe Gly Asp Leu Asp Ser Phe Phe Leu
 35 40 45
 Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Cys
 50 55 60
 Tyr Ser Thr Val Met Arg Pro Gln Val Cys Ala Leu Met Leu Ala Leu
 65 70 75 80
 Cys Trp Val Leu Thr Asn Ile Val Ala Leu Thr His Thr Phe Leu Met
 85 90 95
 Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe Cys
 100 105 110
 Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile Asn
 115 120 125
 Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro Phe
 130 135 140
 Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu Arg
 145 150 155 160
 Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala Tyr
 180 185 190
 Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala Ala
 195 200 205
 Ala Met Tyr Thr Ile Val Thr Pro
 210 215

<210> 2018

<211> 212

<212> PRT

<213> Homo sapien (2921634-1-1-653)

<400> 2018

Cys His Ser Gln Val Ser Arg Leu Ala Gly Leu Gly Tyr Leu Glu Gly
 1 5 10 15
 Arg Arg Leu Ser Ser Ser Tyr Asn Ala Cys Ala Ala Gln Met Phe Phe
 20 25 30
 Phe Val Ala Leu Ala Thr Val Glu Asn Ile Leu Leu Thr Ser Met Ala
 35 40 45
 Tyr Asp His Tyr Ile Ala Val Cys Lys Pro Leu His Tyr Thr Thr Thr
 50 55 60
 Thr Ile Ala Ser Val Cys Ala His Leu Val Ile Gly Ser Tyr Val Cys
 65 70 75 80
 Gly Phe Leu Asn Ala Pro Leu Arg Ile Val Asp Ile Phe Ser Leu Ser
 85 90 95
 Phe Cys Lys Ser Asn Leu Val His His Leu Phe Cys Asp Val Pro Pro

```

      100      105      110
Val Met Ala Val Ser Cys Ser Gly Lys His Ile Ser Lys Lys Ile Leu
      115      120      125
Val Phe Met Ser Ser Phe Asn Val Phe Leu Ala Leu Leu Val Ile Leu
      130      135      140
Thr Ser Tyr Leu Val Ile Phe Ile Thr Ile Leu Lys Met His Ser Ala
      145      150      155      160
Gln Gly His Leu Lys Ala Trp Ser Thr Gly Ala Pro His Leu Ile Ala
      165      170      175
Val Ser Ile Phe Tyr Gly Thr Thr Ile Phe Met Tyr Leu Gln Pro Ser
      180      185      190
Ser Ser His Ser Met Asp Thr Asp Glu Met Ala Ser Leu Phe Tyr Ala
      195      200      205
Val Phe Ile Ser
      210

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<210> 2019
<211> 215
<212> PRT
<213> Homo sapien (2921639-1-1-647)

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<400> 2019
Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser
 1      5      10      15
Asn Ile Arg Thr Gln Ser Lys Val Val Thr Tyr Ala Gly Cys Ile Thr
      20      25      30
Gln Met Tyr Phe Phe Val Leu Phe Ile Val Leu Asp Ser Leu Leu Leu
      35      40      45
Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His Pro Leu His
      50      55      60
Tyr Thr Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
      65      70      75      80
Ser Trp Ile Met Ser Ala Leu Asn Ser Leu Ile Glu Ser Leu Met Val
      85      90      95
Leu Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro His Phe Phe Cys
      100      105      110
Glu Leu Asn Gln Ile Ile Arg Ser Ala Cys Ser Asp Thr Phe Leu Asn
      115      120      125
Asp Met Val Met Tyr Met Ser Ala Val Leu Leu Gly Arg Gly Cys Phe
      130      135      140
Thr Gly Ile Leu Tyr Ser Tyr Phe Lys Thr Val Ser Ser Ile Arg Ala
      145      150      155      160
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
      165      170      175
His Leu Ser Val Val Ser Leu Phe Tyr Cys Met Gly Leu Gly Val Tyr
      180      185      190
Leu Ser Ala Ala Ala Pro Thr Thr His Ser Gln Val Gln Gln Pro Leu
      195      200      205
Met Tyr Thr Val Val Thr Pro
      210      215

```

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<210> 2020
<211> 212
<212> PRT
<213> Homo sapien (2921641-1-1-636)

```

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<220>
<221> VARIANT
<222> (1)...(212)
<223> Xaa = Any Amino Acid

```

<400> 2020
 Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met Ile Val
 1 5 10 15
 Asp Ser Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys Ile Thr
 20 25 30
 Gln Met Phe Thr Phe His Phe Phe Gly Cys Ala Asp Ile Phe Val Leu
 35 40 45
 Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu Arg
 50 55 60
 Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala Ser Leu
 65 70 75 80
 Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu Leu Thr
 85 90 95
 Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr Phe Cys
 100 105 110
 Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Leu Val
 115 120 125
 Ser Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly Cys Phe
 130 135 140
 Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu Gln Lys
 145 150 155 160
 Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly Ser His
 165 170 175
 Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Thr Phe Ile Tyr Arg
 180 185 190
 Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe Tyr Thr
 195 200 205
 Thr Ile Thr Pro
 210

<210> 2021

<211> 216

<212> PRT

<213> Homo sapien (2921661-1-1-649)

<400> 2021
 Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Ala
 1 5 10 15
 Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly Cys Leu Leu
 20 25 30
 Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala Phe Leu Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60
 Tyr Ile Leu Ile Met Ser Pro Gly Leu Arg Ile Phe Leu Val Ser Ala
 65 70 75 80
 Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr Leu Leu Met
 85 90 95
 Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His Phe Leu Cys
 100 105 110
 Asp Ile Asn Pro Leu Leu Gly Leu Ser Cys Thr Asp Pro Phe Thr Asn
 115 120 125
 Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu Ile Cys Val
 130 135 140
 Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr Ile Leu Lys
 145 150 155 160
 Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe Cys Val Asp
 180 185 190
 Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr Val Ala Ser

195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2022
 <211> 216
 <212> PRT
 <213> Homo sapien (2921667-1-1-649)

<400> 2022
 Val Leu Asp Val Gly Cys Ile Thr Val Thr Val Pro Ala Met Leu Gly
 1 5 10 15
 Arg Leu Leu Ser His Lys Ser Thr Ile Ser Tyr Asp Ala Cys Leu Ser
 20 25 30
 Gln Leu Phe Phe Phe His Leu Leu Ala Gly Met Asp Cys Phe Leu Leu
 35 40 45
 Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala Ile Cys Gln Pro Leu Thr
 50 55 60
 Tyr Ser Thr Arg Met Ser Gln Thr Val Gln Arg Met Leu Val Ala Ala
 65 70 75 80
 Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu Thr His Thr Val Ala Met
 85 90 95
 Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu Val Asn His Phe Tyr Cys
 100 105 110
 Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys Ser Ser Thr Gln Leu Asn
 115 120 125
 Glu Leu Leu Leu Phe Val Ala Ala Ala Phe Met Ala Val Ala Pro Leu
 130 135 140
 Val Phe Ile Ser Val Ser Tyr Ala His Val Val Ala Ala Val Pro Gln
 145 150 155 160
 Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Gly Ile Phe Tyr Gly Thr Gly Val Phe Ser Tyr
 180 185 190
 Met Arg Leu Gly Ser Ala Glu Ser Ser Asp Lys Asp Lys Gly Val Gly
 195 200 205
 Val Phe Met Thr Val Ile Asn Pro
 210 215

<210> 2023
 <211> 215
 <212> PRT
 <213> Homo sapien (2921686-1-1-646)

<400> 2023
 Trp Ala Asp Ile Ala Phe Thr Ser Ala Thr Val Pro Lys Met Ile Val
 1 5 10 15
 Asp Met Gln Ser His Arg Val Ile Ser Tyr Ala Ser Cys Leu Thr Gln
 20 25 30
 Met Ser Phe Phe Ala Leu Phe Ala Cys Ile Glu Asp Leu Leu Ile
 35 40 45
 Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Ser Pro His Tyr
 50 55 60
 Pro Val Ile Met Asn Pro Arg Leu Gly Val Phe Phe Val Leu Val Ser
 65 70 75 80
 Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Thr Val Leu
 85 90 95
 Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe Val Cys Asp
 100 105 110
 Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Val Ile Asp Ser
 115 120 125

```

Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Arg Phe Leu Pro Ile Ser
 130          135          140
Gly Ile Leu Leu Ser Tyr Ser Asn Ile Val Pro Ser Ile Leu Arg Ile
145          150          155          160
Ser Ser Ser Asp Gly Lys Ser Lys Ala Phe Ser Thr Cys Arg Ser His
          165          170          175
Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly Val Tyr Leu
          180          185          190
Thr Thr Ala Ala Gly Thr Thr Pro Arg Ser Gly Val Val Val Ser Val
          195          200          205
Met Tyr Thr Val Val Thr Pro
          210          215

```

<210> 2024

<211> 217

<212> PRT

<213> Homo sapien (2921715-1-1-652)

<400> 2024

```

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Lys Val Pro Lys Met Leu Thr
 1          5          10          15
Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
          20          25          30
Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
          35          40          45
Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
          50          55          60
Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
          65          70          75          80
Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
          85          90          95
Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
          100          105          110
Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
          115          120          125
Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro
          130          135          140
Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu
          145          150          155          160
Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
          165          170          175
Ser His Leu Cys Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met
          180          185          190
Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu
          195          200          205
Ser Leu Phe Tyr Ser Leu Phe Asn Pro
          210          215

```

<210> 2025

<211> 311

<212> PRT

<213> Homo sapien (3093312-1-33069-35776)

<400> 2025

```

Met Asn Asp Asp Gly Lys Val Asn Ala Ser Ser Glu Gly Tyr Phe Ile
 1          5          10          15
Leu Val Gly Phe Ser Asn Trp Pro His Leu Glu Val Val Ile Phe Val
          20          25          30
Val Val Leu Ile Phe Tyr Leu Met Thr Leu Ile Gly Asn Leu Phe Ile
          35          40          45
Ile Ile Leu Ser Tyr Leu Asp Ser His Leu His Thr Pro Met Tyr Phe

```

```

      50              55              60
Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser
65              70              75              80
Ile Pro Gln Leu Leu Val Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser
      85              90              95
Tyr Ala Gly Cys Met Ile Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr
      100              105              110
Thr Glu Cys Val Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Ala Ala
      115              120              125
Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Pro Arg Phe Cys
      130              135              140
His Leu Leu Ala Val Ala Ser Trp Val Ser Gly Phe Thr Asn Ser Ala
145              150              155              160
Leu His Ser Ser Phe Thr Phe Trp Val Pro Leu Cys Gly His Arg Gln
      165              170              175
Val Asp His Phe Cys Glu Val Pro Ala Leu Leu Arg Leu Ser Cys
      180              185              190
Val Asp Thr His Val Asn Glu Leu Thr Leu Met Ile Thr Ser Ser Ile
      195              200              205
Phe Val Leu Ile Pro Leu Ile Leu Ile Leu Thr Ser Tyr Gly Ala Ile
      210              215              220
Val Arg Ala Val Leu Arg Met Gln Ser Thr Thr Gly Leu Gln Lys Val
225              230              235              240
Phe Gly Thr Cys Gly Ala His Leu Met Ala Val Ser Leu Phe Phe Ile
      245              250              255
Pro Ala Met Cys Ile Tyr Leu Gln Pro Pro Ser Gly Asn Ser Gln Asp
      260              265              270
Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ser Leu
      275              280              285
Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Val Val Arg Gly Ala Val
      290              295              300
Lys Arg Leu Met Gly Trp Glu
305              310

```

<210> 2026

<211> 330

<212> PRT

<213> Homo sapien (3108020-1-23117-23433)

<220>

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 2026

```

Met Glu Pro Glu Asn Asp Thr Arg Ile Ser Glu Phe Arg Leu Leu Gly
1              5              10              15
Phe Ser Glu Glu Pro Arg Leu Gln Arg Phe Arg Phe Leu Phe Gly Val
      20              25              30
Phe Leu Ser Met Tyr Leu Ile Ile Val Phe Gly Asn Leu Leu Ile Ile
      35              40              45
Leu Val Ile Ile Leu Cys Ser His Leu His Thr Ser Met Tyr Phe Phe
      50              55              60
Leu Ser Asn Leu Ser Phe Val Asp Ile Cys Phe Ala Ser Thr Arg Val
65              70              75              80
Pro Lys Met Leu Val Asn Ile Gln Ala Gln Ser Lys Val Ile Thr Ser
      85              90              95
Ala Gly Cys Ile Thr Gln Met Tyr Phe Phe Ile His Phe Val Gly Leu
      100              105              110
Asp Ser Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile
      115              120              125

```

Cys His Pro Leu Tyr Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly
 130 135 140
 Leu Leu Val Leu Val Ser Trp Ile Thr Ser Val Leu His Ser Leu Leu
 145 150 155 160
 His Ser Leu Met Val Leu Gln Leu Ser Leu Cys Arg Glu Leu Glu Ile
 165 170 175
 Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser
 180 185 190
 Asp Thr Phe Leu Asn Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu
 195 200 205
 Gly Gly Gly Ser Leu Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val
 210 215 220
 Ser Ser Ile Cys Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Pro Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr
 245 250 255
 Ser Leu Gly Val Tyr Leu Ser Ser Ala Ala Ser His Asn Ser His Ser
 260 265 270
 Gly Ala Ile Ala Ser Val Arg Tyr Thr Val Val Thr Pro Met Leu Asn
 275 280 285
 Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys
 290 295 300
 Asn Ser Leu Gly Gly Lys Leu Glu Lys Gly Gln Leu Ser Xaa Gly Leu
 305 310 315 320
 Lys Leu Tyr Pro Xaa Leu Gln Gly Ser Lys
 325 330

<210> 2027

<211> 319

<212> PRT

<213> Homo sapien (3108020-1-37593-38822)

<400> 2027

Met Glu Arg Gly Asn Gln Thr Glu Val Gly Asn Phe Leu Leu Leu Gly
 1 5 10 15
 Phe Ala Glu Asp Ser Asp Met Gln Leu Leu His Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Ile Ile Gly Asn Leu Leu Ile Ile Leu Thr
 35 40 45
 Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly
 85 90 95
 Cys Leu Thr Gln Ile Phe Phe Phe Ile Ala Phe Gly Cys Leu Asp Asn
 100 105 110
 Leu Leu Leu Thr Met Thr Ala Tyr Asp Arg Phe Val Ala Ile Cys Tyr
 115 120 125
 Pro Leu His Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu
 130 135 140
 Val Leu Gly Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr
 145 150 155 160
 Leu Thr Ile Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His
 165 170 175
 Phe Phe Cys Asp Pro Ser Glu Val Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Phe Ile Asn Asn Ile Val Met Tyr Phe Val Thr Ile Val Leu Gly Val
 195 200 205
 Phe Pro Leu Cys Gly Ile Leu Phe Ser Tyr Ser Gln Ile Phe Ser Ser
 210 215 220

Val Leu Arg Val Ser Ala Arg Gly Gln His Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly
 245 250 255
 Val Tyr Leu Ser Ser Ala Val Thr Pro Pro Ser Arg Thr Ser Leu Ala
 260 265 270
 Ala Ser Val Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Ser Leu Gly Arg Leu Leu
 290 295 300
 Leu Arg Ala Thr Ser Leu Lys Glu Gly Thr Ile Ala Lys Leu Ser
 305 310 315

<210> 2028

<211> 315

<212> PRT

<213> Homo sapien (3184261-1-5713-7336)

<400> 2028

Met Glu Pro Glu Lys Gln Thr Glu Ile Ser Glu Phe Phe Leu Gln Gly
 1 5 10 15
 Leu Ser Glu Lys Pro Glu His Gln Thr Leu Leu Phe Thr Met Phe Leu
 20 25 30
 Ser Thr Tyr Leu Val Thr Ile Ile Gly Asn Ala Leu Ile Ile Leu Ala
 35 40 45
 Ile Ile Thr Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Leu Val Asp Thr Leu Leu Ser Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Ala Asn Ile Gln Ala Gln Ser Arg Ala Ile Pro Phe Val Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Ala Phe His Leu Phe Gly Thr Met Asp Ser
 100 105 110
 Phe Leu Leu Ala Val Met Ala Ile Asp Arg Phe Val Ala Ile Val His
 115 120 125
 Pro Gln Arg Tyr Leu Val Leu Met Cys Ser Pro Val Cys Gly Leu Leu
 130 135 140
 Leu Gly Ala Ser Trp Met Ile Thr Asn Leu Gln Ser Leu Ile His Thr
 145 150 155 160
 Cys Leu Met Ala Gln Leu Thr Phe Cys Ala Gly Ser Glu Ile Ser His
 165 170 175
 Phe Phe Cys Asp Leu Met Pro Leu Leu Lys Leu Ser Gly Ser Asp Thr
 180 185 190
 His Thr Asn Glu Leu Val Ile Phe Ala Phe Gly Ile Val Val Gly Thr
 195 200 205
 Ser Pro Phe Ser Cys Ile Leu Leu Ser Tyr Ile Arg Ile Phe Trp Thr
 210 215 220
 Val Phe Lys Ile Pro Ser Thr Arg Gly Lys Trp Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Leu His Leu Thr Val Val Ser Leu Ser Tyr Gly Thr Ile Phe
 245 250 255
 Ala Val Tyr Leu Gln Pro Thr Ser Pro Ser Ser Ser Gln Lys Asp Lys
 260 265 270
 Ala Ala Ala Leu Met Cys Gly Val Phe Ile Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Ile Arg Asn Lys Asp Met Lys Ala Ala Leu Gly Lys Leu
 290 295 300
 Ile Gly Lys Val Ala Val Pro Cys Pro Arg Pro
 305 310 315

<210> 2029

<211> 318

<212> PRT

<213> Homo sapien (3213020-1-101040-103030)

<400> 2029

```

Met Trp Gln Lys Asn Gln Thr Ser Leu Ala Asp Phe Ile Leu Glu Gly
 1           5           10          15
Leu Phe Asp Asp Ser Leu Thr His Leu Phe Leu Phe Ser Leu Thr Met
      20           25           30
Val Val Phe Leu Ile Ala Val Ser Gly Asn Thr Leu Thr Ile Leu Leu
      35           40           45
Ile Cys Ile Asp Pro Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser
      50           55           60
Gln Leu Ser Leu Met Asp Leu Met His Val Ser Thr Thr Ile Leu Lys
      65           70           75           80
Met Ala Thr Asn Tyr Leu Ser Gly Lys Lys Ser Ile Ser Phe Val Gly
      85           90           95
Cys Ala Thr Gln His Phe Leu Tyr Leu Cys Leu Gly Gly Ala Glu Cys
      100          105          110
Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu Arg Tyr Ala Val Leu Met Asn Lys Lys Val Gly Leu Met Met
      130          135          140
Ala Val Met Ser Trp Leu Gly Ala Ser Val Asn Ser Leu Ile His Met
      145          150          155          160
Ala Ile Leu Met His Phe Pro Phe Cys Gly Pro Arg Lys Val Tyr His
      165          170          175
Phe Tyr Cys Glu Phe Pro Ala Val Val Lys Leu Val Cys Gly Asp Ile
      180          185          190
Thr Val Tyr Glu Thr Thr Val Tyr Ile Ser Ser Ile Leu Leu Leu
      195          200          205
Pro Ile Phe Leu Ile Ser Thr Ser Tyr Val Phe Ile Leu Gln Ser Val
      210          215          220
Ile Gln Met Arg Ser Ser Gly Ser Lys Arg Asn Ala Phe Ala Thr Cys
      225          230          235          240
Gly Ser His Leu Thr Val Val Ser Leu Trp Phe Gly Ala Cys Ile Phe
      245          250          255
Ser Tyr Met Arg Pro Arg Ser Gln Cys Thr Leu Leu Gln Asn Lys Val
      260          265          270
Gly Ser Val Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Ser Leu Ile
      275          280          285
Tyr Thr Leu Arg Asn Lys Asp Val Ala Lys Ala Leu Arg Arg Val Leu
      290          295          300
Arg Arg Asp Val Ile Thr Gln Cys Ile Gln Arg Leu Gln Leu
      305          310          315

```

<210> 2030

<211> 114

<212> PRT

<213> Homo sapien (32504-1-1-343)

<400> 2030

```

Val Cys His Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys
 1           5           10          15
Gly Leu Leu Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu
      20           25           30
Leu His Ile Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu
      35           40           45
Ile Pro His Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys
      50           55           60
Ser Asp Thr Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val

```

<400> 2033
Ile Cys Tyr Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Arg Ile Cys
1 5 10 15
Val Ala Leu Ala Val Gly Thr Trp Leu Leu Gly Cys Ile His Ser Ser

```

      20      25      30
Ile Leu Thr Ser Leu Thr Phe Thr Leu Pro Tyr Cys Gly Pro Asn Glu
      35      40      45
Val Asp His Phe Phe Cys Asp Ile Pro Ala Leu Leu Pro Leu Ala Cys
      50      55      60
Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Thr Ser Val Gly Leu
      65      70      75      80
Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr Thr Arg Ile
      85      90      95
Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg Arg Arg Ala
      100      105      110
Phe Ser

```

<210> 2034

<211> 114

<212> PRT

<213> Homo sapien (32518-1-1-343)

<400> 2034

```

Ile Cys Lys Pro Leu Leu Tyr Pro Ala Ile Met Thr Asn Gly Leu Cys
1      5      10      15
Ile Arg Leu Leu Ile Leu Ser Tyr Val Gly Gly Leu Leu His Ala Leu
      20      25      30
Ile His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile
      35      40      45
Val His His Ile Tyr Cys Asp Ile Ile Pro Leu Ser Lys Ile Ser Cys
      50      55      60
Thr Asp Ser Ser Ile Asn Phe Leu Met Val Phe Ile Phe Ser Gly Ser
      65      70      75      80
Ile Gln Val Phe Ser Ile Val Thr Ile Leu Val Ser Tyr Thr Phe Val
      85      90      95
Leu Phe Ala Ile Leu Lys Arg Lys Ser Asp Lys Gly Val Arg Lys Ala
      100      105      110
Phe Ser

```

<210> 2035

<211> 148

<212> PRT

<213> Homo sapien (3289998-1-93404-94343)

<400> 2035

```

Met Val Leu Trp Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe
1      5      10      15
Phe Cys Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe
      20      25      30
Leu Asn Asp Met Gly Met Tyr Phe Ala Ala Gly Leu Leu Ala Gly Gly
      35      40      45
Pro Leu Val Gly Ile Leu Cys Ser Tyr Ser Lys Ile Val Ser Ser Ile
      50      55      60
Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys
      65      70      75      80
Ala Ser His Leu Ser Val Val Ser Leu Phe Cys Cys Thr Gly Leu Gly
      85      90      95
Val Tyr Leu Thr Ser Ala Ala Thr His Asn Ser His Thr Ser Ala Thr
      100      105      110
Ala Ser Val Met Tyr Thr Val Ala Thr Pro Met Leu Asn Pro Phe Ile
      115      120      125
Tyr Ser Leu Arg Asn Lys Asp Ile Lys Arg Ala Leu Lys Met Ser Phe
      130      135      140

```


Arg Gly Lys Gln
145

<210> 2036

<211> 312

<212> PRT

<213> Homo sapien (3402736-1-7079-10933)

<400> 2036

Met Ser Ala Asn Thr Ser Met Val Thr Glu Phe Leu Leu Leu Gly Phe
1 5 10 15
Ser His Leu Ala Asp Leu Gln Gly Leu Leu Phe Ser Val Phe Leu Thr
20 25 30
Ile Tyr Leu Leu Thr Val Ala Gly Asn Phe Leu Ile Val Val Leu Val
35 40 45
Ser Thr Asp Ala Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu Arg Thr
50 55 60
Leu Ser Ala Leu Glu Ile Gly Tyr Thr Ser Val Thr Val Pro Leu Leu
65 70 75 80
Leu His His Leu Leu Thr Gly Arg Arg His Ile Ser Arg Ser Gly Cys
85 90 95
Ala Leu Gln Met Phe Phe Phe Leu Phe Phe Gly Ala Thr Glu Cys Cys
100 105 110
Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro
115 120 125
Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala
130 135 140
Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro
145 150 155 160
Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe
165 170 175
Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser
180 185 190
Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys
195 200 205
Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile
210 215 220
Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys
225 230 235 240
Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe
245 250 255
Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu
260 265 270
Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile
275 280 285
Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile
290 295 300
Gln Lys Thr Val Pro Met Glu Ile
305 310

<210> 2037

<211> 305

<212> PRT

<213> Homo sapien (3522966-1-8581-12533)

<400> 2037

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Gly Leu
1 5 10 15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
20 25 30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu

35 40 45
 His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu
 50 55 60
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser
 65 70 75 80
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
 85 90 95
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
 100 105 110
 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile
 115 120 125
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Ala Trp Gly Ile
 130 135 140
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Pro
 145 150 155 160
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
 165 170 175
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
 180 185 190
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile
 195 200 205
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp
 210 215 220
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
 225 230 235 240
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
 245 250 255
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
 260 265 270
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
 275 280 285
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
 290 295 300
 Phe
 305

<210> 2038

<211> 142

<212> PRT

<213> Homo sapien (3738097-1-24383-25939)

<220>

<221> VARIANT

<222> (1)...(142)

<223> Xaa = Any Amino Acid

<400> 2038

Tyr Ile Glu Met Asp Asn Tyr Phe Leu Thr Xaa Leu Xaa Arg Tyr Leu
 1 5 10 15
 Leu Phe Phe His Phe Ile Ile Ser Thr Gln Tyr Phe Gly Ile Lys Lys
 20 25 30
 Phe Ile Leu Thr Ser Leu Leu Ala Tyr Cys Phe Trp Met Phe Ser Ile
 35 40 45
 Thr Lys Phe Leu Thr Tyr Gly Leu Lys Trp Leu Leu Ile Pro Asp Cys
 50 55 60
 Xaa Ser Trp Tyr Gln His Ala Xaa Phe Asn Pro Xaa Gln Ile Leu Phe
 65 70 75 80
 Leu Gln Asn Ser Xaa Ser Trp Leu Glu Val Tyr Phe Tyr Leu Phe Leu
 85 90 95
 Leu Phe Ala Val Pro Phe Asp Lys Ile Ile Phe Leu Ser Xaa Lys Met
 100 105 110

Tyr Leu Asn Lys Xaa Ile Ile Ser Val Leu Val Gly Thr Arg Trp Thr
 115 120 125
 Phe Gln Arg Cys Val His Thr Leu Cys Ile Leu Ser Leu Phe
 130 135 140

<210> 2039
 <211> 297
 <212> PRT
 <213> Homo sapien (3738097-1-94180-96164)

<220>
 <221> VARIANT
 <222> (1)...(297)
 <223> Xaa = Any Amino Acid

<400> 2039
 Met Lys Xaa Met Ala Val Glu Asn Asn Ser Ser Val Thr Glu Phe Ile
 1 5 10 15
 Leu Val Arg Leu Thr Asn Ser Arg Cys Pro Ser Val Leu Phe Leu Met
 20 25 30
 Trp Ser Leu Trp Gly Glu Phe Glu His Asn Phe Met Ser Leu Asn Ser
 35 40 45
 His Leu His Thr Pro Thr His Phe Phe Leu Phe Thr Leu Ser Phe Ile
 50 55 60
 Asp Val Cys Tyr Ser Phe Val Cys Thr Thr Lys Ile Pro Met Gly Phe
 65 70 75 80
 Ile Ser Glu Arg Asn Ile Ile Ser Phe Val Gly Trp Pro Thr Xaa Leu
 85 90 95
 Tyr Phe Phe Cys Ile Phe Val Lys Glu Pro Lys Asn Gly Val Ile Val
 100 105 110
 Gly Ile Met Phe Ser Ala Lys Met Leu Val Cys Arg Glu Ile Met Asp
 115 120 125
 Xaa Ser Leu Met Xaa Asn Xaa Lys Met His Met Ala Leu Glu Arg Ser
 130 135 140
 Asp Phe Arg Met Gly Xaa Thr Gly Ser Ala Thr Lys Lys His Leu Ile
 145 150 155 160
 Ile Phe Leu Tyr Tyr Ser Asp Tyr Phe Gln Arg Xaa Xaa Gly Cys Arg
 165 170 175
 Ala Leu Gly Gln Gly Ser Leu Ala Lys Gln Asp Thr Xaa Leu Xaa Asn
 180 185 190
 Cys Thr Cys Thr Leu Lys Ser Leu Leu His Ile Ile Ile Cys Phe Tyr
 195 200 205
 Ile Trp Lys Gln Lys Lys Ile Ser Tyr Leu Tyr His Lys Ser Xaa Lys
 210 215 220
 Met Asp Leu Tyr Lys Ile Cys His Val Leu Trp Val Thr His Lys Lys
 225 230 235 240
 Asn Phe Leu Arg Pro Ser Ser Thr Ser Gln Met Val Gln Gly Lys Met
 245 250 255
 Leu Leu Lys Gly Tyr Ile Xaa Phe Trp Arg Met Ser Leu Pro Met Cys
 260 265 270
 Ala Ile Phe Ile Phe Val Arg Arg Tyr Tyr Tyr Leu Leu Lys Lys Leu
 275 280 285
 Lys Thr Leu Leu Tyr Lys Asn Ser Tyr
 290 295

<210> 2040
 <211> 325
 <212> PRT
 <213> Homo sapien (3746441-1-1-1386)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2040

```

Met Ala Asn Glu Asn Tyr Thr Lys Val Thr Xaa Phe Ile Phe Thr Gly
 1           5           10           15
Leu Asn Tyr Asn Pro Gln Leu Arg Val Phe Leu Phe Leu Phe Leu
      20           25           30
Thr Thr Phe Tyr Val Ile Asn Val Thr Gly Asn Leu Gly Met Ile Val
      35           40           45
Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
      50           55           60
Ser His Leu Ser Phe Val Asp Thr Cys Phe Ser Ser Val Val Ser Pro
      65           70           75           80
Lys Met Leu Thr Asp Phe Phe Val Lys Arg Lys Ala Ile Ser Phe Leu
      85           90           95
Gly Cys Ala Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Ala Ala Asp
      100          105          110
Cys Phe Leu Leu Glu Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys
      115          120          125
Asn Pro Leu Leu Tyr Ser Val Ala Met Ser Gln Arg Leu Cys Ile Gln
      130          135          140
Leu Val Val Gly Pro Tyr Val Ile Gly Leu Met Asn Thr Met Thr His
      145          150          155          160
Thr Thr Asn Ala Phe Cys Leu Pro Phe Cys Gly Pro Asn Val Ile Asn
      165          170          175
Pro Phe Phe Cys Asp Met Ser Pro Leu Leu Ser Leu Val Cys Ala Asp
      180          185          190
Thr Arg Leu Asn Lys Leu Ala Val Phe Ile Val Ala Gly Ala Val Gly
      195          200          205
Val Phe Ser Gly Leu Thr Ile Leu Ile Ser Tyr Ile Tyr Ile Leu Met
      210          215          220
Ala Ile Leu Arg Ile Arg Ser Ala Asp Gly Arg Cys Lys Thr Phe Ser
      225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Phe Ile Leu Tyr Gly Thr Leu
      245          250          255
Phe Phe Ile Tyr Val His Pro Ser Ala Thr Phe Ser Leu Asp Leu Asn
      260          265          270
Lys Val Val Ser Val Phe Tyr Thr Ala Val Ile Pro Met Leu Asn Pro
      275          280          285
Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Ile His Arg
      290          295          300
Thr Val Thr Gln Arg Lys Phe Cys Lys Ala Xaa Ile Leu Ile Gln Lys
      305          310          315          320
Glu Leu Gly Arg Lys
      325

```

<210> 2041

<211> 328

<212> PRT

<213> Homo sapien (3766130-1-61888-64085)

<220>

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 2041

```

Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val Ser Glu Phe Ile Leu
 1           5           10           15

```

Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val Ser Leu Phe Ala Leu
 20 25 30
 Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly Asn Thr Leu Ile Leu
 35 40 45
 Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro Met Tyr Phe Ser
 50 55 60
 Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr Thr Lys Ser Ile Val
 65 70 75 80
 Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg Lys Ser Ile Pro Phe
 85 90 95
 Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser Leu Ala Leu Cys Gly Ser
 100 105 110
 Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Tyr Val Ala Val
 115 120 125
 Cys His Pro Leu His Tyr Thr Val Ile Met His Gly Gly Leu Cys Leu
 130 135 140
 Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe Ser Asn Ser Leu Met
 145 150 155 160
 Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser Arg Phe Ile Asn His
 165 170 175
 Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu Ala Cys Val Asp Val
 180 185 190
 Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly Phe Leu Val Ile Leu
 195 200 205
 Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala Cys Ile Val Ala Thr
 210 215 220
 Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Ala Ser His Leu Ile Val Val Cys Met Cys Phe Gly Ala Thr Ile
 245 250 255
 Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser Ala Glu Glu Glu Lys
 260 265 270
 Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala Ala Val Arg Lys Val
 290 295 300
 Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu Arg Thr Ser Cys Tyr
 305 310 315 320
 Leu Ser Ser Lys Pro Lys Arg Arg
 325

<210> 2042

<211> 311

<212> PRT

<213> Homo sapien (3766130-1-85703-88675)

<400> 2042

Met Glu Leu Glu Asn Gln Thr Arg Val Thr Lys Phe Ile Leu Val Gly
 1 5 10 15
 Phe Pro Gly Ser Leu Ser Met Arg Ala Ala Met Phe Leu Ile Phe Leu
 20 25 30
 Val Ala Tyr Ile Leu Thr Val Ala Glu Asn Val Ile Ile Ile Leu Leu
 35 40 45
 Val Leu Gln Asn Arg Pro Leu His Lys Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Leu Glu Thr Trp Tyr Ile Ser Val Thr Val Pro Lys
 65 70 75 80
 Leu Leu Phe Ser Phe Trp Ser Val Asn Asn Ser Ile Ser Phe Thr Leu
 85 90 95
 Cys Met Ile Gln Leu Tyr Phe Phe Ile Ala Leu Met Cys Thr Glu Cys
 100 105 110

Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Thr Ile Met Ser His Gly Leu Cys Phe Arg Leu
 130 135 140
 Ala Leu Gly Ser Trp Ala Ile Gly Phe Gly Ile Ser Leu Ala Lys Ile
 145 150 155 160
 Tyr Phe Ile Ser Cys Leu Ser Phe Cys Gly Pro Asn Val Ile Asn His
 165 170 175
 Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ser Cys Thr Asp Met
 180 185 190
 Ser Ile Thr Glu Leu Val Asp Phe Ile Leu Ala Leu Val Ile Phe Leu
 195 200 205
 Phe Pro Leu Phe Ile Thr Val Leu Ser Tyr Gly Cys Ile Leu Ala Thr
 210 215 220
 Ile Leu Cys Met Pro Thr Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala
 225 230 235 240
 Ser His Leu Val Val Val Thr Ile Phe Tyr Ser Ala Ile Ile Phe Met
 245 250 255
 Tyr Ala Arg Pro Arg Val Ile His Ala Phe Asn Met Asn Lys Ile Ile
 260 265 270
 Ser Ile Phe Tyr Ala Ile Val Thr Pro Ser Leu Asn Pro Phe Ile Tyr
 275 280 285
 Cys Leu Arg Asn Arg Glu Val Lys Glu Ala Leu Lys Lys Leu Ala Tyr
 290 295 300
 Cys Gln Ala Ser Arg Ser Asp
 305 310

<210> 2043

<211> 216

<212> PRT

<213> Homo sapien (3831602-1-1-649)

<400> 2043

Phe Val Asp Val Cys Asn Ser Thr Thr Ile Thr Pro Lys Met Leu Ala
 1 5 10 15
 Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly Cys Phe Leu
 20 25 30
 Gln Met Tyr Phe Phe Ile Ser Leu Ala Thr Thr Glu Cys Ile Leu Phe
 35 40 45
 Gly Leu Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg Pro Leu Leu
 50 55 60
 Tyr Ser Leu Ile Met Ser Arg Thr Val Tyr Leu Lys Met Ala Ala Gly
 65 70 75 80
 Ala Phe Ala Ala Gly Leu Leu Asn Phe Met Val Asn Thr Ser His Val
 85 90 95
 Ser Ser Leu Ser Phe Cys Asp Ser Asn Val Ile His His Phe Phe Cys
 100 105 110
 Asp Ser Pro Pro Leu Phe Lys Leu Ser Cys Ser Asp Thr Ile Leu Lys
 115 120 125
 Glu Ser Ile Ser Ser Ile Leu Ala Gly Val Asn Ile Val Gly Thr Leu
 130 135 140
 Leu Val Ile Leu Ser Ser Tyr Ser Tyr Val Leu Phe Ser Ile Phe Ser
 145 150 155 160
 Met His Ser Gly Glu Gly Arg His Arg Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Thr Ala Ile Ile Leu Phe Tyr Ala Thr Cys Ile Tyr Thr Tyr
 180 185 190
 Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Gln Asp Lys Val Ala Ser
 195 200 205
 Val Phe Tyr Thr Val Val Ile Pro
 210 215

<210> 2044
 <211> 217
 <212> PRT
 <213> Homo sapien (3831605-1-1-652)

<220>
 <221> VARIANT
 <222> (1)...(217)
 <223> Xaa = Any Amino Acid

<400> 2044
 Leu Pro Asp Ile Gly Phe Thr Ser Ala Thr Val Pro Lys Met Ile Glu
 1 5 10 15
 Glu Met Gln Ser His Ser Arg Val Ile Tyr His Gly Asp Cys Leu Thr
 20 25 30
 Gln Met Ser Phe Phe Val Leu Phe Ala Cys Lys Asp Asp Met Ile Leu
 35 40 45
 Thr Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys His Pro Leu Asn
 50 55 60
 Tyr Pro Gly Ile Met Asn Pro His Leu Cys Val Leu Leu Val Leu Val
 65 70 75 80
 Pro Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Leu Ile Val
 85 90 95
 Leu Gln Phe Ile Cys Phe Lys Asn Val Glu Ile Ser Asn Phe Phe Cys
 100 105 110
 Asp Pro Phe Gln Arg Leu Asn Leu Ala Cys Ser Asp Ser Asp Ile Asn
 115 120 125
 Asn Ile Tyr Ile Tyr Leu Asp Ser Thr Ile Phe Gly Phe Leu Arg Ile
 130 135 140
 Ser Gly Ile Leu Leu Cys Tyr Tyr Thr Val Val Phe Pro Ile Leu Arg
 145 150 155 160
 Ile Pro Ser Ser Asp Gly Asn Tyr Lys Ala Phe Ser Thr Xaa Gly Ser
 165 170 175
 Arg Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly Val Tyr
 180 185 190
 Leu Thr Ser Ala Val Ser Ser Ser Pro Arg Asn Asp Val Val Ala Ser
 195 200 205
 Val Met Tyr Ala Val Val Val Thr Pro
 210 215

<210> 2045
 <211> 214
 <212> PRT
 <213> Homo sapien (3831606-1-1-644)

<400> 2045
 Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1 5 10 15
 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly Cys Leu Thr
 20 25 30
 Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Asn Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His
 50 55 60
 Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu Ser Leu
 65 70 75 80
 Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile Leu Leu Met
 85 90 95
 Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr Leu Phe Cys
 100 105 110

Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile His Val Asn
 115 120 125
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Leu
 130 135 140
 Gly Phe Met Ile Thr Ser Asn Ala Arg Ile Val Arg Ala Ile Leu Gln
 145 150 155 160
 Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly Met Val Tyr
 180 185 190
 Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met His Ala Val Val Thr
 210

<210> 2046

<211> 278

<212> PRT

<213> Homo sapien (3831610-1-1-984)

<400> 2046

Met Ala Ile Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe Phe
 1 5 10 15
 Leu Ala Asn Met Ser Phe Leu Glu Ile Trp Tyr Val Thr Val Thr Ile
 20 25 30
 Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly Gln
 35 40 45
 Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu Gly
 50 55 60
 Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Asn Asp Arg
 65 70 75 80
 Tyr Met Ala Ile Cys Tyr Leu Leu His Asn Pro Val Ile Val Ser Gly
 85 90 95
 Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe Gly
 100 105 110
 Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Asn Gly Gly
 115 120 125
 Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu Asn
 130 135 140
 Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile Leu
 145 150 155 160
 Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser Tyr
 165 170 175
 Val Ala Ile Thr Gly Ala Val Met His Ile Pro Ser Ala Ala Gly Arg
 180 185 190
 Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Phe Asn Val Val Ile Ile
 195 200 205
 Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu Ser
 210 215 220
 Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile Val
 225 230 235 240
 Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val Lys
 245 250 255
 Arg Ala Leu Cys Ile Leu His Leu Tyr Gln His Gln Asp Pro Asp
 260 265 270
 Pro Lys Lys Gly Ser Arg
 275

<210> 2047

<211> 227

<212> PRT

<213> Homo sapien (3831615-1-1-684)

<400> 2047

```

Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro Lys Met Leu
 1           5           10           15
Gly Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe Leu Gly Cys Ala
          20           25           30
Thr Gln Met Tyr Phe Phe Phe Phe Gly Val Ala Glu Cys Phe Leu
          35           40           45
Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu
          50           55           60
His Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Ala
65           70           75           80
Ala Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val Gln Thr Thr Trp
          85           90           95
Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val Asn His Phe Phe
          100          105          110
Cys Asp Ser Pro Pro Val Leu Lys Leu Val Cys Ala Asp Thr Ala Leu
          115          120          125
Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Val Met Ile Pro
          130          135          140
Cys Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ala Ile Leu
145           150           155           160
Lys Ile Pro Ser Ala Lys Gly Lys His Lys Ala Phe Ser Thr Cys Ser
          165          170          175
Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser Leu Ser Leu Thr
          180          185          190
Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly Lys Lys Leu Leu
          195          200          205
Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Phe His Leu
          210          215          220
Leu Ser Trp
225

```

<210> 2048

<211> 217

<212> PRT

<213> Homo sapien (3831618-1-1-653)

<400> 2048

```

Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu
 1           5           10           15
Val His Leu Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu Cys Ala
          20           25           30
Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys Ala Leu
          35           40           45
Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu
          50           55           60
Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr
65           70           75           80
Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe
          85           90           95
Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Phe
          100          105          110
Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala
          115          120          125
Ser Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro
          130          135          140
Val Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val
145           150           155           160
Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly

```

165 170 175
 Ser His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr
 180 185 190
 Tyr Met Thr Pro Lys Ser Ser Lys Gln Gln Glu Lys Ser Val Ser Val
 195 200 205
 Phe Tyr Ala Ile Val Thr Pro Met Leu
 210 215

<210> 2049

<211> 279

<212> PRT

<213> Homo sapien (3834584-1-78858-80128)

<400> 2049

Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile
 1 5 10 15
 Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 20 25 30
 Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu
 35 40 45
 Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu
 50 55 60
 Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu
 65 70 75 80
 Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu
 85 90 95
 His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Thr
 100 105 110
 Gly Ser Trp Val Val Ala Asn Ser Ser Ala Leu Leu His Thr Leu Leu
 115 120 125
 Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His Ile Phe
 130 135 140
 Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu
 145 150 155 160
 Ser Glu Val Met Ile Leu Thr Glu Ala Ala Leu Val Thr Ile Thr Pro
 165 170 175
 Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr Cys Val Val Leu
 180 185 190
 Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly
 195 200 205
 Ser His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr Ile Met Ser Pro
 210 215 220
 Tyr Phe Arg Thr Ser Ser His Ser Ala Gln Arg Asp Ile Ala Ala
 225 230 235 240
 Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn Pro Leu Ile Tyr
 245 250 255
 Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val Lys Val Val Ala
 260 265 270
 Val Lys Phe Phe Ser Val Gln
 275

<210> 2050

<211> 310

<212> PRT

<213> Homo sapien (3924656-1-75882-77814)

<400> 2050

Met Glu Pro Gln Asn Thr Thr Gln Val Ser Met Phe Val Leu Leu Gly
 1 5 10 15
 Phe Ser Gln Thr Gln Glu Leu Gln Lys Phe Leu Phe Leu Leu Phe Leu
 20 25 30

Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Ile Met Val Thr
 35 40 45
 Val Thr Phe Asp Cys Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50 55 60
 Asn Leu Ala Leu Ile Asp Leu Cys Tyr Ser Thr Val Thr Ser Pro Lys
 65 70 75 80
 Met Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly
 85 90 95
 Cys Met Ala Gln Ile Phe Phe Phe His Leu Leu Gly Gly Gly Thr Val
 100 105 110
 Phe Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln
 115 120 125
 Pro Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu
 130 135 140
 Val Val Ala Ala Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu
 145 150 155 160
 Ala Leu Ile Leu Pro Leu Pro Phe Cys Gly Pro Asn Ile Leu Asp Asn
 165 170 175
 Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Leu Leu Glu Phe Leu Met Ile Ser Asn Ser Gly Leu Leu Val Ile
 195 200 205
 Ile Trp Phe Leu Leu Leu Leu Ile Ser Tyr Thr Val Ile Leu Val Met
 210 215 220
 Leu Arg Ser His Ser Gly Lys Ala Arg Arg Lys Ala Ala Ser Thr Cys
 225 230 235 240
 Thr Thr His Ile Ile Val Val Ser Met Ile Phe Ile Pro Cys Ile Tyr
 245 250 255
 Ile Tyr Thr Trp Pro Phe Thr Pro Phe Leu Met Asp Lys Ala Val Ser
 260 265 270
 Ile Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Asp Met Lys Ala Ala Met Arg Arg Leu Gly Lys Cys
 290 295 300
 Leu Val Ile Cys Arg Glu
 305 310

<210> 2051

<211> 123

<212> PRT

<213> Homo sapien (3962498-1-83664-84695)

<400> 2051

Met Ser Gly Ser Pro Thr Gln Leu Thr Ala Gly Pro Arg Thr Ala Ser
 1 5 10 15
 Gly Cys Val Ile Met Ile Cys Phe Ala Leu Thr Val Leu Ser Tyr Ile
 20 25 30
 Arg Ile Leu Ala Thr Val Val Gln Ile Arg Ser Ala Ala Ser Arg Arg
 35 40 45
 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Gly Met Val Leu Leu Phe
 50 55 60
 Tyr Gly Thr Gly Ser Ser Thr Tyr Met Arg Pro Thr Thr Arg Tyr Ser
 65 70 75 80
 Pro Leu Glu Gly Arg Leu Ala Ala Val Phe Tyr Ser Ile Leu Ile Pro
 85 90 95
 Thr Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Asp Met Lys Arg
 100 105 110
 Ala Leu Trp Lys Leu Tyr Leu Gln Val Pro Tyr
 115 120

<210> 2052

<211> 343
 <212> PRT
 <213> Homo sapien (3970959-1-83329-85626)

<220>
 <221> VARIANT
 <222> (1)...(343)
 <223> Xaa = Any Amino Acid

<400> 2052

```

Met Val Asn Gln Ser Ser Ala Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1          5          10          15
Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
      20          25          30
Tyr Leu Leu Thr Leu Gly Gly Leu Ile Ile Leu Leu Ser Val Leu Asp
 35          40          45
Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe
 50          55          60
Leu Asp Leu Cys Phe Thr Ile Ser Cys Val Pro Gly Met Leu Val Asn
 65          70          75          80
Leu Trp Glu Pro Lys Lys Thr Ile Ile Leu Leu Gly Cys Ser Val Gln
      85          90          95
Phe Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr
      100          105          110
Val Met Ala Phe Asp Arg Tyr Met Ala Ile Phe Lys Pro Leu Arg His
      115          120          125
Ala Thr Ile Val His Leu Cys Leu Cys Trp Gln Leu Ala Ser Val Ala
      130          135          140
Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser Thr Leu
      145          150          155          160
Arg Leu Pro Phe Cys Pro His Gln Gln Val Asp Asp Phe Val Cys Glu
      165          170          175
Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr Asn Glu
      180          185          190
Ile Gln Met Ala Val Ala Ser Val Phe Ile Leu Ala Val Pro Ser Leu
      195          200          205
Ile Leu Val Ser Tyr Gly Ala Ile Ala Trp Ala Val Leu Arg Ile Thr
      210          215          220
Ala Lys Gly Gln Arg Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr
      225          230          235          240
Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro
      245          250          255
Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr
      260          265          270
Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275          280          285
Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Ala Lys Glu Met Gly
      290          295          300
Leu Ile Gln Ser Xaa Gly Arg Ala Val Xaa Cys Ala Phe Xaa Ile Lys
      305          310          315          320
Lys Lys Leu Phe Ile Leu Leu Xaa Thr Ser Leu Ser Ser Gln Val Tyr
      325          330          335
Tyr Leu Ser Tyr Thr His His
      340

```

<210> 2053
 <211> 312
 <212> PRT
 <213> Homo sapien (3982606-1-1-939)

<400> 2053

```

Met Asp Gly Val Asn Asp Ser Ser Leu Gln Gly Phe Val Leu Met Ser
1      5      10      15
Ile Ser Asp His Pro Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu
20     25     30
Phe Ser Tyr Leu Leu Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu
35     40     45
Ser Arg Leu Glu Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50     55     60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln
65     70     75     80
Met Leu Ile Asn Leu Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly
85     90     95
Cys Ile Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
100    105    110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
115    120    125
Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu
130    135    140
Ala Val Ile Ala Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
145    150    155    160
Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly
165    170    175
Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr
180    185    190
Ser Leu Asn Gln Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala
195    200    205
Val Pro Leu Ser Ile Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala
210    215    220
Val Leu Lys Ile His Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr
225    230    235    240
Cys Leu Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser
245    250    255
Tyr Gly Tyr Leu Leu Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys
260    265    270
Phe Ile Ser Leu Phe Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu
275    280    285
Ile Tyr Thr Leu Arg Asn Met Glu Val Lys Gly Ala Leu Arg Arg Leu
290    295    300
Leu Gly Lys Gly Arg Glu Val Gly
305    310

```

<210> 2054

<211> 104

<212> PRT

<213> Homo sapien (3983513-1-17888-18909)

<220>

<221> VARIANT

<222> (1)...(104)

<223> Xaa = Any Amino Acid

<400> 2054

```

Val Pro Val Arg Cys Pro Gly Arg Val Arg Thr Leu Val Pro Glu Ile
1      5      10      15
Ile Ser Val Asp Phe Pro Xaa Xaa Thr Leu Ile Xaa Gln Glu Val Tyr
20     25     30
Gly Leu Leu Ser Thr Phe Pro Leu Phe Ala Gln Gly Val Cys Gly Pro
35     40     45
Lys Ile Ile Ser Lys Ala Phe Cys Phe Ser Leu Leu Lys Gly Gly Cys
50     55     60
Ser His Ser Leu Gln Leu Ala Lys Gly Gly Gly Val Leu Arg Lys Ala

```

65 70 75 80
Gly Thr Leu Gly Met Leu Lys Val Ala Ser Val Cys Cys Ala Tyr His
 85 90 95
Leu Leu Leu Val Leu Leu Ser Pro
 100

```
<210> 2055
<211> 210
<212> PRT
<213> Homo sapien (4156137-1-118865-120877)
```

```
<220>
<221> VARIANT
<222> (1)...(210)
<223> Xaa = Any Amino Acid
```

<400>	2055
Ser Val Lys Tyr Leu Asn Glu Ser Phe Pro Glu Asp Phe Ile Leu Met 1 5 10 15	
Gly Phe Val Lys Tyr Pro Trp Leu Asp Phe Leu Leu Phe Cys Val Leu 20 25 30	
Leu Thr Phe Tyr Met Phe Thr Leu Gly Asn Ser Ala Ile Ile Leu 35 40 45	
Val Ser Gln Leu Asp Ser Gln Leu His Ser Pro Met Tyr Phe Leu Leu 50 55 60	
Thr Ser Leu Ser Val Leu Tyr Leu Cys Phe Thr Thr Thr Thr Val Pro 65 70 75 80	
Gln Met Leu Phe Asn Leu Gly Gly Thr Asn Lys Asn Ile Thr Xaa Ile 85 90 95	
Gly Cys Met Ala Gln Ala Tyr Val Phe His Trp Leu Ala Cys Thr Glu 100 105 110	
Cys Val Leu Leu Gly Ile Val Ala Leu Asp Cys Tyr Val Ala Val Cys 115 120 125	
Lys Pro Pro Arg Tyr Thr Ile Ile Ile Asp His Lys Val Tyr Leu His 130 135 140	
Leu Ser Ser Thr Ala Trp Leu Ile Gly Leu Ala Asn Ser Leu Leu Gln 145 150 155 160	
Ser Thr Ile Thr Ile Gln Leu Pro Leu Xaa Arg Cys Ile Ala Gln Ile 165 170 175	
Phe Leu Xaa Leu Glu Ser Val Thr Xaa Gln Ser Leu Thr Val Thr Tyr 180 185 190	
Leu Xaa Asp Leu Leu Gln His Ser Ile Xaa Gly Gln Leu His Ala Gly 195 200 205	
Glu Leu 210	

```
<210> 2056
<211> 310
<212> PRT
<213> Homo sapien (4156187-1-109107-111440)
```

```

<400> 2056
Met Gly Asp Asn Ile Thr Ser Ile Thr Glu Phe Leu Leu Leu Gly Phe
 1           5           10           15
Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
 20           25           30
Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
 35           40           45
Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
 50           55           60
Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met

```

```

65          70          75          80
Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
      85          90          95
Met Met Gln Thr Phe Leu Ph Ser Thr Phe Ala Val Thr Glu Cys Leu
      100         105         110
Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
      115         120         125
Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
      130         135         140
Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val
      145         150         155         160
Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
      165         170         175
Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
      180         185         190
Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
      195         200         205
Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
      210         215         220
Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Cys Thr Cys
      225         230         235         240
Phe Ser His Leu Cys Val Ile Gly Leu Phe Tyr Gly Thr Ala Ile Ile
      245         250         255
Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
      260         265         270
Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
      275         280         285
Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu
      290         295         300
Gly Val Glu Arg Ala Leu
305          310

```

<210> 2057

<211> 127

<212> PRT

<213> Homo sapien (4156187-1-27673-28734)

<220>

<221> VARIANT

<222> (1)...(127)

<223> Xaa = Any Amino Acid

<400> 2057

```

Met Gly Gly Lys Gln Pro Trp Val Thr Glu Phe Ile Leu Val Gly Phe
1          5          10          15
Gln Leu Cys Ala Glu Met Glu Ile Phe Leu Ser Cys Ile Phe Ser Arg
      20          25          30
Phe Tyr Ala Phe Ser Leu Leu Arg Asn Gly Met Asn Met Gly Leu Thr
      35          40          45
Tyr Leu Asp Asp Arg Asp Asp Arg Leu His Thr Leu Ile Tyr Ile Phe
      50          55          60
Leu Ser His Leu Ala Ile Asn Asp Met Tyr Tyr Ala Ser Asn Asn Val
      65          70          75          80
Pro Lys Arg Gln Val Asn Gln Met Asn Gln Lys Lys Lys Tyr Phe Val
      85          90          95
Leu Trp Ile Lys Gln Ile Phe Leu Tyr Leu Ala Phe Ala His Thr Glu
      100         105         110
Cys Leu Ile Xaa Ala Met Met Ser Cys Asn Arg Tyr Val Ala Ile
      115         120         125

```

<210> 2058

<211> 312
 <212> PRT
 <213> Homo sapien (4156187-1-8673-10070)

<220>
 <221> VARIANT
 <222> (1)...(312)
 <223> Xaa = Any Amino Acid

<400> 2058
 Met Gly Asp Asn Gln Ser Arg Val Thr Glu Phe Ile Leu Val Gly Phe
 1 5 10 15
 Gln Leu Ser Val Glu Met Glu Val Leu Leu Phe Trp Ile Phe Ser Leu
 20 25 30
 Leu Tyr Leu Phe Ser Leu Leu Ala Asn Gly Met Ile Leu Gly Leu Ile
 35 40 45
 Cys Leu Asp Pro Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Ser His
 50 55 60
 Leu Ala Val Ile Asp Ile Tyr Tyr Ala Ser Ser Asn Leu Leu Asn Met
 65 70 75 80
 Leu Glu Asn Leu Val Lys His Lys Lys Asn Tyr Pro Phe Ile Ser Cys
 85 90 95
 Ile Met Gln Met Ala Leu Tyr Leu Thr Phe Ala Ala Ala Val Cys Met
 100 105 110
 Ile Leu Val Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro
 115 120 125
 Leu His Tyr Thr Val Ile Met Asn Trp Arg Val Cys Thr Val Leu Ala
 130 135 140
 Ile Thr Ser Trp Ala Cys Gly Phe Ser Leu Ala Leu Ile Asn Leu Ile
 145 150 155 160
 Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Gln Glu Val Asn His Phe
 165 170 175
 Phe Gly Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp
 180 185 190
 Ile Asn Glu Ile Phe Val Phe Ala Gly Gly Val Phe Val Leu Val Gly
 195 200 205
 Pro Leu Ser Leu Met Leu Ile Ser Tyr Met Arg Ile Leu Leu Ala Ile
 210 215 220
 Leu Lys Ile Gln Ser Lys Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Cys Val Val Gly Leu Tyr Phe Gly Met Ala Met Val
 245 250 255
 Val Tyr Leu Val Pro Asp Asn Ser Gln Arg Gln Lys Gln Gln Lys Ile
 260 265 270
 Leu Thr Leu Phe Tyr Ser Leu Phe Asn Pro Leu Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Ala Gln Val Lys Gly Ala Leu Tyr Arg Ala Leu
 290 295 300
 Gln Lys Lys Arg Thr Met Xaa Met
 305 310

<210> 2059
 <211> 315
 <212> PRT
 <213> Homo sapien (4160227-1-768-2100)

<220>
 <221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 2059

```

Met Pro Leu Thr Asn Glu Ser His Pro Glu Glu Phe Ile Leu Leu Gly
 1           5           10           15
Phe Ala Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe Thr Ser Leu Leu
      20           25           30
Ile Met Tyr Pro Ile Ala Val Met Gly Asn Ile Thr Ile Ile Leu Met
      35           40           45
Ser Arg Leu Asp Ser Arg Leu His Ser Pro Met Tyr Phe Phe Leu Thr
      50           55           60
Asn Leu Ser Phe Leu Asp Met Cys Tyr Thr Thr Ser Ile Val Pro Gln
      65           70           75           80
Met Leu Phe Asn Leu Gly Ser Ser Lys Lys Thr Ile Ser Tyr Met Gly
      85           90           95
Cys Ala Val Gln Leu Tyr Phe Phe His Ile Met Gly Gly Thr Glu Cys
      100          105          110
Leu Leu Leu Ala Ile Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Arg
      115          120          125
Pro Leu His Tyr Thr Leu Ile Met Asn Gln Arg Val Cys Ile His Xaa
      130          135          140
Phe Pro Pro Cys Trp Leu Ile Gly Ile Ile Tyr Ala Val Ser Glu Ala
      145          150          155          160
Thr Ala Thr Leu Gln Leu Pro Leu Cys Gly Ser Asn Lys Leu Asp His
      165          170          175
Leu Val Cys Glu Ile Pro Val Leu Ile Lys Ile Ala Cys Gly Glu Lys
      180          185          190
Gly Ser Asn Glu Leu Thr Leu Ser Val Val Cys Ile Phe Met Leu Ala
      195          200          205
Val Pro Leu Cys Leu Ile Leu Ala Ser Tyr Ala Ser Ile Gly Ser Ala
      210          215          220
Val Phe Lys Ile Lys Ser Ser Lys Gly Arg Lys Lys Ala Phe Gly Thr
      225          230          235          240
Cys Ser Ser His Leu Ile Val Val Phe Leu Phe Tyr Gly Pro Ala Ile
      245          250          255
Ser Met Tyr Leu Gln Pro Pro Ser Ser Ile Ser Arg Asp Gln Pro Lys
      260          265          270
Phe Met Ala Leu Phe Tyr Gly Val Val Thr Pro Ser Leu Asn Pro Phe
      275          280          285
Ile Tyr Thr Leu Arg Asn Lys Asn Val Lys Gly Ala Leu Arg Asn Leu
      290          295          300
Val Arg Ser Ile Phe Ser Phe Lys Xaa Xaa Trp
      305          310          315

```

<210> 2060

<211> 311

<212> PRT

<213> Homo sapien (4190944-1-137143-138613)

<400> 2060

```

Met Glu Ile Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile Leu Leu
 1           5           10           15
Gly Leu Ser Ser Asn Pro Gln Leu Gln Lys Pro Leu Phe Ala Ile Phe
      20           25           30
Leu Ile Met Tyr Leu Leu Ala Ala Val Gly Asn Val Leu Ile Ile Pro
      35           40           45
Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu
      50           55           60
Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro
      65           70           75           80
Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val
      85           90           95
Gly Cys Leu Ala Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp

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```

      100      105      110
Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys
      115      120      125
Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Arg His Cys Leu Leu
      130      135      140
Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg
      145      150      155      160
Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys
      165      170      175
His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp
      180      185      190
Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile
      195      200      205
Val Thr Pro Phe Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Met Val
      210      215      220
Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser
      225      230      235      240
Thr Cys Gly Ser His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile
      245      250      255
Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp
      260      265      270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275      280      285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Lys Lys
      290      295      300
Leu Gln Asp Arg Ile Tyr Arg
      305      310

```

<210> 2061

<211> 145

<212> PRT

<213> Homo sapien (4190944-1-141327-142434)

<220>

<221> VARIANT

<222> (1)...(145)

<223> Xaa = Any Amino Acid

<400> 2061

```

Met Thr Thr Pro Phe Asn Ser Ser Leu Ile Met Phe Ser Leu Leu Asp
  1      5      10      15
Ser Ser Met Pro Glu Ile Leu Cys Pro Leu Pro Tyr Phe Phe Leu Gly
      20      25      30
Ser His Ala Thr His Ser Ser Xaa Leu Ser Ser Leu Thr Leu Ile Asn
      35      40      45
Arg Xaa Asn Met Phe Ser Glu Leu Asn Ser Pro Tyr Phe Ser Ile Glu
      50      55      60
Leu Asn Leu Lys Tyr Leu Tyr Ile Cys Asn Lys Leu Thr Leu Glu Lys
      65      70      75      80
Pro Asn Thr Phe Phe Xaa Thr Phe Cys Val Leu Ser Thr Asn Glu Arg
      85      90      95
Pro Met Val Leu Phe Leu Tyr Cys Ile Gln Pro Ala Phe Trp Ile Pro
      100      105      110
Ile Trp Xaa Asn Lys Glu Leu Ala Arg Arg Phe Leu Val Tyr Ser Gln
      115      120      125
Gly Leu Cys Ser Ser Ile Xaa Asp Asn Val Thr Arg Cys Pro Glu Ala
      130      135      140
Cys
      145

```

<210> 2062

<211> 318

<212> PRT

<213> Homo sapien (4190944-1-15386-17112)

<400> 2062

```

Met Met Ser Phe Ala Pro Asn Ala Ser His Ser Pro Val Phe Leu Leu
 1          5          10          15
Leu Gly Phe Ser Arg Ala Asn Ile Ser Tyr Thr Leu Leu Phe Phe Leu
          20          25          30
Phe Leu Ala Ile Tyr Leu Thr Thr Ile Leu Gly Asn Val Thr Leu Val
          35          40          45
Leu Leu Ile Ser Trp Asp Ser Arg Leu His Ser Pro Met Tyr Tyr Leu
          50          55          60
Leu Arg Gly Leu Ser Val Ile Asp Met Gly Leu Ser Thr Val Thr Leu
          65          70          75          80
Pro Gln Leu Leu Ala His Leu Val Ser His Tyr Pro Thr Ile Pro Ala
          85          90          95
Ala Arg Cys Leu Ala Gln Phe Phe Phe Phe Tyr Ala Phe Gly Val Thr
          100          105          110
Asp Thr Leu Val Ile Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Asp Pro Leu His Tyr Ala Leu Val Met Asn His Gln Arg Cys Ala
          130          135          140
Cys Leu Leu Ala Leu Ser Trp Val Val Ser Ile Leu His Thr Met Leu
          145          150          155          160
Arg Val Gly Leu Val Leu Pro Leu Cys Trp Thr Gly Asp Ala Gly Gly
          165          170          175
Asn Val Asn Leu Pro His Phe Phe Cys Asp His Arg Pro Leu Leu Arg
          180          185          190
Ala Ser Cys Ser Asp Ile His Ser Asn Glu Leu Ala Ile Phe Phe Glu
          195          200          205
Gly Gly Phe Leu Met Leu Gly Pro Cys Ala Leu Ile Val Leu Ser Tyr
          210          215          220
Val Arg Ile Gly Ala Ala Ile Leu Arg Leu Pro Ser Ala Ala Gly Arg
          225          230          235          240
Arg Arg Ala Val Ser Thr Cys Gly Ser His Leu Thr Met Val Gly Phe
          245          250          255
Leu Tyr Gly Thr Ile Ile Cys Val Tyr Phe Gln Pro Pro Phe Gln Asn
          260          265          270
Ser Gln Tyr Gln Asp Met Val Ala Ser Val Met Tyr Thr Ala Ile Thr
          275          280          285
Pro Leu Ala Asn Pro Phe Val Tyr Ser Leu His Asn Lys Asp Val Lys
          290          295          300
Gly Ala Leu Cys Arg Leu Leu Glu Trp Val Lys Val Asp Pro
          305          310          315

```

<210> 2063

<211> 317

<212> PRT

<213> Homo sapien (4190944-1-176262-177597)

<400> 2063

```

Met Asn Ser Glu Asn Leu Thr Arg Ala Ala Val Ala Pro Ala Glu Phe
 1          5          10          15
Val Leu Leu Gly Ile Thr Asn Arg Trp Asp Leu Arg Val Ala Leu Phe
          20          25          30
Leu Thr Cys Leu Pro Val Tyr Leu Val Ser Leu Leu Gly Asn Met Gly
          35          40          45
Met Ala Leu Leu Ile Arg Met Asp Ala Arg Leu His Thr Pro Met Tyr
          50          55          60
Phe Phe Leu Ala Asn Leu Ser Leu Leu Asp Ala Cys Tyr Ser Ser Ala

```

```

65          70          75          80
Ile Gly Pro Lys Met Leu Val Asp Leu Leu Leu Pro Arg Ala Thr Ile
      85          90          95
Pro Tyr Thr Ala Cys Ala Leu Gln Met Phe Val Phe Ala Gly Leu Ala
      100        105        110
Asp Thr Glu Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
      115        120        125
Ala Ile Arg Asn Pro Leu Leu Tyr Thr Thr Ala Met Ser Gln Arg Leu
      130        135        140
Cys Leu Ala Leu Leu Gly Ala Ser Gly Leu Gly Gly Ala Val Ser Ala
145          150        155        160
Phe Val His Thr Thr Leu Thr Phe Arg Leu Ser Phe Cys Arg Ser Arg
      165        170        175
Lys Ile Asn Ser Phe Phe Cys Asp Ile Pro Pro Leu Leu Ala Ile Ser
      180        185        190
Cys Ser Asp Thr Ser Leu Asn Glu Leu Leu Leu Phe Ala Ile Cys Gly
      195        200        205
Phe Ile Gln Thr Ala Thr Val Leu Ala Ile Thr Val Ser Tyr Gly Phe
      210        215        220
Ile Ala Gly Ala Val Ile His Met Arg Ser Val Glu Gly Ser Arg Arg
225          230        235        240
Ala Ala Ser Thr Gly Gly Ser His Leu Thr Ala Val Ala Met Met Tyr
      245        250        255
Gly Thr Leu Ile Phe Met Tyr Leu Arg Pro Ser Ser Ser Tyr Ala Leu
      260        265        270
Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Ser
      275        280        285
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala
      290        295        300
Leu Arg Gln Thr Trp Ser Arg Phe His Cys Pro Gly Gln
305          310        315

```

<210> 2064

<211> 314

<212> PRT

<213> Homo sapien (4190944-1-2029-4183)

<400> 2064

```

Met Asp Asn Ser Asn Trp Thr Ser Val Ser His Phe Val Leu Leu Gly
1          5          10          15
Ile Ser Thr His Pro Glu Glu Gln Ile Pro Leu Phe Leu Val Phe Ser
      20          25          30
Leu Met Tyr Ala Ile Asn Ile Ser Gly Asn Leu Ala Ile Ile Thr Leu
      35          40          45
Ile Leu Ser Ala Pro Arg Leu His Ile Pro Met Tyr Ile Phe Leu Ser
      50          55          60
Asn Leu Ala Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys
65          70          75          80
Met Leu Gln Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr Thr Gly
      85          90          95
Cys Leu Ala Gln Thr Tyr Phe Phe Ile Cys Phe Ala Val Met Glu Asn
      100        105        110
Phe Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His
      115        120        125
Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val Lys Met
      130        135        140
Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu His Thr
145          150        155        160
Phe Leu Ile Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile Pro His
      165        170        175
Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr Ser Thr

```

180 185 190
 Tyr Leu Asn Thr Leu Met Ile His Thr Glu Gly Ala Val Val Ile Ser
 195 200 205
 Gly Ala Leu Ala Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile Leu Val
 210 215 220
 Val Leu Arg Ile Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly Thr Leu Ser
 245 250 255
 Trp Val Tyr Phe Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys Gly Arg
 260 265 270
 Ile Ile Thr Val Val Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gly Asp Val Lys Gly Gly Phe Met Lys Trp
 290 295 300
 Met Ser Arg Met Gln Thr Phe Phe Phe Arg
 305 310

<210> 2065

<211> 216

<212> PRT

<213> Homo sapien (438406-1-1-648)

<400> 2065

Val Leu Asp Val Gly Cys Ile Thr Val Thr Val Pro Ala Met Leu Gly
 1 5 10 15
 Arg Leu Leu Ser His Lys Ser Thr Ile Ser Tyr Asp Ala Cys Leu Ser
 20 25 30
 Gln Leu Phe Phe Phe His Leu Leu Ala Gly Met Asp Cys Phe Leu Leu
 35 40 45
 Thr Ala Met Ala Tyr Asp Arg Leu Leu Gly Ile Cys Gln Ala Leu Thr
 50 55 60
 Tyr Arg Thr Arg Met Ser Gln Thr Val Gln Arg Met Leu Val Ala Ala
 65 70 75 80
 Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu Thr His Thr Val Gly Met
 85 90 95
 Ser Thr Leu Asn Phe Cys Gly Pro Asn Val Ile Asn His Phe Tyr Cys
 100 105 110
 Asp Leu Pro Gln Leu Phe Lys Leu Ser Cys Ser Ser Thr Gln Leu Asn
 115 120 125
 Glu Leu Leu Leu Phe Ala Val Gly Phe Ile Met Ala Gly Thr Pro Met
 130 135 140
 Ala Leu Ile Val Ile Ser Tyr Ile His Val Ala Ala Val Leu Arg
 145 150 155 160
 Ile Arg Ser Val Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Ala Ile Phe Tyr Gly Ser Gly Ile Phe Asn Tyr
 180 185 190
 Met Arg Leu Gly Ser Thr Lys Leu Ser Asp Lys Asp Lys Ala Val Gly
 195 200 205
 Ile Phe Asn Thr Val Ile Asn Pro
 210 215

<210> 2066

<211> 318

<212> PRT

<213> Homo sapien (4581418-1-11548-14170)

<400> 2066

Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly
 1 5 10 15

Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala
 20 25 30
 Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala
 35 40 45
 Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln
 65 70 75 80
 Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly
 85 90 95
 Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys
 100 105 110
 Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met
 130 135 140
 Ile Ile Met Ile Trp Ser Ile Ser Leu Ala Asn Ser Val Val Leu Cys
 145 150 155 160
 Thr Leu Thr Leu Asn Leu Pro Thr Cys Gly Asn Asn Ile Leu Asp His
 165 170 175
 Phe Leu Cys Glu Leu Pro Ala Leu Val Lys Ile Ala Cys Val Asp Thr
 180 185 190
 Thr Thr Val Glu Met Ser Val Phe Ala Leu Gly Ile Ile Ile Val Leu
 195 200 205
 Thr Pro Leu Ile Leu Ile Leu Ile Ser Tyr Gly Tyr Ile Ala Lys Ala
 210 215 220
 Val Leu Arg Thr Lys Ser Lys Ala Ser Gln Arg Lys Ala Met Asn Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Ser Met Phe Tyr Gly Thr Ile Ile
 245 250 255
 Tyr Met Tyr Leu Gln Pro Gly Asn Arg Ala Ser Lys Asp Gln Gly Lys
 260 265 270
 Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Leu
 290 295 300
 Met Arg Phe His His Lys Ser Thr Lys Ile Lys Arg Asn Cys
 305 310 315

<210> 2067

<211> 257

<212> PRT

<213> Homo sapien (4581418-1-39007-42459)

<220>

<221> VARIANT

<222> (1)...(257)

<223> Xaa = Any Amino Acid

<400> 2067

Phe Ile Leu Trp Gly Phe Phe Asp His Pro Xaa Pro Glu Met Phe Leu
 1 5 10 15
 Phe Ile Met Gly Leu Val Gly Leu Ser Leu His Thr Gly Gly Gln His
 20 25 30
 Leu Asn Tyr Cys Gly Thr Gln Gly Ile Phe Xaa Gly Ser Thr Lys Cys
 35 40 45
 Ile Ile Leu Ala Val Thr Ser Leu Asp Pro Tyr Ile Ala Ile Cys Lys
 50 55 60
 His Leu Arg Tyr Pro Ala Ile Met His Gln Gln Leu Cys Val Leu Leu
 65 70 75 80
 Val Ala Met Ala Trp Leu Ser Ser Leu Ala Asn Ser Leu Gln Ser Ser

[illegible]

```
<210> 2068
<211> 309
<212> PRT
<213> Homo sapien (5081803-1-1-930)
```

<400> 2068																
Met	Lys	Lys	Glu	Asn	Gln	Ser	Phe	Asn	Leu	Asp	Phe	Ile	Leu	Leu	Gly	
1				5					10					15		
Val	Thr	Ser	Gln	Gln	Glu	Gln	Asn	Asn	Val	Phe	Phe	Val	Ile	Phe	Leu	
			20					25					30			
Cys	Ile	Tyr	Pro	Ile	Thr	Leu	Thr	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala	
		35					40					45				
Ile	Cys	Ala	Asp	Ile	Arg	Leu	His	Asn	Pro	Met	Tyr	Phe	Leu	Leu	Ala	
		50				55					60					
Asn	Leu	Ser	Leu	Val	Asp	Ile	Ile	Phe	Ser	Ser	Val	Thr	Ile	Pro	Lys	
65					70					75					80	
Val	Leu	Ala	Asn	His	Leu	Leu	Gly	Ser	Lys	Phe	Ile	Ser	Phe	Gly	Gly	
				85					90					95		
Cys	Leu	Met	Gln	Met	Tyr	Phe	Met	Ile	Ala	Leu	Ala	Lys	Ala	Asp	Ser	
			100					105					110			
Tyr	Thr	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Ala	Val	Ala	Ile	Ser	Cys	
		115					120					125				
Pro	Leu	His	Tyr	Thr	Thr	Ile	Met	Ser	Pro	Arg	Ser	Cys	Ile	Leu	Leu	
	130					135					140					
Ile	Ala	Gly	Ser	Trp	Val	Ile	Gly	Asn	Thr	Ser	Ala	Leu	Pro	His	Thr	
145					150					155					160	
Leu	Leu	Thr	Ala	Ser	Leu	Ser	Phe	Cys	Gly	Asn	Gln	Glu	Val	Ala	Asn	
				165					170					175		
Phe	Tyr	Cys	Asp	Ile	Met	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Val	
			180					185					190			
His	Phe	Asn	Val	Lys	Met	Met	Tyr	Leu	Gly	Val	Gly	Val	Phe	Ser	Leu	
		195					200					205				
Pro	Leu	Leu	Cys	Ile	Ile	Val	Ser	Tyr	Val	Gln	Val	Phe	Ser	Thr	Val	
		210				215						220				
Phe	Gln	Val	Pro	S	r	Thr	Lys	Ser	Leu	Phe	Lys	Ala	Phe	Cys	Thr	Cys
225						230					235					240
Gly	Ser	His	Leu	Thr	Val	Val	Phe	Leu	Tyr	Tyr	Gly	Thr	Thr	Met	Gly	

```

          245          250          255
Met Tyr Phe Arg Pro Leu Thr Ser Tyr Ser Pro Lys Asp Ala Val Ile
          260          265          270
Thr Val Met Tyr Val Ala Val Thr Pro Ala Leu Asn Pro Phe Ile Tyr
          275          280          285
Ser Leu Arg Asn Trp Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Ser
          290          295          300
Lys Arg Ile Ser Ser
305

```

<210> 2069

<211> 272

<212> PRT

<213> Homo sapien (5262456-1-1-1993)

<400> 2069

```

Met Trp Ile Asn Asn Gln Ser Ser Leu Asp Asp Phe Ile Leu Leu Gly
 1          5          10          15
Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Val Ile Phe Leu Val
          20          25          30
Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val Ser
          35          40          45
His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser Asn
          50          55          60
Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln Met
          65          70          75          80
Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys
          85          90          95
Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile
          100          105          110
Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys Pro
          115          120          125
Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met Ala
          130          135          140
Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser Thr
          145          150          155          160
Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His Phe
          165          170          175
Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile Arg
          180          185          190
Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Met
          195          200          205
Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala Val
          210          215          220
Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr Cys
          225          230          235          240
Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser
          245          250          255
Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys Ile
          260          265          270

```

<210> 2070

<211> 356

<212> PRT

<213> Homo sapien (5262456-1-22068-24947)

<220>

<221> VARIANT

<222> (1)...(356)

<223> Xaa = Any Amino Acid

<400> 2070

```

Met Ile Asn Asp Ser His Phe Ser Gly Phe Ile Leu Leu Gly Phe Thr
 1           5           10           15
Gly Gln Pro Gln Leu Gln Met Met Ile Ser Gly Val Val Phe Phe Phe
          20           25           30
Tyr Thr Ile Ala Phe Met Gly Asn Met Ala Ile Ile Leu Leu Ser Phe
          35           40           45
Leu Asp Asp His Leu Gln Val Pro Met Tyr Phe Phe Leu Arg Asn Leu
          50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
65           70           75           80
Val Ser Ile Trp Gly Lys Asp Lys Arg Ile Thr Phe Gly Gly Cys Ala
          85           90           95
Phe Gln Leu Phe Ile Asp Val Ala Leu Tyr Ser Val Glu Cys Ile Leu
          100          105          110
Leu Ser Met Met Ser Tyr Asp Arg Leu Asn Ala Ile Cys Lys Pro Leu
          115          120          125
His His Met Thr Ile Met Asn Leu Gln Leu Cys Gln Gly Leu Val Val
          130          135          140
Ile Ser Trp Val Val Gly Val Ile Asn Cys Ile Ile Pro Ser Pro Tyr
145          150          155          160
Ala Thr Ser Leu Pro Arg Cys Arg Asn His His Leu Asp His Phe Phe
          165          170          175
Val Cys Val Lys Cys Leu Gln Xaa Ser Arg Phe Lys Ile Ala Cys Val
          180          185          190
Asp Thr Thr Ala Met Glu Val Thr Thr Phe Ala Met Cys Leu Ile Ile
          195          200          205
Val Leu Val Pro Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
          210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
225          230          235          240
Gly Thr Cys Ser Ser His Leu Val Val Val Ser Ile Phe Cys Gly Thr
          245          250          255
Val Thr Tyr Met Tyr Ile Gln Pro Gly Asn Ser Pro Asn Gln Asn Glu
          260          265          270
Gly Lys Leu Leu Ser Ile Phe Tyr Ser Ile Val Thr Pro Ser Leu Asn
          275          280          285
Pro Leu Ile Tyr Thr Val Arg Asn Lys Glu Phe Lys Gly Ala Met Lys
          290          295          300
Arg Leu Thr Gly Lys Glu Lys Asp Cys Met Glu Lys Arg Gly His Xaa
305          310          315          320
Phe Phe Leu Pro Ala Ile Ser Asn Met Ala Ile Asp Leu Pro Asn Leu
          325          330          335
Lys Cys Arg Gln Phe Ile Leu Xaa Ile Asn Cys Leu His Leu Arg Xaa
          340          345          350
Arg Xaa Tyr Pro
          355

```

<210> 2071

<211> 338

<212> PRT

<213> Homo sapien (5679453-1-2929-5456)

<220>

<221> VARIANT

<222> (1)...(338)

<223> Xaa = Any Amino Acid

<400> 2071

```

Met Ile Leu Pro Ala Ser Phe Ser Xaa Gly Thr Met Glu Thr Ser Ser
 1           5           10           15

```

Val Ser Ser Gly Thr Asp Phe Ile Leu Leu Gly Phe Ser Asp Arg Pro
 20 25 30
 Gln Leu Glu His Ile Ile Ser Val Val Val Phe Ile Ile Tyr Ile Val
 35 40 45
 Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val Ser Tyr Leu Asp Thr
 50 55 60
 Gln Leu His Thr Phe Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu
 65 70 75 80
 Asp Leu Cys Tyr Thr Thr Ser Ile Ile Pro Gln Met Leu Ala Asn Gln
 85 90 95
 Trp Gly Pro Lys Lys Ser Ile Thr Tyr Gly Gly Cys Val Leu Gln Phe
 100 105 110
 Phe Phe Val Leu Asp Leu Gly Ala Thr Glu Cys Leu Leu Leu Ala Val
 115 120 125
 Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Gln Pro Leu His Tyr Thr
 130 135 140
 Leu Lys Cys Thr Leu Ser Phe Ala Thr Ala Trp Leu Ser Gly Leu Ala
 145 150 155 160
 Ser Ala Leu Ile Val Cys Ser Leu Thr Leu Lys Leu Pro Arg Cys Gly
 165 170 175
 His Arg Glu Val Asp Asn Phe Phe Cys Glu Met Pro Ala Leu Ile Lys
 180 185 190
 Met Ala Cys Val Tyr Ser Lys Val Ile Glu Ile Val Val Phe Ala Phe
 195 200 205
 Gly Val Val Phe Leu Phe Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr
 210 215 220
 Gly Val Ile Thr Gln Ala Val Met Arg Ile Lys Ser Ala Thr Arg Leu
 225 230 235 240
 Gln Lys Ile Leu Asn Thr Cys Gly Ser His Leu Thr Val Val Ile Leu
 245 250 255
 Phe Tyr Gly Thr Ile Ile Tyr Ile Tyr Met Lys Pro Gln Asn Thr Ile
 260 265 270
 Ser Gln Asp Glu Gly Lys Phe Ser Leu Phe Tyr Thr Ile Ile Thr Pro
 275 280 285
 Ser Leu Asn Leu Pro Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ser
 290 295 300
 Ala Leu Lys Arg Ile Leu Trp Met Lys Lys Ser Ser Ala Glu Xaa Met
 305 310 315 320
 Asn Xaa Met Glu Lys Ser Arg Met Xaa Ser Thr Lys Glu Ile Leu Ala
 325 330 335
 Phe Ile

<210> 2072

<211> 308

<212> PRT

<213> Homo sapien (5791525-1-119325-122054)

<400> 2072

Met Ala Met Asp Asn Val Thr Ala Val Phe Gln Phe Leu Leu Ile Gly
 1 5 10 15
 Ile Ser Asn Tyr Pro Gln Trp Arg Asp Thr Phe Phe Thr Leu Val Leu
 20 25 30
 Ile Ile Tyr Leu Ser Thr Leu Leu Gly Asn Gly Phe Met Ile Phe Leu
 35 40 45
 Ile His Phe Asp Pro Asn Leu His Thr Pro Ile Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Gly Thr Ala Ser Met Pro Gln
 65 70 75 80
 Ala Leu Val His Cys Phe Ser Thr His Pro Tyr Leu Ser Tyr Pro Arg
 85 90 95

Cys Leu Ala Gln Thr Ser Val Ser Leu Ala Leu Ala Thr Ala Glu Cys
 100 105 110
 Leu Leu L u Ala Ala Met Ala Tyr Asp Arg Val Val Ala Ile Ser Asn
 115 120 125
 Pro Leu Arg Tyr Ser Val Val Met Asn Gly Pro Val Cys Val Cys Leu
 130 135 140
 Val Ala Thr Ser Trp Gly Thr Ser Leu Val Leu Thr Ala Met Leu Ile
 145 150 155 160
 Leu Ser Leu Arg Leu His Phe Cys Gly Ala Asn Val Ile Asn His Phe
 165 170 175
 Ala Cys Glu Ile Leu Ser Leu Ile Lys Leu Thr Cys Ser Asp Thr Ser
 180 185 190
 Leu Asn Glu Phe Met Ile Leu Ile Thr Ser Ile Phe Thr Leu Leu Leu
 195 200 205
 Pro Phe Gly Phe Val Leu Leu Ser Tyr Ile Arg Ile Ala Met Ala Ile
 210 215 220
 Ile Arg Ile Arg Ser Leu Gln Gly Arg Leu Lys Ala Phe Thr Thr Cys
 225 230 235 240
 Gly Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Ser Ala Ile Ser
 245 250 255
 Met Tyr Met Lys Thr Gln Ser Lys Ser Tyr Pro Asp Gln Asp Lys Phe
 260 265 270
 Ile Ser Val Phe Tyr Gly Ala Leu Thr Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Lys Lys Asp Val Lys Arg Ala Ile Arg Lys Val Met
 290 295 300
 Leu Lys Arg Thr
 305

<210> 2073

<211> 314

<212> PRT

<213> Homo sapien (5791525-1-456-2065)

<220>

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 2073

Met His Gln Gly Asn Xaa Thr Thr Val Ser Lys Phe Phe Leu Leu Gly
 1 5 10 15
 Ile Thr Thr Lys Pro Lys Glu Gln Gln Phe Ile Phe Met Leu Phe Leu
 20 25 30
 Cys Thr Tyr Leu Val Thr Met Val Arg Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Val Val Ser Asp Ala His Leu His Gly Pro Ile Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asn Val Cys Ile Thr Thr Thr Thr Val Pro Lys
 65 70 75 80
 Ile Leu Ala Asp Ile Gln Ser Gln Asn Ser Thr Ile Ser Phe Glu Gly
 85 90 95
 Cys Pro Ala Gln Met Xaa Phe Xaa Ile Phe Leu Val Asp Leu Asp Asn
 100 105 110
 Phe Leu Leu Val Asp Met Ala Tyr Asn Xaa Tyr Ile Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Thr Val Val Val Leu Ser Pro Lys Asn Cys Ala Leu
 130 135 140
 Leu Val Val Thr Pro Trp Val Ile Ser Asn Leu Val Ser Ile Leu His
 145 150 155 160
 Leu Ser Leu Leu Ser His Leu Thr Phe Cys Ile Ser His Ile Phe Tyr

165 170 175
 Asp Leu Glu Pro Ile Leu Gly Leu Ala Cys Ser Asp Thr Gln Ile Asn
 180 185 190
 Asn Leu Ile Ile Thr Ala Ile Gly Glu Val Val Ile Phe Ile Pro Phe
 195 200 205
 Thr Cys His Ile Leu Val Ser Tyr Gly Leu Ile Gly Ser Thr Met Leu
 210 215 220
 Gly Val Pro Ser Ala Lys Gly Lys Xaa Lys Thr Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Ser Val Val Pro Gln Val Phe Tyr Gly Phe Ile Ile Gly
 245 250 255
 Val Tyr Phe Leu Ser Phe Phe Ala Tyr Ser Ala Glu Arg Asp Glu Val
 260 265 270
 Ala Ala Ile Met Tyr Thr Thr Val Thr His Leu Ile Lys Ser Phe Ile
 275 280 285
 Cys Ser Leu Arg Asn Glu Asp Met Lys Gly Ala Leu Arg Arg Pro Leu
 290 295 300
 Ser Arg Gln Gly Phe Ser Gly Val Val Ser
 305 310

<210> 2074
 <211> 138
 <212> PRT
 <213> Homo sapien (5823349-1-32238-32756)

<220>
 <221> VARIANT
 <222> (1)...(138)
 <223> Xaa = Any Amino Acid

<400> 2074
 Leu Met Leu Leu Asp Leu Leu Ser Asp Ala Glu Val His Ala Val Ser
 1 5 10 15
 Ser Ser His Cys Ser Leu His Leu Thr Lys Glu Ile Phe Ser Ile Val
 20 25 30
 Ser Asn Gln Ala Leu Ser Pro Glu Ser Thr Leu Gly Leu His Met His
 35 40 45
 Leu Cys Ala Phe Leu Thr Leu Phe Pro Leu Pro Arg Thr Pro Leu Pro
 50 55 60
 Ser Phe Leu Ile His Arg Asn Leu Ile His Leu Ser Ser His Ala Gln
 65 70 75 80
 Gln Leu Ser Phe Pro Xaa Leu Leu Xaa Lys Tyr Ser Leu Phe Asn Leu
 85 90 95
 Tyr Val Ile Leu Ser Arg Ile Leu Phe Pro Leu His Pro Leu Val Tyr
 100 105 110
 Glu Gln Phe Lys Ser Gly Cys Tyr Gly Xaa Phe Ile Ile Lys Ile Leu
 115 120 125
 Asn Phe Cys Leu Leu Xaa Val Met Asn Leu
 130 135

<210> 2075
 <211> 162
 <212> PRT
 <213> Homo sapien (5931513-1-1-2929)

<400> 2075
 Met Asn Val Ser Glu Pro Asn Ser Ser Phe Ala Phe Val Asn Glu Phe
 1 5 10 15
 Ile Leu Gln Gly Phe Ser Cys Glu Trp Thr Ile Gln Ile Phe Leu Phe
 20 25 30
 Ser Leu Phe Thr Thr Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala

35 40 45
 Ile Ala Phe Val Leu Trp Cys Asp Arg Arg Leu His Thr Pro Met Tyr
 50 55 60
 Met Phe Leu Gly Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser
 65 70 75 80
 Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser Glu Lys Lys Asn Ile
 85 90 95
 Ser Phe Ala Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
 100 105 110
 Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala Phe Asp Gln Tyr Leu
 115 120 125
 Ala Ile Cys Arg Pro Leu Leu Tyr Pro Asn Ile Met Thr Gly His Leu
 130 135 140
 Tyr Ala Lys Leu Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe
 145 150 155 160
 Leu Ile

<210> 2076

<211> 318

<212> PRT

<213> Homo sapien (6087993-15-1-2211)

<400> 2076

Met Ile Gln Pro Met Ala Ser Pro Ser Asn Ser Ser Thr Val Pro Val
 1 5 10 15
 Ser Glu Phe Leu Thr Cys Phe Pro Asn Phe Gln Ser Trp Gln His
 20 25 30
 Trp Leu Ser Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala
 35 40 45
 Asn Thr Thr Leu Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln
 50 55 60
 Pro Leu Tyr Tyr Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu
 65 70 75 80
 Cys Leu Thr Val Ile Pro Lys Val Leu Ala Ile Phe Trp Tyr Asp Leu
 85 90 95
 Arg Ser Ile Ser Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn
 100 105 110
 Ser Phe Leu Pro Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp
 115 120 125
 Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr
 130 135 140
 Asn Gln Phe Val Ala Lys Ala Ser Val Phe Ile Val Val Arg Asn Ala
 145 150 155 160
 Leu Leu Thr Ala Pro Ile Pro Ile Leu Thr Ser Leu Leu His Tyr Cys
 165 170 175
 Gly Glu Asn Val Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser
 180 185 190
 Arg Leu Ser Cys Asp Asn Phe Thr Leu Asn Arg Ile Tyr Gln Phe Val
 195 200 205
 Ala Gly Trp Thr Leu Leu Gly Ser Asp Leu Phe Leu Ile Phe Leu Ser
 210 215 220
 Tyr Thr Phe Ile Leu Arg Ala Val Leu Arg Phe Lys Ala Glu Gly Ala
 225 230 235 240
 Ala Val Lys Ala Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu
 245 250 255
 Phe Phe Ser Thr Ile Leu Leu Val Val Leu Thr Asn Val Ala Arg
 260 265 270
 Lys Lys Val Pro Met Asp Ile Leu Ile Leu Leu Asn Val Leu His His
 275 280 285
 Leu Ile Pro Pro Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys

290 295 300
 Glu Ile Lys Gln Gly Ile Gln Lys Leu Leu Gln Arg Gly Arg
 305 310 315

<210> 2077

<211> 314

<212> PRT

<213> Homo sapien (6087993-21-1-3660)

<400> 2077

Met Leu Leu Ser Asn Ser Ser Trp Arg Leu Ser Gln Pro Ser Phe Leu
 1 5 10 15
 Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu
 20 25 30
 Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
 35 40 45
 Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
 50 55 60
 Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr
 65 70 75 80
 Ala Pro Lys Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly
 85 90 95
 Tyr Ile Val Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser
 100 105 110
 Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
 130 135 140
 Gly Arg Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile
 145 150 155 160
 Pro Phe Pro Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile
 165 170 175
 Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
 180 185 190
 Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu
 195 200 205
 Val Ile Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
 210 215 220
 Leu Gln Ala Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Val
 245 250 255
 Pro Gly Ile Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
 260 265 270
 His His Val His Val Leu Leu Ala Thr Arg Tyr Leu Leu Met Pro Pro
 275 280 285
 Ala Leu Asn Pro Leu Val Tyr Gly Val Lys Thr Gln Gln Ile Arg Gln
 290 295 300
 Arg Val Leu Arg Val Phe Thr Gln Lys Asp
 305 310

<210> 2078

<211> 327

<212> PRT

<213> Homo sapien (6087993-34-2575-6318)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 2078

Phe Phe Ser Asn Asn Ser Val Leu Phe Pro His Thr Phe Phe Leu Ala
 1 5 10 15
 Gly Ile Pro Gly Leu Thr Ala Thr His Ile Trp Ile Leu Leu Pro Phe
 20 25 30
 Cys Phe Met Phe Phe Leu Ser Leu Thr Gly Asn Gly Val Leu Leu Phe
 35 40 45
 Leu Ile Arg Thr Glu Cys Ser Leu Arg Gln Pro Met Phe Leu Phe Leu
 50 55 60
 Ala Met Leu Ser Phe Val Asp Leu Val Leu Ser Leu Ser Thr Leu Pro
 65 70 75 80
 Lys Met Leu Ala Ile Phe Trp Phe Gly Ala Thr Ala Ile Ser Ser His
 85 90 95
 Ser Cys Leu Ser Gln Met Phe Phe Ile His Ala Phe Ser Ala Met Glu
 100 105 110
 Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Ser Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Arg Tyr Ala Thr Ile Leu Pro Pro Val Val Val Ala Lys
 130 135 140
 Ile Gly Gly Leu Val Val Leu Xaa Gly Val Gly Leu Thr Ile Ser Phe
 145 150 155 160
 Pro Ser Leu Ala His Arg Leu His Tyr His Gly Ser His Met Ile Ala
 165 170 175
 Tyr Thr Phe Cys Glu His Met Ala Val Val Lys Leu Ala Cys Glu Ala
 180 185 190
 Thr Thr Val Asp Asn Leu Tyr Ala Phe Val Val Ala Ile Phe Leu Gly
 195 200 205
 Gly Gly Asp Val Val Cys Ile Ala Tyr Ser Tyr Gly Leu Ile Val Arg
 210 215 220
 Thr Val Met His Phe Pro Ser Pro Glu Glu Arg Ala Lys Ala Gly Ser
 225 230 235 240
 Thr Cys Thr Ala His Val Cys Val Ile Leu Phe Phe Tyr Gly Leu Gly
 245 250 255
 Phe Leu Ser Val Val Met Gln Arg Phe Gly Ala Pro Thr Ala Ser Thr
 260 265 270
 Ala Lys Val Ile Leu Ala Asn Leu Tyr Leu Leu Phe Pro Pro Ala Leu
 275 280 285
 Asp Pro Ile Val Tyr Gly Met Glu Thr Lys Gln Ile Xaa Glu Arg Leu
 290 295 300
 Leu Met Ile Leu Ser Pro Lys Gln Ile Glu Leu Thr Xaa Val Xaa Leu
 305 310 315 320
 Ser Pro Ala Gly Leu Gln Gly
 325

<210> 2079

<211> 135

<212> PRT

<213> Homo sapien (6087993-36-10518-12399)

<220>

<221> VARIANT

<222> (1)...(135)

<223> Xaa = Any Amino Acid

<400> 2079

Lys Asp Leu Xaa Arg Arg Ser Asn Ile Asn Phe Arg Ile Glu Arg Leu
 1 5 10 15
 Tyr Phe Phe Ile Xaa Gly Trp Glu Met Lys Met Gly Leu Xaa Asn Xaa
 20 25 30
 Leu Leu Met Phe Cys Glu Ser Phe Xaa Xaa Xaa Lys Thr Val Leu Arg
 35 40 45

```

Ile Lys Gly Glu Gly Asp Met Ala Lys Ala Leu Gly Thr Cys Gly Ser
 50          55          60
His Phe Ile Leu Ile Leu Phe Phe Thr Thr Val Leu Leu Val Leu Val
65          70          75          80
Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro Pro Asp Val Pro Ile Leu
          85          90          95
Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val
          100          105          110
Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu
          115          120          125
Arg Arg Leu Xaa Lys Ile Lys
          130          135

```

<210> 2080
 <211> 141
 <212> PRT
 <213> Homo sapien (6094601-37-1-3120)

<220>
 <221> VARIANT
 <222> (1)...(141)
 <223> Xaa = Any Amino Acid

```

<400> 2080
Met Leu Thr Cys Phe Trp Lys His Leu Xaa Tyr Leu Pro Leu Xaa Phe
 1          5          10          15
Val Asp Phe Val Leu Ser Lys Lys Lys Pro Ser Asn Xaa Ser Val Ser
          20          25          30
Ile Asn Val Phe Leu Leu Leu Thr Tyr Xaa Xaa Ser Phe Ala Leu Val
          35          40          45
Tyr Leu Cys Phe Asp Lys Leu Phe Trp Ile Cys Asn Pro Leu Ser Gly
          50          55          60
Leu Met Thr Leu Arg Arg Thr Arg Cys Ala Gly Ile Leu Gly Ala Cys
65          70          75          80
Trp Thr Tyr Ala Phe Thr Ser Thr Ile Arg Xaa Val Phe Phe Phe Phe
          85          90          95
Asn Leu Lys Asp Lys Leu Phe Phe Gln Met Ser Asn Phe Leu Ser Leu
          100          105          110
Xaa Glu Leu Met Xaa Gly Pro Phe Leu Glu Asn Ser His Met Tyr
          115          120          125
Ser Tyr Thr His Lys Leu Cys Leu Leu Phe Xaa Gly Val
          130          135          140

```

<210> 2081
 <211> 315
 <212> PRT
 <213> Homo sapien (6249440-1-23422-29767)

<220>
 <221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

```

<400> 2081
Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1          5          10          15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
          20          25          30
Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
          35          40          45
Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe

```


50		55		60
Phe Phe Leu Ser Thr	Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser			
65	70	75		80
Trp Glu Leu Xaa Val	Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile			
	85	90		95
Ser Tyr Asn Ser Cys Ser Val Gln Met Ile Thr His Leu Phe Leu Gly				
	100	105		110
Thr Ala Gln Cys Leu Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val				
	115	120		125
Glu Ile Ser Tyr Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val				
	130	135		140
Cys Ile Gln Leu Ala Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala				
145	150	155		160
Val Thr Leu Ile Ile Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val				
	165	170		175
Ile Asn His Phe Thr Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys				
	180	185		190
Ser Asp Thr Leu Val Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe				
	195	200		205
Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile				
	210	215		220
Phe Val Arg Ala Val Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly				
225	230	235		240
Ser His Leu Thr Gly Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met				
	245	250		255
Tyr Leu Lys Pro Gln Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val				
	260	265		270
Ser Lys Leu Tyr Gly Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr				
	275	280		285
Ile Gln Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys				
	290	295		300
Gly Asn Glu Lys Ser Xaa Gln Phe Ser Leu Asn				
305	310	315		

<210> 2082

<211> 295

<212> PRT

<213> Homo sapien (6739493-1-1-1041)

<400> 2082

Met Tyr Ser Phe Met Ala Gly Ser Ile Phe Ile Thr Ile Phe Gly Asn	
1	5
Leu Ala Met Ile Ile Ser Ile Ser Tyr Phe Lys Gln Leu His Thr Pro	
	20
Thr Asn Phe Leu Ile Leu Ser Met Ala Ile Thr Asp Phe Leu Leu Gly	
	35
Phe Thr Ile Met Pro Tyr Ser Met Ile Arg Ser Val Glu Asn Cys Trp	
	50
Tyr Phe Gly Leu Thr Phe Cys Lys Ile Tyr Tyr Ser Phe Asp Leu Met	
65	70
Leu Ser Ile Thr Ser Ile Phe His Leu Cys Ser Val Ala Ile Asp Arg	
	85
Phe Tyr Ala Ile Cys Tyr Pro Leu Leu Tyr Ser Thr Lys Ile Thr Ile	
	100
Pro Val Ile Lys Arg Leu Leu Leu Leu Cys Trp Ser Val Pro Gly Ala	
	115
Phe Ala Phe Gly Ala Val Phe Ser Glu Ala Tyr Ala Asp Gly Ile Glu	
	130
Gly Tyr Asp Ile Leu Val Ala Cys Ser Ser Ser Cys Pro Val Met Phe	
145	150
Asn Lys Leu Trp Gly Thr Thr Leu Phe Met Ala Gly Phe Phe Thr Pro	

<210> 2083
<211> 302
<212> PRT
<213> Homo sapien (6911343-1-10351-11487)

```
<220>  
<221> VARIANT  
<222> (1)...(302)  
<223> Xaa = Any Amino Acid
```

Leu 1	Ser	Ser	Met	Cys 5	Leu	Thr	Ile	Val	Met 10	His	Cys	Glu	Phe	Phe 15	Leu
Met	Asp	Leu	Thr	Asp	Asp	Pro	Gln	Leu	His	Pro	Thr	Phe	Ser	Ala	Leu
			20					25					30		
Phe	Leu	Pro	Ile	Tyr	Val	Val	Met	Val	Met	Ala	Asn	Leu	Gly	Leu	Leu
		35					40					45			
Ala	Phe	Ile	Val	Val	Ser	Pro	Gln	Phe	Leu	Thr	Pro	Met	Tyr	Phe	Phe
		50				55					60				
Leu	Ser	Asn	Trp	Ser	Ser	Val	Asp	Phe	Cys	Tyr	Ser	Ser	Val	Thr	Val
65					70					75					80
Pro	Lys	Ile	Ser	Met	Gly	Phe	Phe	Ser	Asp	Cys	Gln	Val	Phe	Ser	Phe
				85					90					95	
Ser	Gly	Cys	Met	Ala	Gln	Leu	Ser	Cys	Phe	Xaa	Ile	Phe	Ala	Asp	Thr
			100					105					110		
Glu	Phe	Phe	Leu	Leu	Ala	Ser	Met	Val	Tyr	Tyr	Arg	Xaa	Glu	Ala	Val
		115					120					125			
Cys	Asn	Pro	Leu	Leu	Tyr	His	Ile	Thr	Met	Ser	Pro	Lys	Leu	Cys	Leu
		130				135					140				
Gln	Leu	Val	Ala	Thr	Ser	Met	Asn	Met	Val	Leu	Pro	Ser	Ser	Thr	Ile
145					150					155					160
Phe	His	Leu	Ile	Phe	Cys	Lys	Ser	Arg	Ala	Ile	Ile	His	Xaa	Phe	Cys
			165						170					175	
Tyr	Phe	Ser	Pro	Pro	Pro	Arg	Leu	Xaa	Lys	Leu	Ser	Cys	Ser	Asp	Met
			180					185					190		
Gln	Gly	Leu	Gln	Leu	Leu	Thr	Phe	Ala	Ser	Ser	Ser	Phe	Asn	Val	Ser
		195					200					205			
Val	Ser	Arg	Thr	Ile	Phe	Leu	Val	Ser	Tyr	Leu	Ile	Met	Arg	Met	Pro
		210				215					220				
Ser	Val	Xaa	Gly	Lys	His	Cys	Ala	Ser	His	Leu	Thr	Ala	Val	Ser	Leu
225					230					235					240
Cys	Tyr	Gly	Thr	Thr	Val	Phe	Leu	His	Leu	His	Leu	Ser	Leu	Lys	Cys
			245						250					255	

Ser Pro Asp Arg Asp Met Leu Val Ser Val Leu His Ser Ala Ile Leu
 260 265 270
 Met Leu Asn Pro Met Val Gln Ser Leu Arg Asn Lys Asp Val Lys Lys
 275 280 285
 Thr Phe Gly Thr Ser Ser Xaa Arg Phe Thr Ile Pro Leu Leu
 290 295 300

<210> 2084

<211> 274

<212> PRT

<213> Homo sapien (6911343-1-22015-25112)

<220>

<221> VARIANT

<222> (1)...(274)

<223> Xaa = Any Amino Acid

<400> 2084

Glu Arg Asn Pro Ser Val Ala Glu Lys Cys Leu Gln Gly Met Thr Asp
 1 5 10 15
 Ser Ser His His Tyr Leu Xaa Leu Arg Leu Pro Leu Phe Arg Leu Leu
 20 25 30
 Ile Leu Leu Tyr Thr Ile Ile Thr Ile Gly Asn Leu Gly Thr Val Ile
 35 40 45
 Leu Ile Gly Ile Ser Leu Gly Leu Tyr Val Cys Pro Pro Arg Phe Leu
 50 55 60
 Leu Phe Thr Phe Ser Met Leu Arg Val Leu Val Lys Cys Phe Xaa Ser
 65 70 75 80
 Thr Val Leu Pro Phe Ser Phe Trp Ser Leu Glu Ala Gln Ile Asn Phe
 85 90 95
 Phe Ser Ile Leu Cys Ile Thr Glu Phe Phe Pro Leu Ala Thr Met Ala
 100 105 110
 Tyr Asp Asp Asn Val Ala Thr Cys Glu Pro Leu Phe His Pro Phe Thr
 115 120 125
 Ser Leu Arg Leu Asn Ser Ala Phe Val Xaa Glu Lys Leu Tyr Leu Arg
 130 135 140
 Ala Phe Thr Ser Ala Leu Pro Ser Thr Leu Pro Phe His Leu Pro Phe
 145 150 155 160
 Phe Asn Ser His Leu Cys Ser Leu Gln Xaa His Tyr Phe Leu Gly Gln
 165 170 175
 Val Val Leu Xaa Asn Met Thr Pro Asn Phe Lys Leu Pro Asp Phe Ser
 180 185 190
 Asn Ser Asn Val Asn Leu Val Ser Leu Cys Cys Pro Thr Ile Cys Cys
 195 200 205
 Tyr Pro Ile Ile Leu Arg Ser Leu Ser Ser His Asn Xaa Ser Glu Asn
 210 215 220
 Lys Leu Leu Ile Ile Ile Phe Phe Gln Asn Ser Thr Xaa Leu Leu Phe
 225 230 235 240
 Ile Phe Cys Ser Asp Glu Asn Val Tyr Xaa Thr Ile Xaa Gly Ile Thr
 245 250 255
 Asp Xaa Phe Ile Lys Ser Lys His Cys Val His Ile Pro Leu Met Gln
 260 265 270
 Ile Leu

<210> 2085

<211> 323

<212> PRT

<213> Homo sapien (6911343-1-65670-69060)

<220>

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 2085

```

Val Glu Asn Ser Pro Met Val Thr Asp Phe Ile Phe Leu Gly Met Thr
 1          5          10          15
Asp Asn Ser Gln Leu Glu Val Leu Leu Phe Gly Val Phe Leu Ile Ala
      20          25          30
Tyr Ile Ile Thr Val Leu Glu Asn Leu Gly Leu Val Val Leu Ile Arg
      35          40          45
Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Gln
      50          55          60
Ser Phe Leu Asp Val Cys Phe Ser Ser Ile Thr Ile Pro Gln Asn Leu
      65          70          75          80
Ala His Leu Phe Ser Lys Leu Gln Tyr Val Ser Phe Leu Phe Pro Tyr
      85          90          95
Thr Xaa Met Ser Leu Phe Val Ile Phe Ala Ser Ala Glu Cys Asn Phe
      100          105          110
Leu Asn Leu Met Ala Tyr Asp Arg Phe Thr Ala Ile Cys His Pro Leu
      115          120          125
Phe Tyr His Ile Thr Met Ser Arg Gly His Tyr Leu Phe Leu Val Ala
      130          135          140
Gly Cys Tyr Leu Gly Gly Leu Val Lys Met Val Thr Val Thr Thr Ser
      145          150          155          160
Ile Thr Gln Leu Ser Leu Cys Gln Pro Cys Val Leu Pro Ala Phe Phe
      165          170          175
Cys Asp Ile Pro Ser Leu Leu Val Leu Val Cys Ser Asp Pro Trp Ile
      180          185          190
Thr Ser Ser Ile Leu Val Val Gly Cys Gly Gly Phe Thr Leu Val Thr
      195          200          205
Ser Val Val Val Ile Leu Val Ser Tyr Met Ser Ser Leu Met Thr Ile
      210          215          220
Leu Gly Ile Pro Leu Ala Ser Gly Lys Gln Arg Ala Phe Ser Thr Cys
      225          230          235          240
Ala Ser His Leu Thr Ala Val Ser Leu Tyr Tyr Glu Thr Thr Met Tyr
      245          250          255
Thr Tyr Leu Pro Ala Ser Arg His Gly Ser Gly Ala Gly Asn Gln Ile
      260          265          270
Val Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile
      275          280          285
Tyr Ser Leu Arg Asn Glu Glu Val Lys Val Ala Leu Xaa Lys Thr Leu
      290          295          300
Arg His Ser Pro Xaa Ser Ser Leu Ser Val Ser Lys Met Gln Asn Ile
      305          310          315          320
Leu Xaa Arg

```

<210> 2086

<211> 318

<212> PRT

<213> Homo sapien (7024122-10-14004-16338)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2086

```

Met Lys Ser Glu Leu Asn Arg Asn Tyr Ser Glu Val Thr Glu Phe Ile
 1          5          10          15

```

Leu Leu Gly Phe Arg Thr Ser Pro Glu Ala Gln Ile Leu Leu Phe Phe
 20 25 30
 Leu Phe Leu Leu Ile Tyr Met Val Ile Val Leu Arg Asn Leu Ser Met
 35 40 45
 Leu Val Val Ile Glu Ile Asp Ser Arg Leu His Thr Pro Val Tyr Phe
 50 55 60
 Phe Leu Arg Asn Leu Ser Tyr Leu Asp Leu Arg Tyr Ser Thr Val Ile
 65 70 75 80
 Ala Pro Lys Leu Thr Thr Leu Phe Ser Lys Glu Lys Lys Ile Ser Tyr
 85 90 95
 Asn Gly Xaa Ala Thr Gln Leu Phe Phe Phe Ala Leu Phe Val Gly Thr
 100 105 110
 Glu Gly Phe Phe Leu Asp Met Met Ala Tyr Asp Arg Phe Ser Ala Ile
 115 120 125
 Cys Ser Pro Phe Phe Tyr Thr Val Cys Met Ser Gln Gln Ala Cys Val
 130 135 140
 Cys Leu Val Val Gly Ser Ser Ile Cys Gly Cys Ile Asn Ser Met Ile
 145 150 155 160
 Gln Thr Gly Phe Thr Phe Ser Leu His Phe Cys Gly Glu Asn Arg Leu
 165 170 175
 Glu His Phe Phe Cys Asp Val Ser Val Met Ile Lys Ile Ser Cys Ile
 180 185 190
 Asp Ile Leu Val Asn Glu Val Val Leu Phe Ile Leu Ser Ala Leu Ile
 195 200 205
 Thr Thr Thr Thr Thr Val Ile Leu Ala Ser Tyr Val His Ile Leu Ser
 210 215 220
 Thr Val Leu Lys Ile Leu Ser Thr His Gly Arg Arg Lys Thr Phe Ser
 225 230 235 240
 Thr Cys Ser Ser His Ile Thr Val Val Ser Leu Phe Tyr Gly Thr Val
 245 250 255
 Phe Phe Met Tyr Ala Gln Pro Gly Ala Ile Pro Lys Ser Lys Val Ile
 260 265 270
 Val Val Phe Xaa Thr Leu Val Ile Pro Met Leu Asn Thr Leu Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Val Gln Asn Ala Leu Lys Arg Tyr Ile Asp Lys
 290 295 300
 Lys Asn Ile Phe His Trp Pro Leu Ala Ile Tyr Lys Thr Ile
 305 310 315

<210> 2087

<211> 318

<212> PRT

<213> Homo sapien (7024122-5-2648-5354)

<400> 2087

Met Phe Ser Ser Glu Pro Thr Ile Asp Gly Asn Gln Ser Leu Cys Ala
 1 5 10 15
 Lys Phe Thr Phe Val Ala Phe Ser Ser Ile Glu Glu Leu Gln Leu Val
 20 25 30
 Leu Phe Ile Val Phe Leu Ile Ile Tyr Leu Cys Thr Ile Gly Gly Asn
 35 40 45
 Ile Ile Ile Ile Ser Leu Ile Trp Ile Thr Pro Ala Leu His Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Val Asn Leu Ser Phe Leu Glu Met Cys Tyr Thr
 65 70 75 80
 Thr Ser Val Val Pro Leu Leu Val His Leu Leu Val Glu Thr Lys Thr
 85 90 95
 Ile Ser Val Gly Gly Cys Ala Thr Gln Met Tyr Ile Phe Ala Ile Leu
 100 105 110
 Gly Leu Thr Glu Cys Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Phe
 115 120 125

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Leu Phe Met Gly Pro Arg
 130 135 140
 Val Cys Leu Lys Leu Ala Ala Ser Trp Phe Thr Gly Val Val Val
 145 150 155 160
 Glu Ser Ala Gln Ile Thr Leu Ile Phe Thr Leu Pro Phe Cys Gly Thr
 165 170 175
 Gly Lys Ile Pro Thr Leu Phe Cys Asp Ile Met Pro Val Leu Lys Leu
 180 185 190
 Ala Cys Ile Asp Thr Ser Gln Ile Glu Ile Val Met Phe Ser Leu Ser
 195 200 205
 Val Leu Phe Ile Val Ser Pro Cys Phe Leu Ile Leu Cys Ser His Met
 210 215 220
 His Ile Pro Val Thr Ile Leu Arg Ile Pro Ser Ala Ala Gly Arg His
 225 230 235 240
 Lys Ala Phe Ser Thr Cys Ser Ser His Ile Leu Val Val Ser Leu Phe
 245 250 255
 Tyr Gly Thr Ala Leu Phe Thr Tyr Leu Gln Pro Lys Thr Ala His Thr
 260 265 270
 Pro Glu Thr Asp Lys Ala Thr Ala Leu Met Tyr Thr Met Val Thr Pro
 275 280 285
 Ala Leu Asn Pro Val Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu
 290 295 300
 Ala Phe Gln Arg Ile Thr Gln Arg Asn Ser Leu Arg Gln Thr
 305 310 315

<210> 2088

<211> 317

<212> PRT

<213> Homo sapien (7024122-6-11866-14009)

<220>

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 2088

Met Gly Asp Lys Gly Thr Gly Asn His Ser Asp Val Thr Asp Phe Ile
 1 5 10 15
 Leu Glu Gly Phe Arg Val Arg Pro Glu Phe Tyr Ile Leu Leu Phe Phe
 20 25 30
 Leu Phe Leu Leu Ile Tyr Ser Met Val Leu Leu Gly Asn Ile Ser Val
 35 40 45
 Met Thr Ile Ile Val Thr Asp Ser Gln Leu Asn Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Gly Asn Leu Ser Phe Ile Asp Val Ser Tyr Ser Thr Val Ile
 65 70 75 80
 Ala Pro Lys Ala Met Ala His Phe Leu Ser Glu Lys Lys Thr Val Ser
 85 90 95
 Phe Ala Gly Cys Val Ala Gln Leu Phe Leu Phe Ala Leu Phe Ile Val
 100 105 110
 Thr Glu Gly Phe Val Leu Ala Ala Met Ala Tyr Asp Arg Phe Ser Ala
 115 120 125
 Ile Cys Asn Pro Leu Leu His Ser Val His Met Ser Arg Arg Leu Cys
 130 135 140
 Thr Gln Leu Val Ala Gly Ser Tyr Phe Cys Gly Trp Ala Ser Ser Ile
 145 150 155 160
 Leu Gln Val Ser Val Thr Phe Ser Val Ser Phe Cys Ala Ser Arg Val
 165 170 175
 Ile Ala His Phe Tyr Cys Asp Ser Tyr Gln Ile Glu Lys Ile Ser Cys
 180 185 190
 Ser Asn Leu Phe Val Asn Lys Met Val Ser Leu Ser Leu Ser Val Ile

195	200	205
Ile Ile Leu Pro Thr Ile Val Val Ile Ile Val Ser Tyr Leu Tyr Ile		
210	215	220
Val Ser Ser Val Leu Lys Ile Pro Ser Ser Glu Gly Arg Lys Lys Asp		
225	230	235
Phe Ser Thr Cys Ser Ser His Arg Gly Val Val Ser Leu Leu Xaa Gly		
245	250	255
Thr Val Ser Phe Val Tyr Leu Thr Pro Pro Ser Asn Pro Glu Leu Arg		
260	265	270
Lys Val Ala Ser Val Phe Tyr Ile Cys Val Thr Pro Met Leu Asn Pro		
275	280	285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys		
290	295	300
Ile Leu Cys Asn Lys Lys Ala Leu Ser Xaa Phe Tyr Phe		
305	310	315

<210> 2089

<211> 315

<212> PRT

<213> Homo sapien (7107785-12-32121-33524)

<400> 2089

Met Ser Pro Asp Gly Asn His Ser Ser Asp Pro Thr Glu Phe Val Leu		
1	5	10
Ala Gly Leu Pro Asn Leu Asn Ser Ala Arg Val Glu Leu Phe Ser Val		
20	25	30
Phe Leu Leu Val Tyr Leu Leu Asn Leu Thr Gly Asn Val Leu Ile Val		
35	40	45
Gly Val Val Arg Ala Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe		
50	55	60
Leu Gly Asn Leu Ser Cys Leu Glu Ile Leu Leu Thr Ser Val Ile Ile		
65	70	75
Pro Lys Met Leu Ser Asn Phe Leu Ser Arg Gln His Thr Ile Ser Phe		
85	90	95
Ala Ala Cys Ile Thr Gln Phe Tyr Phe Tyr Phe Phe Leu Gly Ala Ser		
100	105	110
Glu Phe Leu Leu Leu Ala Val Met Ser Ala Asp Arg Tyr Leu Ala Ile		
115	120	125
Cys His Pro Leu Arg Tyr Pro Leu Leu Met Ser Gly Ala Val Cys Phe		
130	135	140
Arg Val Ala Leu Ala Cys Trp Val Gly Gly Leu Val Pro Val Leu Gly		
145	150	155
Pro Thr Val Ala Val Ala Leu Leu Pro Phe Cys Lys Gln Gly Ala Val		
165	170	175
Val Gln His Phe Phe Cys Asp Ser Gly Pro Leu Leu Arg Leu Ala Cys		
180	185	190
Thr Asn Thr Lys Lys Leu Glu Glu Thr Asp Phe Val Leu Ala Ser Leu		
195	200	205
Val Ile Val Ser Ser Leu Leu Ile Thr Ala Val Ser Tyr Gly Leu Ile		
210	215	220
Val Leu Ala Val Leu Ser Ile Pro Ser Ala Ser Gly Arg Gln Lys Ala		
225	230	235
Phe Ser Thr Cys Thr Ser His Leu Ile Val Val Thr Leu Phe Tyr Gly		
245	250	255
Ser Ala Ile Phe Leu Tyr Val Arg Pro Ser Gln Ser Gly Ser Val Asp		
260	265	270
Thr Asn Trp Ala Val Thr Val Ile Thr Thr Phe Val Thr Pro Leu Leu		
275	280	285
Asn Pro Phe Ile Tyr Ala Leu Arg Asn Glu Gln Val Lys Glu Ala Leu		
290	295	300
Lys Asp Met Phe Arg Lys Val Val Ala Gly Val		

305

310

315

<210> 2090
 <211> 141
 <212> PRT
 <213> Homo sapien (7107785-6-1204-2472)

<220>
 <221> VARIANT
 <222> (1)...(141)
 <223> Xaa = Any Amino Acid

<400> 2090
 Arg Asn Ile Arg Ile Ser Leu Pro Ile Tyr Phe Leu Ser Val Xaa Glu
 1 5 10 15
 Glu Arg Phe Gly Arg Glu Glu Phe Leu Arg Val Trp Thr Tyr Xaa Leu
 20 25 30
 Ile Ser Met Arg Asn Cys Phe Leu Arg Gly Cys Leu Met Tyr Xaa Met
 35 40 45
 Ile Phe Ser Trp Ser Cys Thr Glu Tyr Val Val His Met Phe Phe Ser
 50 55 60
 Leu Leu Asn Ser Gly Ile Ser Thr Glu Cys Gln Ile Ser Tyr Gln Gln
 65 70 75 80
 Asn Lys Asp Ile Ala Ile Phe Phe Leu His Asn Leu Xaa Xaa Lys Glu
 85 90 95
 Asn Phe Glu Ile Phe Leu Tyr Glu Asp Tyr Cys Ser His Ile Arg Asp
 100 105 110
 Leu Thr Lys Ile Ser Leu Gly Glu Ala Gly Xaa Asn Tyr Xaa Gly Lys
 115 120 125
 Ser Thr Thr Ile Glu Phe Leu Phe Leu Ala Leu Leu Phe
 130 135 140

<210> 2091
 <211> 202
 <212> PRT
 <213> Homo sapien (7134787-10-3417-6169)

<220>
 <221> VARIANT
 <222> (1)...(202)
 <223> Xaa = Any Amino Acid

<400> 2091
 Ile Phe Ala Ile Leu Thr Thr Ile Asp Cys Cys Val Phe Val Trp Glu
 1 5 10 15
 Phe Leu Glu Cys Thr Val Phe Val Asn Lys Arg Ala Cys Ala Gln Leu
 20 25 30
 Ala Cys Gly Ala Phe Cys Ile Gly Leu Ile Met Thr Val Val Xaa Ile
 35 40 45
 Thr Thr Val Ser Gln Arg Tyr Lys Arg Ser Thr Tyr Ala Ile Val Asp
 50 55 60
 Cys Phe Leu Phe Asp Thr Leu Leu Val Met Lys Leu Ser Cys Ile Asp
 65 70 75 80
 Asn Thr Ile Tyr Glu Ile Ile Gln Tyr Phe Ile His His Thr Cys Val
 85 90 95
 Gln Val Ser Met Gly Leu Val Cys Ile Ser Tyr Ile Asp Ile Pro Val
 100 105 110
 Thr Ser Ile Val Leu Arg Ile Ser Xaa Ser Glu Val Phe Ala Thr Cys
 115 120 125
 Val Pro Gln Pro Pro Pro His His Gly His Cys Leu Tyr Val Cys Ala
 130 135 140

Cys Thr Ala Tyr Leu Lys His Lys Pro Met Asn Ser Ile Glu Lys Gly
 145 150 155 160
 Leu Leu Xaa Glu Thr Tyr Ile Ile Ile His Ser Ala Ser Gly Pro
 165 170 175
 Val Val Tyr Thr Leu Arg Tyr Met Glu Ala Lys Asp Thr Met Tyr Arg
 180 185 190
 Ala Val Asp Arg Asn Ile Ser Xaa Gln Ile
 195 200

<210> 2092

<211> 276

<212> PRT

<213> Homo sapien (7134787-7-358-5219)

<400> 2092

Met Arg Arg Lys Asn Leu Thr Glu Val Thr Glu Phe Val Phe Leu Gly
 1 5 10 15
 Phe Ser Arg Phe His Lys His His Ile Thr Leu Phe Val Val Phe Leu
 20 25 30
 Ile Leu Tyr Thr Leu Thr Val Ala Gly Asn Ala Ile Ile Met Thr Ile
 35 40 45
 Ile Cys Ile Asp Arg His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Met Leu Ala Ser Ser Lys Thr Val Tyr Thr Leu Phe Ile Ile Pro Gln
 65 70 75 80
 Met Leu Ser Ser Phe Val Thr Gln Thr Gln Pro Ile Ser Leu Ala Gly
 85 90 95
 Cys Thr Thr Gln Thr Phe Phe Phe Val Thr Leu Ala Ile Asn Asn Cys
 100 105 110
 Phe Leu Leu Thr Val Met Gly Tyr Asp His Tyr Met Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Arg Val Ile Thr Ser Lys Lys Val Cys Val Gln Leu
 130 135 140
 Val Cys Gly Ala Phe Ser Ile Gly Leu Ala Met Ala Ala Val Gln Val
 145 150 155 160
 Thr Ser Ile Phe Thr Leu Pro Phe Cys His Thr Val Val Gly His Phe
 165 170 175
 Phe Cys Asp Ile Leu Pro Val Met Lys Leu Ser Cys Ile Asn Thr Thr
 180 185 190
 Ile Asn Glu Ile Ile Asn Phe Val Val Arg Leu Phe Val Ile Leu Val
 195 200 205
 Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Val
 210 215 220
 Leu Lys Ile Ala Ser Ala Glu Gly Trp Lys Lys Thr Phe Ala Thr Cys
 225 230 235 240
 Ala Phe His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile
 245 250 255
 Ala Tyr Leu Met Pro Lys Ser Glu Asn Ser Ile Glu Gln Asp Leu Leu
 260 265 270
 Leu Ser Val Thr
 275

<210> 2093

<211> 310

<212> PRT

<213> Homo sapien (7139676-7-1545-4565)

<400> 2093

Met Gln Leu Asn Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Gln Asp Pro Phe Trp Lys Lys Ile Val Phe Val Ile Phe Leu Arg Leu

```

      20      25      30
Tyr Leu Gly Thr Leu Leu Gly Asn Leu Leu Ile Ile Ile Ser Val Lys
      35      40      45
Ala Ser Gln Ala Leu Lys Asn Pro Met Phe Phe Phe Leu Phe Tyr Leu
      50      55      60
Ser Leu Ser Asp Thr Cys Leu Ser Thr Ser Ile Ala Pro Arg Met Ile
65      70      75      80
Val Asp Ala Leu Leu Lys Lys Thr Thr Ile Ser Phe Ser Glu Cys Met
      85      90      95
Ile Gln Val Phe Ser Ser His Val Phe Gly Cys Leu Glu Ile Phe Ile
      100      105      110
Leu Ile Leu Thr Ala Val Asp Arg Tyr Val Asp Ile Cys Lys Pro Leu
      115      120      125
His Tyr Met Thr Ile Ile Ser Gln Trp Val Cys Gly Val Leu Met Ala
      130      135      140
Val Ala Trp Val Gly Ser Cys Val His Ser Leu Val Gln Ile Phe Leu
145      150      155      160
Ala Leu Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Cys Phe
      165      170      175
Cys Asp Leu Gln Pro Leu Leu Lys Gln Ala Cys Ser Glu Thr Tyr Val
      180      185      190
Val Asn Leu Leu Leu Val Ser Asn Ser Gly Ala Ile Cys Ala Val Ser
      195      200      205
Tyr Val Met Leu Ile Phe Ser Tyr Val Ile Phe Leu His Ser Leu Arg
      210      215      220
Asn His Ser Ala Glu Val Ile Lys Lys Ala Leu Ser Thr Cys Val Ser
225      230      235      240
His Ile Ile Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe Met Tyr
      245      250      255
Thr Cys Pro Ala Thr Val Phe Pro Met Asp Lys Met Ile Ala Val Phe
      260      265      270
Tyr Thr Val Gly Thr Ser Phe Leu Asn Pro Val Ile Tyr Thr Leu Lys
      275      280      285
Asn Thr Glu Val Lys Ser Ala Met Arg Lys Leu Trp Ser Lys Lys Leu
      290      295      300
Ile Thr Asp Asp Lys Arg
305      310

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<210> 2094

<211> 311

<212> PRT

<213> Homo sapien (7139676-9-1-2285)

<400> 2094

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Met Glu Lys Ser Asn Asn Ser Thr Leu Phe Ile Leu Leu Gly Phe Ser
1      5      10      15
Gln Asn Lys Asn Ile Glu Val Leu Cys Phe Val Leu Phe Leu Phe Cys
      20      25      30
Tyr Ile Ala Ile Trp Met Gly Asn Leu Leu Ile Met Ile Ser Ile Thr
      35      40      45
Cys Thr Gln Leu Ile His Gln Pro Met Tyr Phe Phe Leu Asn Tyr Leu
      50      55      60
Ser Leu Ser Asp Leu Cys Tyr Thr Ser Thr Val Thr Pro Lys Leu Met
65      70      75      80
Val Asp Leu Leu Ala Glu Arg Lys Thr Ile Ser Tyr Asn Asn Cys Met
      85      90      95
Ile Gln Leu Phe Thr Thr His Phe Phe Gly Gly Ile Glu Ile Phe Ile
      100      105      110
Leu Thr Gly Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115      120      125
His Tyr Thr Ile Ile Met Ser Arg Gln Lys Cys Asn Thr Ile Ile Ile

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130	135	140
Val Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu Leu		
145	150	155
Thr Ile Ph Val Pro Phe Cys Gly Pro Asn Glu Ile Asp His Tyr Phe		160
	165	170
Cys Asp Val Tyr Pro Leu Leu Lys Leu Ala Cys Ser Asn Ile His Met		175
	180	185
Ile Gly Leu Leu Val Ile Ala Asn Ser Gly Leu Ile Ala Leu Val Thr		190
	195	200
Phe Val Val Leu Leu Leu Ser Tyr Val Phe Ile Leu Tyr Thr Ile Arg		205
	210	215
Ala Tyr Ser Ala Glu Arg Arg Ser Lys Ala Leu Ala Thr Cys Ser Ser		220
225	230	235
His Val Ile Val Val Val Leu Phe Phe Ala Pro Ala Leu Phe Ile Tyr		240
	245	250
Ile Arg Pro Val Thr Thr Phe Ser Glu Asp Lys Val Phe Ala Leu Phe		255
	260	265
Tyr Thr Ile Ile Ala Pro Met Phe Asn Pro Leu Ile Tyr Thr Leu Arg		270
	275	280
Asn Thr Glu Met Lys Asn Ala Met Arg Lys Val Trp Cys Cys Gln Ile		285
	290	295
Leu Leu Lys Arg Asn Gln Leu		300
305	310	

<210> 2095

<211> 319

<212> PRT

<213> Homo sapien (7144617-1-1-995)

<400> 2095

Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly	
1	5
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys	10
	15
	20
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala	25
	30
	35
Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu	40
	45
	50
Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro	55
65	60
Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln	65
	70
	75
Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu	80
	85
	90
Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys	95
	100
	105
Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser	110
	115
	120
Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His	125
145	130
	135
Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg	140
	145
	150
Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp	155
	160
	165
Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val	170
	175
	180
Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val	185
	190
	195
Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly	200
225	205
	210
Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser	215
	220
	225
	230
	235
	240

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<210> 2096
<211> 316
<212> PRT
<213> Homo sapien (7144637-1-1-993)
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<220>
<221> VARIANT
<222> (1)...(316)
<223> Xaa = Any Amino Acid
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1231

<210> 2097
 <211> 247
 <212> PRT
 <213> Homo sapien (7144976-1-1-1194)

<220>
 <221> VARIANT
 <222> (1)...(247)
 <223> Xaa = Any Amino Acid

<400> 2097
 Met Gly Asn Ile Asn Ile Ser Leu Glu Asn Tyr Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Asn Xaa Pro Pro Leu Glu Ile Val Ile Phe Val Val Leu Leu
 20 25 30
 Ile Phe Cys Phe Met Thr Leu Ile Gly Lys Leu Phe Ser Ile Ile Leu
 35 40 45
 Ser Tyr Leu Asp Ser His Pro His Thr Pro Arg Tyr Leu Phe Ser Phe
 50 55 60
 Leu Asp Phe Cys Tyr Thr Ile Ser Ser Ile Phe Xaa Leu Gln Tyr Asn
 65 70 75 80
 Leu Trp Gly Pro Gln Lys Asn Ile Ser Tyr Ala Ser Gly Met Ile Gln
 85 90 95
 Ile Tyr Phe Val Leu Thr Leu Gly Thr Met Asp Cys Ala Leu Leu Val
 100 105 110
 Val Met Ser Arg Thr Val Tyr Ala Ala Gly His Arg His Leu Pro Tyr
 115 120 125
 Thr Val Val Met Ala Val Ala Phe Trp Val Ser Ser Phe Thr Asn Ser
 130 135 140
 Ala Phe Asp Ser Phe Phe Thr Phe Trp Val Thr Leu Cys Gly His His
 145 150 155 160
 Tyr Tyr Ala Tyr Ile Phe Ile Phe Thr Ser Leu Leu Val Xaa Arg Trp
 165 170 175
 Phe Ile Asn Arg Lys Lys Gln Ser Val Phe Ser Leu Asn His Ala Ala
 180 185 190
 Leu Leu Thr Leu Ser Phe Pro Leu Xaa Asn Asp Cys Phe Gln Glu Ile
 195 200 205
 Glu Lys Asn Met Leu Arg Lys His Ser Ile Gly Glu Cys Xaa Lys His
 210 215 220
 Val Met Leu Val Gln Leu Asn Gln Val Ser Lys Thr Cys Ile Phe Met
 225 230 235 240
 Arg Pro Ile Leu Gly Asn Ser
 245

<210> 2098
 <211> 329
 <212> PRT
 <213> Homo sapien (7145001-12-25597-26388)

<220>
 <221> VARIANT
 <222> (1)...(329)
 <223> Xaa = Any Amino Acid

<400> 2098
 Lys Ser Met Lys Lys Met Asn Asn Val Ile Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr His Asn Pro Glu Leu Gln Lys Phe Leu Phe Val Met Phe Leu
 20 25 30
 Ile Thr Tyr Leu Ile Thr Leu Ala Gly Asn Leu Phe Ile Ser Val Ile

```
<210> 2099
<211> 264
<212> PRT
<213> Homo sapien (7145001-12-45102-50811)
```

<400> 2099																
Met	Val	Asp	Asn	Leu	Ile	Ile	Val	Val	Thr	Ile	Thr	Thr	Ser	Pro	Ala	
1				5					10					15		
Leu	Asp	Ser	Pro	Val	Tyr	Phe	Phe	Leu	Ser	Phe	Phe	Ser	Phe	Ile	Asp	
			20					25					30			
Gly	Cys	Ser	Ser	Ser	Thr	Met	Ala	Pro	Lys	Met	Ile	Phe	Asp	Leu	Leu	
		35					40					45				
Thr	Glu	Lys	Lys	Thr	Ile	Ser	Phe	Ser	Gly	Cys	Met	Thr	Gln	Leu	Phe	
	50					55					60					
Val	Glu	His	Phe	Phe	Gly	Gly	Val	Glu	Ile	Ile	Leu	Leu	Val	Val	Met	
65					70					75					80	
Ala	Tyr	Asp	Cys	Tyr	Val	Ala	Ile	Cys	Lys	Pro	Leu	Tyr	Tyr	Leu	Ile	
			85						90					95		
Thr	Met	Asn	Arg	Gln	Val	Cys	Gly	Leu	Leu	Val	Ala	Met	Ala	Trp	Val	
		100						105					110			
Gly	Gly	Phe	Leu	His	Ala	Leu	Ile	Gln	Met	Leu	Leu	Ile	Val	Trp	Leu	
		115					120					125				
Pro	Phe	Cys	Gly	Pro	Asn	Val	Ile	Asp	His	Phe	Ile	Cys	Asp	Leu	Phe	

130	135	140
Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr His Val Phe Gly Leu Phe		
145	150	155
Val Ala Ala Asn Ser Gly Leu Met Cys Met Leu Ile Phe Ser Ile Leu		160
	165	170
Ile Thr Ser Tyr Val Leu Ile Leu Cys Ser Gln Arg Lys Ala Leu Ser		175
	180	185
Thr Cys Ala Phe His Ile Thr Val Val Leu Phe Phe Val Pro Cys		190
	195	200
Ile Leu Val Tyr Leu Arg Pro Met Ile Thr Phe Pro Ile Asp Lys Ala		205
	210	215
Val Ser Val Phe Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu Ile		220
225	230	235
Tyr Thr Leu Arg Asn Thr Glu Val Lys Asn Ala Met Lys Gln Leu Trp		240
	245	250
Ser Gln Ile Ile Trp Gly Asn Asn		255
	260	

<210> 2100

<211> 309

<212> PRT

<213> Homo sapien (7145001-8-11112-14684)

<400> 2100

Met Gly Ala Lys Asn Asn Val Thr Glu Phe Val Leu Phe Gly Leu Phe		
1	5	10
Glu Ser Arg Glu Met Gln His Thr Cys Phe Val Val Phe Phe Leu Phe		15
	20	25
His Val Leu Thr Val Leu Gly Asn Leu Val Ile Ile Thr Ile Asn		30
	35	40
Ala Arg Lys Thr Leu Lys Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu		45
	50	55
Ser Phe Ala Asp Ile Cys Tyr Pro Ser Thr Thr Ile Pro Lys Met Ile		60
65	70	75
Ala Asp Thr Phe Val Glu His Lys Ile Ile Ser Phe Asn Gly Cys Met		80
	85	90
Thr Gln Leu Phe Ser Ala His Phe Phe Gly Gly Thr Glu Ile Phe Leu		95
	100	105
Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu		110
	115	120
His Tyr Thr Ala Ile Met Asp Cys Arg Lys Cys Gly Leu Leu Ala Gly		125
	130	135
Ala Ser Trp Leu Ala Gly Phe Leu His Ser Ile Leu Gln Thr Leu Leu		140
145	150	155
Thr Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp Asn Phe Phe		160
	165	170
Cys Asp Val His Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr Tyr Met		175
	180	185
Val Gly Leu Ile Val Val Ala Asn Ser Gly Met Ile Ser Leu Ala Ser		190
	195	200
Phe Phe Ile Leu Ile Ile Ser Tyr Val Ile Ile Leu Leu Asn Leu Arg		205
	210	215
Ser Gln Ser Ser Glu Asp Arg Arg Lys Ala Val Ser Thr Cys Gly Ser		220
225	230	235
His Val Ile Thr Val Leu Leu Val Leu Met Pro Pro Met Phe Met Tyr		240
	245	250
Ile Arg Pro Ser Thr Thr Leu Ala Ala Asp Lys Leu Ile Ile Leu Phe		255
	260	265
Asn Ile Val Met Pro Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg		270
	275	280
Asn Asn Asp Val Lys Asn Ala Met Arg Lys Leu Phe Arg Val Lys Arg		285

290
Ser Leu Gly Glu Lys
305

295

300

<210> 2101
<211> 296
<212> PRT
<213> Homo sapien (7145013-16-7265-9434)

<400> 2101

Leu Leu Leu Leu Val Leu Leu Leu Pro Thr Phe Leu Leu Ser Leu Met
1 5 10 15
Gly Asn Met Leu Ile Ile Ser Thr Val Leu Ser Cys Ser Arg Leu His
20 25 30
Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Ile Leu Asp Ile Leu
35 40 45
Phe Thr Ser Val Ile Ser Pro Lys Val Leu Ala Asn Leu Gly Ser Arg
50 55 60
Asp Lys Thr Ile Ser Phe Ala Gly Cys Ile Thr Gln Cys Tyr Phe Tyr
65 70 75 80
Phe Phe Leu Gly Thr Val Glu Phe Leu Leu Leu Thr Val Met Ser Tyr
85 90 95
Asp Cys Tyr Ala Ala Ile Cys Cys Pro Leu Arg Tyr Thr Thr Ile Met
100 105 110
Arg Pro Tyr Val Cys Ile Gly Thr Val Val Phe Ser Trp Val Gly Gly
115 120 125
Phe Leu Ser Val Leu Phe Pro Thr Ile Leu Ile Ser Gln Leu Pro Phe
130 135 140
Cys Gly Ser Asn Ile Ile Asn His Phe Phe Cys Asp Ser Gly Pro Leu
145 150 155 160
Leu Ala Leu Ala Cys Ala Asp Thr Thr Ala Ile Glu Leu Met Asp Phe
165 170 175
Met Leu Ser Ser Met Val Ile Leu Cys Cys Ile Val Leu Val Ala Tyr
180 185 190
Ser Tyr Thr Tyr Ile Ile Leu Thr Ile Met Arg Ile Pro Ser Ala Ser
195 200 205
Gly Arg Lys Lys Ala Phe Asn Thr Cys Ala Ser His Leu Thr Ile Val
210 215 220
Ile Ile Ser Ser Gly Ile Thr Val Phe Ile Tyr Val Thr Pro Ser Gln
225 230 235 240
Lys Glu Tyr Leu Glu Ile Asn Lys Ile Pro Ser Val Leu Ser Ser Leu
245 250 255
Val Thr Pro Phe Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn Asp Thr
260 265 270
Val Gln Gly Val Leu Arg Asp Val Trp Val Arg Val Arg Gly Val Phe
275 280 285
Glu Lys Arg Met Arg Ala Val Leu
290 295

<210> 2102
<211> 162
<212> PRT
<213> Homo sapien (7211526-1-1-487)

<400> 2102

Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
1 5 10 15
Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
20 25 30
Pro Leu Val His Val Ser Leu Leu Arg Leu Thr Phe Cys Arg Phe
35 40 45


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Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
 50                      55                      60
Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Ile Ile Phe Ile Phe Gly
65                      70                      75                      80
Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Thr
                      85                      90                      95
Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
                      100                      105                      110
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
                      115                      120                      125
Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
                      130                      135                      140
Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
145                      150                      155                      160
Leu Leu

```

<210> 2103

<211> 162

<212> PRT

<213> Homo sapien (7211533-1-1-487)

<220>

<221> VARIANT

<222> (1)...(162)

<223> Xaa = Any Amino Acid

<400> 2103

```

Met Ala Ile Val Asn Pro Leu Leu Tyr Thr Val Ala Met Thr Lys Ile
 1                      5                      10                      15
Val Cys Ile Val Leu Ala Phe Gly Ser Cys Met Gly Gly Leu Ile Ser
                      20                      25                      30
Ser Leu Thr His Thr Ile Gly Leu Val Lys Leu Ser Phe Cys Gly Pro
                      35                      40                      45
Asn Val Ile Ser His Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu
                      50                      55                      60
Ser Cys Ser Glu Thr Ser Met Asn Glu Leu Leu Leu Leu Ile Phe Ser
65                      70                      75                      80
Gly Ile Ile Ala Thr Leu Thr Phe Leu Thr Val Val Ile Ser Tyr Ile
                      85                      90                      95
Phe Ile Val Ala Ala Ile Leu Arg Ile Arg Xaa Glu Ala Gly Arg Arg
                      100                      105                      110
Lys Ala Phe Ser Thr Cys Thr Ser His Leu Ile Thr Val Thr Leu Phe
                      115                      120                      125
Tyr Gly Ser Ile Ser Phe Ser Tyr Ile Gln Pro Asn Ser Gln Tyr Ser
                      130                      135                      140
Leu Glu Gln Glu Lys Val Val Ser Val Phe Tyr Thr Leu Val Val Pro
145                      150                      155                      160
Met Leu

```

<210> 2104

<211> 162

<212> PRT

<213> Homo sapien (7211534-1-1-485)

<400> 2104

```

Val Gly Ile Cys Asn Pro Leu Leu Tyr Thr Val Thr Met Ser Pro Gln
 1                      5                      10                      15
Lys Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ile Phe Gly
                      20                      25                      30

```

Ala Val Ala His Met Gly Asn Ile Met Phe Met Ser Phe Cys Gly Asp
 35 40 45
 Asn Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu
 50 55 60
 Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Val Phe Ile Ile Val
 65 70 75 80
 Thr Val Gly Ile Gly Val Pro Ile Val Thr Ile Phe Leu Ser Tyr Gly
 85 90 95
 Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
 100 105 110
 Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
 115 120 125
 Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
 130 135 140
 Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Cys Thr Ala Val Val Pro
 145 150 155 160
 Met Phe

<210> 2105

<211> 162

<212> PRT

<213> Homo sapien (7211536-1-1-487)

<400> 2105

Val Ala Ile Cys Lys Pro Leu His Tyr Val Val Ile Met Asn Asn Arg
 1 5 10 15
 Val Cys Thr Leu Leu Val Leu Cys Cys Trp Val Ala Gly Leu Met Ile
 20 25 30
 Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Asp Ser
 35 40 45
 Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
 50 55 60
 Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala
 65 70 75 80
 Val Phe Ala Leu Ile Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu
 85 90 95
 Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys
 100 105 110
 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
 115 120 125
 Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu
 130 135 140
 Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
 145 150 155 160
 Leu Leu

<210> 2106

<211> 162

<212> PRT

<213> Homo sapien (7211538-1-1-487)

<400> 2106

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
 1 5 10 15
 Leu Cys Val Phe Leu Val Ala Val Thr Trp Ile Leu Ser Cys Ala Ser
 20 25 30
 Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
 35 40 45
 Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu

```

      50              55              60
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65              70              75              80
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
      85              90              95
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
      100             105             110
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
      115             120             125
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
      130             135             140
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145              150              155              160
Met Leu

```

<210> 2107

<211> 159

<212> PRT

<213> Homo sapien (7211540-1-1-478)

<400> 2107

```

Val Ala Ile Cys Asn Pro Leu Arg Tyr Leu Thr Val Met Asn Pro Gln
1              5              10              15
Leu Cys Leu Trp Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His
      20              25              30
Ser Ile Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro
      35              40              45
Asn Glu Leu Asp Asn Phe Tyr Cys Asp Val Leu Gln Ile Ile Lys Leu
      50              55              60
Ala Cys Met Asp Thr Tyr Val Val Glu Val Leu Val Ile Ala Asn Ser
65              70              75              80
Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala
      85              90              95
Ile Ile Leu Ile Thr Leu Arg Thr Arg Phe Cys Gln Gly Gln Asn Lys
      100             105             110
Val Leu Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe
      115             120             125
Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val
      130             135             140
Asp Lys Ile Phe Ser Leu Phe Tyr Thr Val Ile Thr Pro Met Leu
145              150              155

```

<210> 2108

<211> 162

<212> PRT

<213> Homo sapien (7211541-1-1-488)

<400> 2108

```

Met Ala Ile Cys Lys Pro Leu Leu Tyr Gly Ser Lys Met Thr Arg Cys
1              5              10              15
Val Cys Leu Cys Leu Ala Ala Ala Pro Tyr Ile Tyr Gly Phe Ala Asn
      20              25              30
Gly Leu Ser Gln Thr Thr Leu Met Leu Arg Leu Ser Phe Cys Gly Pro
      35              40              45
Asn Asp Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Leu Val Leu
      50              55              60
Ala Cys Ser Asp Thr Tyr Val Lys Glu Thr Ala Met Leu Val Val Ala
65              70              75              80
Gly Ser Asn Leu Ile Cys Ser Leu Thr Val Ile Leu Ile Ser Tyr Thr
      85              90              95

```

Phe Ile Phe Thr Ala Ile Leu Arg Ile His Thr Ala Glu Gly Arg Arg
 100 105 110
 Lys Ala Phe Ser Thr Cys Gly Ser His Val Thr Ala Val Thr Val Phe
 115 120 125
 Tyr Gly Thr Leu Phe Cys Met Tyr Leu Arg Pro Pro Ser Glu Thr Ser
 130 135 140
 Ile Gln Gln Gly Lys Ile Val Ala Val Phe Tyr Ile Phe Val Ser Pro
 145 150 155 160
 Met Leu

<210> 2109

<211> 162

<212> PRT

<213> Homo sapien (7211542-1-1-487)

<400> 2109

Val Ala Ile Cys Lys Pro Leu His Tyr Thr Ser Ile Met Asn Arg Lys
 1 5 10 15
 Leu Cys Thr Leu Val Leu Cys Ala Trp Leu Ser Gly Phe Leu Thr
 20 25 30
 Ile Phe Pro Pro Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Ala Ser
 35 40 45
 Asn Val Ile Asp His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu
 50 55 60
 Ser Cys Ser Asp Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala
 65 70 75 80
 Leu Val Thr Leu Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met
 85 90 95
 Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys
 100 105 110
 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
 115 120 125
 Tyr Gly Ser Cys Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys
 130 135 140
 Ala Ser Leu Thr Lys Gly Ile Ala Ile Leu Asn Thr Ser Val Ala Pro
 145 150 155 160
 Met Leu

<210> 2110

<211> 243

<212> PRT

<213> Homo sapien (7230851-8-1-2360)

<220>

<221> VARIANT

<222> (1)...(243)

<223> Xaa = Any Amino Acid

<400> 2110

Met Gln Ser Glu His Leu Ala Glu Phe Ser Glu Phe Leu Ile Leu Ser
 1 5 10 15
 Leu Ser Glu Ile Gln Asn Cys Ser Pro Phe Phe Gly Leu Phe Leu Ser
 20 25 30
 Met Asn Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile
 35 40 45
 Ser Ser Asp Ser His Leu His Lys Pro Met Tyr Phe Leu Leu Ser Lys
 50 55 60
 Leu Ser Met Ala Ala Ile Cys Phe Val Phe Thr Met Ile Gln Lys Met
 65 70 75 80

```

Met Val Asn Leu Arg Ala Gln Ser Lys Asp Ile Phe Thr Gln Pro Ser
      85                      90                      95
Gly Ser Pro Ile Pro Phe Xaa Met Cys Ser Leu Ile Arg Phe Leu Leu
      100                    105                    110
Ile Gln Gln Lys Ser Val Val Leu Ile Phe Glu Tyr Ser Leu Val Leu
      115                    120                    125
Ile His Pro Ile Xaa Ile Xaa Arg Cys Lys Leu Ile Ile Leu Leu Tyr
      130                    135                    140
Glu Pro Phe Lys Ile Ile Glu Asp Ser Tyr Val Leu Phe Leu Ile Ile
145      150                    155                    160
Thr Ile Leu Ser Ser His Xaa Leu Ile His Asn Cys Xaa Xaa Val Met
      165                    170                    175
Asp Phe Leu Leu Lys Gln Pro Leu Phe Tyr His Leu Met Leu Leu Val
      180                    185                    190
Met Gln Gln Leu Thr Leu Asn Ala Leu Phe Ile Phe Xaa Thr Xaa Xaa
      195                    200                    205
Leu Leu Leu Thr Ser Leu Xaa Asp Leu Lys Ile Ser Leu Cys Thr Val
      210                    215                    220
Val Ser Gln Xaa Ile Thr Thr Ile Ile Leu Lys Asn Lys Ile Lys Val
225      230                    235                    240
Val Ser Met

```

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<210> 2111
<211> 313
<212> PRT
<213> Homo sapien (7239533-11-790-4930)

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<220>
<221> VARIANT
<222> (1)...(313)
<223> Xaa = Any Amino Acid

```

```

<400> 2111
Met Glu Ser Gln Arg Asn Ile Xaa Lys Phe Ile Leu Met Ser Leu Ser
 1      5      10      15
Ser Ile Gln Asn Ile Gln Ile Phe Val Phe Val Phe Leu Phe Cys Asn
      20      25      30
Val Ala Ile Leu Val Gly Asn Phe Leu Ile Leu Ile Ser Ile Xaa Cys
      35      40      45
Ser Pro Leu Phe Asn Gln Pro Met His Tyr Phe Leu Gly Tyr Met Asn
      50      55      60
Ile Tyr Tyr Thr Ser Cys Val Thr Pro Lys Ile Ile Gly Asp Leu Val
      65      70      75      80
Val Gly Arg Ile Asn Ile Ser Tyr Asp Arg Ile Phe Pro Met His Phe
      85      90      95
Phe Gly Ile Ile Glu Ile Phe Ile Leu Thr Val Met Ala Phe Asp His
      100     105     110
Tyr Val Ala Ile Cys Lys Pro Pro Arg Tyr Leu Ile Ile Met Asn Arg
      115     120     125
Thr Lys Tyr Asn Thr Leu Ile Ser Val Ala Trp Leu Leu Gly Leu Ile
      130     135     140
His Ser Leu Phe Gln Phe Ser Met Lys Ile Trp Leu Pro Phe Cys Gly
145     150     155     160
Ser Asn Lys Ile Asp Asp Xaa Tyr Xaa Asp Ile Phe Pro Leu Leu Lys
      165     170     175
Val Ala Cys Thr Asp Thr Cys Ile Thr Gly Val Leu Val Val Ala Asn
      180     185     190
Ser Gly Met Phe Ala Leu Val Thr Phe Val Leu Ser Phe Gly Ser Tyr
      195     200     205
Val Ile Ile Leu Phe Pro Leu Lys Asn His Ser Val Glu Gly Arg Cys

```

```

      210              215              220
Lys Ala Leu Ser Thr Cys Gly Ser His Ile Thr Met Val Ile Phe Phe
225              230              235              240
Phe Glu Pro Ser Ile Phe Ala Tyr Leu Arg Pro Ser Thr Phe Pro Glu
      245              250              255
Asp Lys Ile Ser Ala Leu Phe Tyr Thr Ile Ile Ala Pro Met Phe Asn
      260              265              270
His Leu Ile Tyr Asn Leu Arg Asn Thr Glu Met Lys Lys Ala Met Arg
      275              280              285
Lys Val Trp Tyr Gln Ile Ser Phe Ser Glu Glu Lys Gln Leu Ile Cys
      290              295              300
Pro Thr Xaa Cys Thr Lys Glu Leu Tyr
305              310

```

<210> 2112

<211> 311

<212> PRT

<213> Homo sapien (7239533-19-11510-15318)

<400> 2112

```

Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly
1              5              10              15
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu
      20              25              30
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu
      35              40              45
Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50              55              60
His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys
      65              70              75              80
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly
      85              90              95
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val
      100              105              110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
      115              120              125
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu
      130              135              140
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu
      145              150              155              160
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His
      165              170              175
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile
      180              185              190
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser
      195              200              205
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr
      210              215              220
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
      225              230              235              240
Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu
      245              250              255
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys
      260              265              270
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val
      275              280              285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Val
      290              295              300
Met Gly Ser Lys Ile His Ser
305              310

```

<210> 2113
 <211> 287
 <212> PRT
 <213> Homo sapien (7239533-20-19626-20657)

<220>
 <221> VARIANT
 <222> (1)...(287)
 <223> Xaa = Any Amino Acid

<400> 2113
 Tyr Ile Leu Leu Asp Ile Tyr Ile Cys Leu Asn Asn Thr His Val Xaa
 1 5 10 15
 Leu Cys Val Glu Ser Gln Arg Gln Phe Lys Ile Ser Phe Tyr Phe Ser
 20 25 30
 Phe Phe Leu Leu Ala Ile Thr Xaa Phe Xaa Xaa Xaa Ile Leu Ile Ile
 35 40 45
 Met Lys Thr Xaa Gln Tyr Phe Leu Lys His Lys His Leu Lys Lys Lys
 50 55 60
 Phe Ser Xaa Cys Leu Val Tyr Ile Leu Thr Tyr Ile Leu Ser Leu Xaa
 65 70 75 80
 Ser Lys Phe Phe Ala Leu Cys Xaa Ile Phe Ala Asp Lys Ala Phe Gln
 85 90 95
 Glu Gln Val Ser Gly Asn Xaa Xaa Ser Arg Ser Xaa Glu Ser Pro Val
 100 105 110
 His Tyr Thr Leu Thr Met Ser Gln Lys Phe Cys Ser Ile His Pro Ala
 115 120 125
 Gly Cys Tyr Asp Gln Gly Ile Xaa Ser Ile Pro Gly His Ser Phe Ser
 130 135 140
 His Cys Ile Ala Tyr Cys Gly His Asn Val Val Asn Ile Phe Xaa Asn
 145 150 155 160
 Lys Tyr Ser Val Ala Ile Ser Asp Ser Cys Ser Ser Ser Trp Ile Ala
 165 170 175
 Asp Phe Cys Leu Phe Val Cys Phe Ala Leu Val Asn Phe Asp Xaa Leu
 180 185 190
 Arg Asn Leu Arg Val Leu Leu Leu Ser Phe His Phe Gln Leu Val Xaa
 195 200 205
 Lys Ala Leu Ser Ala Ser Ala His Gln Pro Ser Pro Pro Ile Ser His
 210 215 220
 Ile Ser Thr Ile Phe Leu Thr Leu Val Pro Asn Ser Lys Asn Ser Gln
 225 230 235 240
 Ala Ile Val Lys Ala His Ser Val Cys Tyr Ala Met Leu Ile Pro Met
 245 250 255
 Leu Asn Ser Gln Thr Cys Ser Met Arg Tyr Lys Asn Val Asn Glu Ser
 260 265 270
 Leu Gln Lys Leu Met Asp Phe Lys Ile Phe Xaa His Xaa Lys Gln
 275 280 285

<210> 2114
 <211> 256
 <212> PRT
 <213> Homo sapien (7239533-8-1261-3491)

<400> 2114
 Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Asp Thr Cys Tyr Ser
 1 5 10 15
 Asn Val Phe Thr Pro Lys Leu Leu Glu Ile Leu Val Val Glu Asp Arg
 20 25 30
 Thr Ile Ser Phe Lys Gly Cys Met Val Gln Phe Phe Phe Gly Cys Ala
 35 40 45
 Phe Val Ile Thr Glu Met Phe Met Leu Ala Val Met Ala Tyr Asp Leu

50 55 60
 Phe Met Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro
 65 70 75 80
 Lys Leu Cys Ala Leu Leu Val Ala Gly Thr Tyr Thr Trp Gly Gly Leu
 85 90 95
 Cys Ser Leu Thr Leu Thr Tyr Ser Leu Leu Val Leu Ser Tyr Cys Gly
 100 105 110
 Ser Asn Ile Ile Asn His Phe Gly Cys Glu Tyr Ser Ala Ile Leu Ser
 115 120 125
 Leu Ser Cys Ser Asp Pro Tyr Phe Asn Gln Met Ala Cys Leu Val Ile
 130 135 140
 Ser Ile Phe Ser Glu Ala Cys Ser Leu Leu Ala Ile Leu Ala Phe Tyr
 145 150 155 160
 Val Phe Ile Val Ala Thr Val Ile Lys Met Leu Ser Thr Gly Gly Pro
 165 170 175
 Gln Lys Ala Ile Ser Thr Cys Ala Ser His Leu Thr Thr Val Ser Ile
 180 185 190
 Phe His Gly Val Ile Leu Leu Leu Tyr Cys Val Pro Asn Ser Lys Ser
 195 200 205
 Ser Trp Leu Leu Val Lys Val Ala Thr Val Leu Phe Thr Val Ile Ile
 210 215 220
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 225 230 235 240
 Gly Thr Val Arg Lys Leu Ile Asn Ser Gln Ser Pro Phe His Ser Lys
 245 250 255

<210> 2115

<211> 314

<212> PRT

<213> Homo sapien (7239533-9-1-1650)

<400> 2115

Met Met Met Val Leu Arg Asn Leu Ser Met Glu Pro Thr Phe Ala Leu
 1 5 10 15
 Leu Gly Phe Thr Asp Tyr Pro Lys Leu Gln Ile Pro Leu Phe Leu Val
 20 25 30
 Phe Leu Leu Met Tyr Val Ile Thr Val Val Gly Asn Leu Gly Met Ile
 35 40 45
 Ile Ile Ile Lys Ile Asn Pro Lys Phe His Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Val Thr
 65 70 75 80
 Pro Lys Leu Leu Glu Asn Leu Val Met Ala Asp Lys Ser Ile Phe Tyr
 85 90 95
 Phe Ser Cys Met Met Gln Tyr Phe Leu Ser Cys Thr Ala Val Val Thr
 100 105 110
 Glu Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ala
 130 135 140
 Leu Leu Val Ala Gly Ser Tyr Leu Trp Gly Met Phe Gly Pro Leu Val
 145 150 155 160
 Leu Leu Cys Tyr Ala Leu Arg Leu Asn Phe Ser Gly Pro Asn Val Ile
 165 170 175
 Asn His Phe Phe Cys Glu Tyr Thr Ala Leu Ile Ser Val Ser Gly Ser
 180 185 190
 Asp Ile Leu Ile Pro His Leu Leu Phe Ser Phe Ala Thr Phe Asn
 195 200 205
 Glu Met Cys Thr Leu Leu Ile Ile Leu Thr Ser Tyr Val Phe Ile Phe
 210 215 220
 Val Thr Val Leu Lys Ile Arg Ser Val Ser Gly Arg His Lys Ala Phe

225 230 235 240
 Ser Thr Trp Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
 245 250 255
 Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg Gln Thr
 260 265 270
 Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Asn Pro Met Leu Asn
 275 280 285
 Pro Pro Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Trp
 290 295 300
 Lys Leu Ile His Thr Gln Val Pro Phe His
 305 310

<210> 2116

<211> 308

<212> PRT

<213> Homo sapien (7239554-20-1-1871)

<400> 2116

Met Met Ser Asn Gln Thr Leu Val Thr Glu Phe Ile Leu Gln Gly Phe
 1 5 10 15
 Ser Glu His Pro Glu Tyr Arg Val Phe Leu Phe Ser Cys Phe Leu Phe
 20 25 30
 Leu Tyr Ser Gly Ala Leu Thr Gly Asn Val Leu Ile Thr Leu Ala Ile
 35 40 45
 Thr Phe Asn Pro Gly Leu His Ala Pro Met Tyr Phe Phe Leu Leu Asn
 50 55 60
 Leu Ala Thr Met Asp Ile Ile Cys Thr Ser Ser Ile Met Pro Lys Ala
 65 70 75 80
 Leu Ala Ser Leu Val Ser Glu Glu Ser Ser Ile Ser Tyr Gly Gly Cys
 85 90 95
 Met Ala Gln Leu Tyr Phe Leu Thr Trp Ala Ala Ser Ser Glu Leu Leu
 100 105 110
 Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro
 115 120 125
 Leu His Tyr Ser Ser Met Met Ser Lys Val Phe Cys Ser Gly Leu Ala
 130 135 140
 Thr Ala Val Trp Leu Leu Cys Ala Val Asn Thr Ala Ile His Thr Gly
 145 150 155 160
 Leu Met Leu Arg Leu Asp Phe Cys Gly Pro Asn Val Ile Ile His Phe
 165 170 175
 Phe Cys Glu Val Pro Pro Leu Leu Leu Ser Cys Ser Ser Thr Tyr
 180 185 190
 Val Asn Gly Val Met Ile Val Leu Ala Asp Ala Phe Tyr Gly Ile Val
 195 200 205
 Asn Phe Leu Met Thr Ile Ala Ser Tyr Gly Phe Ile Val Ser Ser Ile
 210 215 220
 Leu Lys Val Lys Thr Ala Trp Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Thr Val Val Cys Met Tyr Tyr Thr Ala Val Phe Tyr
 245 250 255
 Ala Tyr Ile Ser Pro Val Ser Gly Tyr Ser Ala Gly Lys Ser Lys Leu
 260 265 270
 Ala Gly Leu Leu Tyr Thr Val Leu Ser Pro Thr Leu Asn Pro Leu Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Leu Arg Lys Leu Phe
 290 295 300
 Pro Phe Phe Arg
 305

<210> 2117

<211> 157

<212> PRT

<213> Homo sapien (7239554-9-1-1342)

<220>

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 2117

```

Met Gly Glu Ala Arg Asn Arg Thr Val Val Gln Glu Phe Ile Leu Glu
 1           5           10           15
Gly Phe Pro Ala Val Gln His Leu Gly Asn Val Leu Phe Leu Val His
      20           25           30
Leu Leu Ala Tyr Leu Ala Ser Ile Met Ala Asn Met Leu Ile Ile Thr
      35           40           45
Ile Thr Trp Ala Asp His His Leu Gln Thr Pro Met Tyr Phe Phe Leu
      50           55           60
Ser Ser Phe Ser Phe Cys Glu Cys Cys Phe Ile Thr Thr Val Ile Pro
65           70           75           80
Lys Leu Leu Val Ile Leu Leu Ser Gly Arg Ala Lys Ile Pro Leu Ser
      85           90           95
Thr Thr Leu Ser His Ala Val Pro Phe Ser Phe Leu Tyr Ser Trp Val
      100          105          110
Asn Ser Phe Ser Ser Leu Asn Gly Cys Asp Val Pro Leu Asp Xaa Tyr
      115          120          125
Leu Ala Ile Cys Lys Pro Leu His Tyr Ser Thr Ile Met Ser Leu Arg
      130          135          140
Thr Ser Phe His Lys Val Thr Ala Trp Leu Cys Pro Gly
145           150           155

```

<210> 2118

<211> 129

<212> PRT

<213> Homo sapien (7239558-10-440-1325)

<400> 2118

```

Met Gln Gly Glu Asn Phe Thr Ile Trp Ser Ile Phe Phe Leu Glu Gly
 1           5           10           15
Phe Ser Gln Tyr Pro Gly Leu Glu Val Val Leu Phe Val Phe Ser Leu
      20           25           30
Val Met Tyr Leu Thr Thr Leu Leu Gly Asn Ser Thr Leu Ile Leu Ile
      35           40           45
Thr Ile Leu Asp Ser Arg Leu Lys Thr Pro Met Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ser Phe Met Asp Ile Cys Tyr Thr Ser Ala Ser Val Pro Thr
65           70           75           80
Leu Leu Val Asn Leu Leu Ser Ser Gln Lys Thr Ile Ile Phe Ser Gly
      85           90           95
Cys Ala Val Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
      100          105          110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115          120          125
Pro

```

<210> 2119

<211> 313

<212> PRT

<213> Homo sapien (7248974-19-1-3170)

<220>

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 2119

```

Met Leu Gly Asn Tyr Ser Ser Ala Thr Glu Phe Phe Leu Leu Gly Phe
 1           5           10           15
Pro Gly Ser Gln Glu Val Arg Arg Ile Leu Phe Val Asn Phe Phe Phe
          20           25           30
Leu Tyr Ala Val Thr Val Met Gly Asn Thr Val Ile Ile Val Thr Val
          35           40           45
Cys Val Asp Lys His Leu Gln Ser Pro Met Tyr Phe Phe Leu Gly His
          50           55           60
Leu Cys Val Leu Glu Ile Leu Ile Thr Ser Thr Ala Ala Pro Phe Met
          65           70           75           80
Leu Trp Gly Leu Leu Leu Pro Ser Thr Gln Ile Met Ser Leu Thr Ala
          85           90           95
Cys Ala Ala Gln Leu Leu Tyr Leu Ser Leu Gly Thr Ser Glu Leu Ala
          100          105          110
Leu Met Gly Val Met Ala Val Asp His Tyr Val Ala Val Cys Asn Pro
          115          120          125
Leu Arg Tyr Asn Ile Ile Met Asn Ser Ser Thr Cys Val Trp Met Val
          130          135          140
Ile Val Ser Trp Val Phe Gly Phe Leu Phe Gln Ile Trp Pro Val Tyr
          145          150          155          160
Ala Thr Phe Gln Leu Thr Phe Cys Lys Ser Asn Val Leu Asp His Phe
          165          170          175
Tyr Cys Asp Xaa Gly Gln Leu Leu Lys Val Ser Cys Glu Asp Thr Leu
          180          185          190
Phe Thr Glu Phe Ile Leu Phe Leu Met Ala Val Phe Ile Ile Ile Gly
          195          200          205
Ser Leu Ile Pro Thr Ile Val Ser Tyr Thr Tyr Ile Ile Ser Thr Ile
          210          215          220
Leu Lys Ile Pro Leu Ala Ser Gly Trp Arg Lys Ser Phe Ser Thr Cys
          225          230          235          240
Ala Ser His Phe Thr Cys Val Val Ile Gly Tyr Ser Ser Cys Leu Phe
          245          250          255
Leu Tyr Thr Lys Pro Lys Gln Thr Gln Ala Ala Lys Tyr Asn Arg Ile
          260          265          270
Ala Ser Leu Leu Val Leu Val Val Thr Pro Phe Leu Asn Pro Phe Ile
          275          280          285
Phe Thr Leu Arg Asn Asp Lys Phe Ile Gln Ala Phe Gly Asp Gly Met
          290          295          300
Lys His Cys Tyr Gln Leu Leu Arg Ile
          305          310

```

<210> 2120

<211> 138

<212> PRT

<213> Homo sapien (7248974-26-1-596)

<220>

<221> VARIANT

<222> (1)...(138)

<223> Xaa = Any Amino Acid

<400> 2120

```

Leu Leu Ser Leu Trp Ile Phe Thr Leu Phe Cys Tyr Tyr Val Xaa Tyr
 1           5           10           15
Cys Asp Glu Lys Pro Leu Phe Val Thr Leu Ile Pro Lys Cys Val
          20           25           30

```

Ser Asp Ile Xaa Gly Met Asn Phe Tyr Lys Cys Asn Cys Trp Val Met
 35 40 45
 Gly Met Ser Asn Phe Asn Ser Phe Tyr Gln Val Phe Ile Glu His Arg
 50 55 60
 Val Phe Ile Val Xaa Pro Ala Val Gly Gly Cys Phe Phe Ile Val Ser
 65 70 75 80
 Asn Ile Val Cys Xaa Xaa Thr Leu Gly Lys Lys Leu Asn Ile Phe Ile
 85 90 95
 Lys Ser Asn Ser His Leu Thr Thr Ile Ser Ile Tyr Gln Arg Gly Gly
 100 105 110
 Met Val Thr Trp Ile Gly His Ser Asn Ser Ser Ser Tyr Gln Xaa Thr
 115 120 125
 Xaa Asp Tyr Ser Leu Leu Tyr Xaa Leu Ile
 130 135

<210> 2121

<211> 161

<212> PRT

<213> Homo sapien (7248974-31-3444-4455)

<220>

<221> VARIANT

<222> (1)...(161)

<223> Xaa = Any Amino Acid

<400> 2121

Ile Cys Gly Ser His Ser Gly Val Thr Glu Phe Cys Leu Leu Gly Phe
 1 5 10 15
 Pro Gly Ser Gln Xaa Val Cys His Leu Leu Pro Ser Ser Phe Val Ser
 20 25 30
 Ile Val Ile Arg Asn Tyr Val Ile Ile Ile Val Cys Val Glu Lys Cys
 35 40 45
 Leu Leu Phe Leu Leu Tyr Leu Phe Tyr Gly Asp Leu Ser Val Met Glu
 50 55 60
 Ile Leu Ile Thr Tyr Thr Ala Val Pro Leu Met Leu Arg Gly Cys Tyr
 65 70 75 80
 Phe Pro Xaa Phe Lys Gln Tyr Leu Xaa Xaa His Val Ser Val Gln Leu
 85 90 95
 Tyr Met Asn Phe Phe Gly Gly Thr Gln Glu Phe Ala Leu Leu Gly Val
 100 105 110
 Met Thr Val Asn His Tyr Val Ala Leu Cys Asn Ser Leu Lys Xaa Asn
 115 120 125
 Ile Ile Met Ser Ser Thr His Cys Ile Trp Leu Val Ile Val Leu Leu
 130 135 140
 Ile Gly Phe Leu Ser Glu Ile Trp Ser Val Tyr Ala Thr Phe Gln Leu
 145 150 155 160
 Pro

<210> 2122

<211> 169

<212> PRT

<213> Homo sapien (7249005-11-1-1318)

<220>

<221> VARIANT

<222> (1)...(169)

<223> Xaa = Any Amino Acid

<400> 2122

Asn Ser Glu Ser Lys His Phe Leu Leu Leu Lys Leu Cys Ser Met Phe

```

1           5           10           15
Ala Val Thr Phe Leu Ser Leu Ile Leu Ser Gly Lys Gly Leu Gln Phe
                20           25           30
Pro Phe Tyr Phe Ser Glu Cys Asn Cys Lys Val Ser Asp Val Phe Thr
                35           40           45
Val Glu Thr Arg Glu Gln Glu Ala Pro Met Lys Thr Thr Gly Phe Tyr
                50           55           60
Gly Gly Ile Met Val Trp Xaa Val Glu Ala Cys Tyr Ser Ser Cys Ile
65           70           75           80
Ser Leu Gly Ser Asn Pro Asp Tyr Thr Ala Tyr Gly Ala Leu Thr Ala
                85           90           95
Arg Xaa Pro Gln Glu Phe Leu Cys Trp Xaa Asn Arg Phe Ile Ile Met
                100          105          110
Pro Val Asn Leu Lys Met Leu Xaa Val Lys Thr Ile Trp Cys Phe Ser
                115          120          125
Arg Thr Gln Xaa Ser Leu Thr Val Ile Thr Ile Phe Pro Leu Pro Thr
130          135          140
Phe Asn Lys Xaa Ile Ile Tyr Ile Tyr Xaa Thr Lys Glu Ile Xaa Ser
145          150          155          160
Cys Phe Ser Glu Thr Thr Gln Phe Tyr
                165

```

<210> 2123
 <211> 110
 <212> PRT
 <213> Homo sapien (7249007-9-15200-16107)

<220>
 <221> VARIANT
 <222> (1)...(110)
 <223> Xaa = Any Amino Acid

```

<400> 2123
Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
1           5           10           15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Trp Leu
                20           25           30
Ser Leu Ser Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile
                35           40           45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Ile Tyr Phe Phe
50           55           60
Leu Phe Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Ala Met Val
65           70           75           80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr
                85           90           95
Ala Gly Cys Leu Thr Xaa Met Ser Phe Phe Val Leu Phe Phe
                100          105          110

```

<210> 2124
 <211> 241
 <212> PRT
 <213> Homo sapien (7249007-9-22951-24848)

<220>
 <221> VARIANT
 <222> (1)...(241)
 <223> Xaa = Any Amino Acid

```

<400> 2124
Leu Arg Gln Leu His Asn Leu Phe Leu Pro Val Gly Phe Phe Leu Ser
1           5           10           15

```

Ser Tyr Ser Phe Xaa Val Ile Trp His Asn Leu Asn Ser Val Thr Lys
 20 25 30
 Phe Ser Ser Lys Thr Asp Glu Ser Lys Leu Lys Ser Xaa Cys Lys Val
 35 40 45
 Lys Ser Leu Phe Phe Thr Tyr Ala Gly Cys Cys Glu Lys Leu Leu Leu
 50 55 60
 Ala Val Glu Lys Arg Asp Arg Ser Phe Leu Phe Ile His Phe Leu Leu
 65 70 75 80
 His Xaa Ser Thr Ala Val Ser Asp His Ala Lys Val Glu Pro Gly Val
 85 90 95
 Gly Arg Arg Glu Arg Gly Xaa Gly Lys Ser His Xaa Leu Thr Leu Lys
 100 105 110
 Xaa Asp Gly Phe Thr Phe Ser Gly Pro Gly Gln Cys Leu Leu Phe Leu
 115 120 125
 Thr His Ile Lys Pro Leu Xaa Met His Leu Thr Met Gly Ala Ser Pro
 130 135 140
 Leu Pro Glu Val Arg Pro Pro Asp Phe Phe Gln Phe Pro Val Val Pro
 145 150 155 160
 His Asn Pro His Ser Trp Thr Phe Thr Gln Tyr Val Arg Leu Pro Ser
 165 170 175
 Trp Val Gln Ser Leu Ser Lys Gln Leu Thr His Phe Ser Phe His Gly
 180 185 190
 Gln Ser Phe Lys Ser Ala Tyr Ile Xaa Leu Ala Ile Ser Gly Ala Val
 195 200 205
 Thr Pro Ile Leu Leu Gln Arg Pro Arg Gly Gln Ser Ser Val Ala Val
 210 215 220
 Xaa His Ile Pro Asp Asp Arg Ile His Thr Leu Lys Pro Leu Ser Gly
 225 230 235 240
 Pro

<210> 2125

<211> 318

<212> PRT

<213> Homo sapien (7249162-23-8972-11111)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2125

Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
 1 5 10 15
 Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
 20 25 30
 Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
 35 40 45
 Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe
 50 55 60
 Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val
 65 70 75 80
 Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu
 85 90 95
 Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu
 100 105 110
 Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr
 130 135 140
 Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro

145				150				155				160			
Asp	Val	Phe	Leu	Val	Lys	Arg	Leu	Pro	Phe	Cys	His	Ser	Asn	Leu	Leu
				165					170					175	
Pro	His	Thr	Tyr	Cys	Glu	His	Met	Ala	Val	Ala	Lys	Phe	Ala	Cys	Ala
			180					185					190		
Asp	Ile	His	Val	Asn	Val	Trp	Tyr	Gly	Leu	Ser	Val	Leu	Leu	Tyr	Thr
	195						200					205			
Val	Val	Leu	Asp	Ala	Leu	Leu	Ile	Leu	Val	Ser	Xaa	Ser	Phe	Ile	Leu
	210					215					220				
Tyr	Thr	Gly	Phe	His	Leu	Pro	Ser	Pro	Gly	Ala	Arg	Gln	Lys	Ala	Leu
225					230					235				240	
Gly	Thr	Cys	Gly	Ser	Pro	Leu	Arg	Val	Ile	Ser	Met	Phe	Tyr	Leu	Pro
				245					250					255	
Gly	Ile	Phe	Thr	Ile	Ile	Thr	Gln	Arg	Phe	Gly	His	His	Val	Pro	Phe
			260				265						270		
His	Thr	His	Ile	Leu	Leu	Gly	Asn	Val	Trp	Val	Leu	Ala	Pro	Pro	Met
	275						280					285			
Leu	Asn	Pro	Ile	Ile	Tyr	Gly	Ile	Asn	Thr	Arg	Gln	Ile	Gln	Glu	Cys
	290					295					300				
Val	Leu	Ser	Leu	Leu	Ser	Ser	Gln	Arg	Lys	Xaa	Cys	Xaa	Ile		
305					310					315					

<210> 2126

<211> 322

<212> PRT

<213> Homo sapien (7249220-22-20773-24242)

<220>

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 2126

Met	Ser	Val	Val	Glu	Ala	Asn	Asn	Ile	Ser	Gly	Pro	Val	Ser	Glu	Phe
1				5				10						15	
Ile	Leu	Leu	Gly	Phe	Pro	Cys	Arg	Cys	Arg	Glu	Thr	Lys	Ile	Leu	Leu
			20				25					30			
Phe	Val	Val	Phe	Ser	Leu	Ile	Tyr	Leu	Leu	Thr	Leu	Met	Gly	Asn	Thr
	35					40					45				
Ser	Ile	Ile	Cys	Ala	Val	Trp	Ser	Ser	Gln	Lys	Leu	His	Thr	Pro	Met
	50					55					60				
Tyr	Ile	Leu	Leu	Ala	Asn	Phe	Ser	Phe	Leu	Glu	Ile	Cys	Cys	Ile	Ser
65				70						75				80	
Ser	Asp	Val	Pro	Asn	Met	Leu	Ala	Asn	Leu	Ile	Ser	His	Ile	Lys	Ser
				85					90					95	
Ile	Ser	Tyr	Ala	Gly	Cys	Leu	Leu	Gln	Phe	Phe	Tyr	Phe	Ser	Met	Cys
			100					105					110		
Ala	Ala	Glu	Gly	Tyr	Phe	Leu	Ser	Val	Met	Ser	Phe	Asp	Arg	Phe	Leu
	115						120					125			
Thr	Ile	Cys	Arg	Pro	Leu	His	Tyr	Pro	Thr	Val	Met	Thr	His	His	Leu
	130					135					140				
Cys	Val	Xaa	Leu	Val	Ala	Phe	Cys	Arg	Ala	Gly	Gly	Phe	Leu	Ser	Ile
145					150					155				160	
Leu	Met	Pro	Ala	Val	Leu	Met	Ser	Arg	Val	Pro	Phe	Cys	Gly	Pro	Asn
				165					170					175	
Ile	Thr	Asp	His	Phe	Phe	Cys	Asn	Leu	Gly	Pro	Leu	Leu	Ala	Leu	Ser
			180					185					190		
Cys	Ala	Pro	Val	Pro	Lys	Thr	Thr	Leu	Thr	Cys	Ala	Thr	Val	Ser	Ser
	195						200					205			
Leu	Ile	Ile	Phe	Ile	Thr	Phe	Leu	Tyr	Ile	Leu	Gly	Ser	His	Ile	Leu
	210					215					220				

Val Leu Arg Ala Val Leu Trp Val Pro Ala Gly Ser Gly Arg Asn Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Ala Ser His Phe Leu Val Val Ser Phe Phe Tyr
 245 250 255
 Gly Ser Val Met Val Met Tyr Val Ser Pro Gly Ser Arg Ser Arg Pro
 260 265 270
 Gly Thr Gln Lys Phe Val Thr Leu Phe Tyr Cys Thr Ala Thr Pro Phe
 275 280 285
 Phe Asn Pro Leu Thr Tyr Ser Leu Trp Asn Lys Asp Met Thr Asp Ala
 290 295 300
 Leu Lys Lys Val Leu Gly Val Pro Ser Lys Glu Ile Ser Trp Asn Thr
 305 310 315 320
 Leu Lys

<210> 2127

<211> 311

<212> PRT

<213> Homo sapien (7249282-10-14985-16332)

<400> 2127

Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly
 1 5 10 15
 Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu
 20 25 30
 Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile
 35 40 45
 Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys
 65 70 75 80
 Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys
 85 90 95
 Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe
 100 105 110
 Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro
 115 120 125
 Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val
 130 135 140
 Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val
 145 150 155 160
 Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe
 165 170 175
 Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr
 180 185 190
 Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val
 195 200 205
 Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile
 210 215 220
 Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Ala Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile Phe
 245 250 255
 Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln Val
 260 265 270
 Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Leu Ile Arg Val Met
 290 295 300
 Gln Arg Arg Gln Asp Ser Arg
 305 310

<210> 2128
 <211> 306
 <212> PRT
 <213> Homo sapien (7249282-10-21300-24858)

<220>
 <221> VARIANT
 <222> (1)...(306)
 <223> Xaa = Any Amino Acid

<400> 2128
 Thr Ala Gly Ser Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly
 1 5 10 15
 Tyr Ala Asn His Pro Glu Leu Gln Val Ser Phe Phe Leu Met Phe Leu
 20 25 30
 Phe Ile Tyr Leu Phe Thr Ile Leu Gly Asn Leu Gly Leu Ile Met Leu
 35 40 45
 Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Val Thr Pro Lys
 65 70 75 80
 Thr Leu Ala Asn Phe Gln Ser Asn Gln Arg Ser Ile Ser Phe Val Gly
 85 90 95
 Cys Phe Val Gln Met Tyr Phe Ser Val Gly Leu Val Cys Thr Glu Cys
 100 105 110
 Phe Leu Leu Gly Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Trp Asn
 115 120 125
 Pro Tyr Ser Val Val Ile Ser Xaa Lys Ala Cys Asn Trp Leu Gly Val
 130 135 140
 Met Ser Tyr Thr Ile Gly Phe Thr Asn Ser Leu Val Ser Val Trp Val
 145 150 155 160
 Ile Ser Gly Leu Phe Cys Asp Ser Ser Ile Asn Phe Phe Phe Cys Asp
 165 170 175
 Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Ala Phe Ser Thr Glu
 180 185 190
 Met Val Ser Phe Ala Leu Ala Gly Phe Thr Leu Leu Gly Ser Ile Leu
 195 200 205
 Ile Ile Thr Val Thr Tyr Ile Ala Ile Thr Ser Ala Ile Leu Lys Asn
 210 215 220
 Gln Trp Ala Ala Gly Trp Gln Lys Ala Phe Ser Thr Cys Ala Phe His
 225 230 235 240
 Leu Met Ala Leu Thr Ile Phe Tyr Gly Ser Leu Ile Phe Thr Tyr Leu
 245 250 255
 Gln Leu Asp Lys Thr Ser Ser Leu Ile His Ala Gln Leu Ala Phe Val
 260 265 270
 Phe Tyr Met Thr Val Ile Pro Met Leu Asn Pro Leu Ile Xaa Ser Leu
 275 280 285
 Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Val Ile His Arg Lys
 290 295 300
 Leu Phe
 305

<210> 2129
 <211> 327
 <212> PRT
 <213> Homo sapien (7249282-10-488-2060)

<220>
 <221> VARIANT
 <222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 2129

Lys Leu Gln Leu Asn Asn Phe Thr Glu Val Thr Met Phe Ile Leu Ile
 1 5 10 15
 Ser Phe Thr Glu Glu Phe Asp Val Gln Val Phe Leu Phe Leu Leu Phe
 20 25 30
 Leu Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val
 35 40 45
 Pro Ile Ile Gly Asp Phe Trp Leu His Ser Pro Met Tyr Tyr Phe Leu
 50 55 60
 Gly Val Leu Ser Phe Leu Asp Val Cys Tyr Ser Thr Val Val Thr Pro
 65 70 75 80
 Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Leu
 85 90 95
 Gly Cys Ala Thr Gln Met Phe Leu Ala Cys Thr Phe Gly Thr Thr Glu
 100 105 110
 Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr
 115 120 125
 Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro
 130 135 140
 Leu Ile Thr Ala Ser Tyr Val Ala Ser Ile Leu His Ala Thr Ile His
 145 150 155 160
 Thr Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg
 165 170 175
 His Val Phe Cys Asn Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp
 180 185 190
 Thr His Val Ile Gln Leu Leu Phe Phe Tyr Phe Val Gly Ser Ile Glu
 195 200 205
 Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu
 210 215 220
 Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser
 225 230 235 240
 Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile
 245 250 255
 Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp
 260 265 270
 Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro
 275 280 285
 Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg
 290 295 300
 Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu Xaa Phe Xaa Asn Xaa
 305 310 315 320
 Val Lys Leu Gln Ile Ile Leu
 325

<210> 2130

<211> 319

<212> PRT

<213> Homo sapien (7249282-11-14537-16718)

<400> 2130

Met Asn His Val Val Lys His Asn His Thr Ala Val Thr Lys Val Thr
 1 5 10 15
 Glu Phe Ile Leu Met Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro
 20 25 30
 Leu Phe Gly Leu Phe Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn
 35 40 45
 Leu Gly Met Val Ile Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Arg His Leu Ser Ile Thr Asp Leu Gly Tyr Ser

65					70					75				80	
Thr	Val	Ile	Ala	Pro	Lys	Met	Leu	Val	Asn	Phe	Ile	Val	His	Lys	Asn
				85					90					95	
Thr	Ile	Ser	Tyr	Asn	Trp	Tyr	Ala	Thr	Gln	Leu	Ala	Phe	Phe	Glu	Ile
			100					105					110		
Phe	Ile	Ile	Ser	Glu	Leu	Phe	Ile	Leu	Ser	Ala	Met	Ala	Tyr	Asp	Arg
		115					120					125			
Tyr	Val	Ala	Ile	Cys	Lys	Pro	Leu	Leu	Tyr	Val	Ile	Ile	Met	Ala	Glu
	130						135				140				
Lys	Val	Leu	Trp	Val	Leu	Val	Ile	Val	Pro	Tyr	Leu	Tyr	Ser	Thr	Phe
145					150				155						160
Val	Ser	Leu	Phe	Leu	Thr	Ile	Lys	Leu	Phe	Lys	Leu	Ser	Phe	Cys	Gly
			165						170					175	
Ser	Asn	Ile	Ile	Ser	Tyr	Phe	Tyr	Cys	Asp	Cys	Ile	Pro	Leu	Met	Ser
		180						185					190		
Ile	Leu	Cys	Ser	Asp	Thr	Asn	Glu	Leu	Glu	Leu	Ile	Ile	Leu	Ile	Phe
	195						200					205			
Ser	Gly	Cys	Asn	Leu	Leu	Phe	Ser	Leu	Ser	Ile	Val	Leu	Ile	Ser	Tyr
	210					215					220				
Met	Phe	Ile	Leu	Val	Ala	Ile	Leu	Arg	Met	Asn	Ser	Arg	Lys	Gly	Arg
225					230					235					240
Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Ser	Ser	His	Leu	Thr	Val	Val	Ile	Met
			245						250					255	
Phe	Tyr	Gly	Thr	Leu	Leu	Phe	Ile	Tyr	Leu	Gln	Pro	Lys	Ser	Ser	His
		260						265					270		
Thr	Leu	Ala	Ile	Asp	Lys	Met	Ala	Ser	Val	Phe	Tyr	Thr	Leu	Leu	Ile
	275						280					285			
Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys
	290					295					300				
Asp	Ala	Leu	Lys	Arg	Thr	Leu	Thr	Asn	Arg	Phe	Lys	Ile	Pro	Ile	
305					310					315					

<210> 2131

<211> 317

<212> PRT

<213> Homo sapien (7249282-11-25530-27263)

<220>

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 2131

Met	Gly	Gln	Lys	Asn	Leu	Thr	Val	Leu	Thr	Glu	Leu	Ile	Leu	Met	Glu
1				5					10					15	
Ile	Thr	Arg	Arg	Leu	Glu	Leu	Gln	Leu	Ser	Leu	Phe	Trp	Val	Phe	Leu
		20						25				30			
Ile	Ile	Cys	Thr	Phe	Thr	Val	Val	Ser	Lys	Glu	Cys	Ile	Ile	Ile	Leu
	35						40				45				
Asn	Asn	Val	Asp	Leu	Gly	Leu	Gln	Thr	Phe	Val	Tyr	Phe	Leu	Ile	Arg
	50					55					60				
Tyr	Leu	Asn	Phe	Ile	Asn	Leu	Gly	Asn	Ser	Met	Val	Ile	Tyr	Pro	Lys
65					70				75					80	
Ile	Leu	Val	Asn	Phe	Val	Val	Ala	Gln	Asn	Ala	Ile	Pro	Cys	Tyr	Ala
			85						90					95	
Cys	Thr	Met	Gln	Met	Ala	Phe	Phe	Ile	Met	Phe	Ile	Ile	Cys	Glu	Leu
		100						105				110			
Phe	Val	Ser	Ser	Ala	Met	Ala	Tyr	Asp	His	Tyr	Val	Asp	Ile	His	Ser
		115					120					125			
Leu	Leu	Pro	Xaa	Asn	Val	Met	Ser	Gln	Glu	Leu	Cys	His	Val	Leu	Val
	130					135					140				

Ala Ile Pro Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Val Thr Ile
 145 150 155 160
 Lys Ile Phe Ile Leu Ala Phe Tyr Gly Ser Asn Val Ile Ser Tyr Phe
 165 170 175
 Tyr Cys Xaa Asp Val Ser Leu Leu Ala Met Val Asp Ser Asn Ala Xaa
 180 185 190
 Gly Ile Glu Met Leu Ile Thr Leu Phe Ser Val Leu Asn Leu Ile Phe
 195 200 205
 Phe Leu Leu Val Val Leu Met Ser Ser Met Leu Ile Leu Leu Thr Val
 210 215 220
 Cys Xaa Met His Ser Ala Gly Glu Gln Xaa Lys Thr Phe Phe Thr Tyr
 225 230 235 240
 Val Ser Cys Leu Ile Val Val Val Val Phe Cys Gly Phe Leu Tyr Phe
 245 250 255
 Met Tyr Leu Gln Leu Lys Phe Ser Ser Phe Phe Phe Asp Asn Asn Lys
 260 265 270
 Met Thr Ser Met Phe Ser Ser Leu Val Ile Thr Met Leu Tyr His Leu
 275 280 285
 Val Cys Ser Val Lys Asn Lys Gly Ser Lys Lys Asn Ala Phe Tyr Ser
 290 295 300
 Phe Phe Met Lys Gln Xaa Lys Leu Cys Asn Leu Met Val
 305 310 315

<210> 2132

<211> 318

<212> PRT

<213> Homo sapien (7249282-5-5312-7865)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2132

Met Lys Pro Thr Ile Gln Met Ala Ser Gly Asn Leu Thr Trp Val Thr
 1 5 10 15
 Glu Phe Ile Leu Val Gly Val Ser Asp Asp Pro Glu Leu Gln Ile Pro
 20 25 30
 Leu Phe Leu Val Phe Leu Val Leu Tyr Leu Leu Thr Val Ala Gly Asn
 35 40 45
 Leu Gly Ile Ile Thr Leu Thr Ser Val Asp Pro Gln Leu Gln Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Xaa His Leu Ala Ile Ile Asn Leu Cys Asn Ser
 65 70 75 80
 Thr Val Val Ala Pro Lys Met Leu Val Asn Phe Leu Val Thr Lys Lys
 85 90 95
 Thr Ile Ser Tyr Tyr Gly Cys Ala Ala Gln Leu Gly Gly Phe Leu Val
 100 105 110
 Phe Ile Val Ala Glu Ile Phe Thr Leu Ala Ala Met Ala Tyr Asp Arg
 115 120 125
 Tyr Val Ala Ile Trp Ser Pro Leu Leu Tyr Ala Val Val Val Ser Pro
 130 135 140
 Lys Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile
 145 150 155 160
 Thr Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser
 165 170 175
 Ser Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala
 180 185 190
 Leu Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe
 195 200 205
 Ser Gly Thr Asn Leu Leu Phe Ser Met Ile Val Val Leu Ile Ser Tyr

210	215	220
Phe Asn Ile Val Ile Thr	Ile Leu Arg Ile Arg	Ser Ser Glu Gly Arg
225	230	235
Gln Lys Ala Phe Ser Thr	Cys Ala Ser His Met	Ile Ala Val Val Val
	245	250
Phe Tyr Gly Thr Leu Leu	Phe Met Tyr Leu Gln Pro	Arg Ser Asn His
	260	265
Ser Leu Asp Thr Asp Lys	Met Ala Ser Val Phe Tyr	Thr Leu Val Ile
	275	280
Pro Val Leu Asn Pro Leu	Ile Tyr Ser Leu Arg	Asn Lys Asn Val Lys
	290	295
Asp Ala Leu Lys Arg Phe	Leu Asp Asn Pro Cys	Arg Ser Leu
305	310	315

<210> 2133

<211> 279

<212> PRT

<213> Homo sapien (7264174-61-26274-29247)

<220>

<221> VARIANT

<222> (1)...(279)

<223> Xaa = Any Amino Acid

<400> 2133

Leu Pro Pro Leu Phe Phe Arg Val Phe Val Ile Leu Phe Val Ser Leu
1 5 10 15
Leu Phe Val Lys Leu Cys Ile Leu Phe Leu Ile Ile Leu Leu Val Lys
20 25 30
Phe Leu Leu Lys Thr Lys Ile Ala Met Thr Tyr Phe Thr Tyr Leu Ser
35 40 45
Asn Tyr Lys Leu Lys Ala Xaa Asn Ser Ile Asp Phe His Ile His Met
50 55 60
Phe Val Tyr Val Tyr Ile Met Asn Lys Leu Val His Leu Lys Tyr Glu
65 70 75 80
Thr Leu Thr Ser Leu Pro Phe Phe Trp Asn Ser Leu Gly Cys Leu Asp
85 90 95
Thr Ser Xaa Phe Cys Phe Thr Phe Tyr Val Thr Tyr Ser Ser Leu Ile
100 105 110
Val Ile Asn Met Leu Tyr Phe Leu Ala Val Leu Ala Lys Ser Ser Phe
115 120 125
Ile Leu Cys Phe Asn Ser Leu Ser Val Asn Cys Asp Thr Phe Cys Val
130 135 140
Trp Leu Ser Cys Phe Gly Ile Val Tyr Leu Asp Val His Pro Ile Ala
145 150 155 160
His Cys Leu Phe Leu Lys Arg Leu Phe Lys Cys Tyr Val Phe Leu Xaa
165 170 175
Ser Leu Val Phe Cys Phe Met His Ala Leu Leu Pro Xaa Thr Leu Lys
180 185 190
Asn Thr Cys Phe Asp Val Leu Phe Ile Phe Ile Cys Glu Lys Ser Leu
195 200 205
Leu Ala Asn Met Ser Phe Val Thr Ile Val Ser Ser Leu Ile Leu Leu
210 215 220
Thr Asn Xaa Glu Ile Ile Ser Phe Ser Ser Val Ile Leu Cys Gly Thr
225 230 235 240
Ile His Leu Asn Leu Ser Ser Phe Phe Leu His Arg Phe Phe Ile Phe
245 250 255
Phe Phe Cys Leu Lys Ser Ala Asn Ile Tyr Leu Asn Val Asp Leu Leu
260 265 270
Ser Ile Ile Leu Thr Leu Val
275

<210> 2134
 <211> 314
 <212> PRT
 <213> Homo sapien (7283250-10-5473-8590)

<400> 2134
 Met Glu Arg Gly Asn Trp Thr Leu Val Thr Glu Phe Ile Leu Val Gly
 1 5 10 15
 Ile Pro Thr Thr Arg Ala Leu Gly Gly Leu Leu Phe Val Ile Phe Tyr
 20 25 30
 Pro Ala Tyr Leu Val Thr Val Leu Gly Asn Thr Leu Ile Ile Ile Leu
 35 40 45
 Ile Leu Val Asp Tyr Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Glu Thr Leu Thr Ile Thr Cys Ala Val Pro Lys
 65 70 75 80
 Met Leu Glu Gly Phe Pro Ser Glu Arg Lys Ser Ile Thr Ser Gly Glu
 85 90 95
 Cys Ser Ala Gln Ser Tyr Phe Tyr Phe Leu Ser Gly Cys Thr Glu Phe
 100 105 110
 Ile Pro Phe Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Ser
 115 120 125
 Pro Leu Gln Tyr Pro Ala Ile Met Thr Ser Ser Leu Cys Ala His Leu
 130 135 140
 Val Ile Leu Ser Trp Val Gly Gly Phe Leu Leu Met Leu Pro Ser Thr
 145 150 155 160
 Ile Leu Lys Ala Gly Leu Pro His Cys Gly Pro Asn Val Ile Glu His
 165 170 175
 Phe Phe Cys Asp Ser Ala Pro Leu Leu His Leu Ala Cys Ala Asp Ile
 180 185 190
 Arg Ala Ile Glu Leu Leu Asp Phe Leu Ser Ser Leu Val Leu Ile Leu
 195 200 205
 Ser Ser Leu Ser Leu Thr Val Val Ser Tyr Val Tyr Ile Ile Ser Thr
 210 215 220
 Ile Leu Lys Ile Pro Ser Gly Gln Gly Gln Arg Lys Ala Phe Ala Thr
 225 230 235 240
 Cys Ala Ser His Phe Thr Val Val Ser Val Gly Tyr Gly Ile Ser Ile
 245 250 255
 Phe Val Tyr Val His Pro Ser Gln Lys Ser Ser Leu His Leu Asn Lys
 260 265 270
 Ile Leu Phe Ile Leu Ser Ser Ile Ile Thr Pro Leu Leu Asn Pro Phe
 275 280 285
 Val Phe Ser Leu Trp Asn Glu Pro Met Lys Asp Ala Leu Lys Asp Ala
 290 295 300
 Val Gly Arg Arg Thr Glu Leu Ala Gln Arg
 305 310

<210> 2135
 <211> 309
 <212> PRT
 <213> Homo sapien (7283250-11-11521-16137)

<400> 2135
 Met Ala Asn Leu Thr Ile Val Thr Glu Phe Ile Leu Met Gly Phe Ser
 1 5 10 15
 Thr Asn Lys Asn Met Cys Ile Leu His Ser Ile Leu Phe Leu Leu Ile
 20 25 30
 Tyr Leu Cys Ala Leu Met Gly Asn Val Leu Ile Ile Met Ile Thr Thr
 35 40 45
 Leu Asp His His Leu His Thr Pro Val Tyr Phe Phe Leu Lys Asn Leu

```

      50              55              60
Ser Phe Leu Asp Leu Cys Leu Ile Ser Val Thr Ala Pro Lys Ser Ile
65              70              75              80
Ala Asn Ser Leu Ile His Asn Asn Ser Ile Ser Phe Leu Gly Cys Val
      85              90              95
Ser Gln Val Phe Leu Leu Leu Ser Ser Ala Ser Ala Glu Leu Leu Leu
      100              105              110
Leu Thr Val Met Ser Phe Asp Arg Tyr Thr Ala Ile Cys His Pro Leu
      115              120              125
His Tyr Asp Val Ile Met Asp Arg Ser Thr Cys Val Gln Arg Ala Thr
      130              135              140
Val Ser Trp Leu Tyr Gly Gly Leu Ile Ala Val Met His Thr Ala Gly
145              150              155              160
Thr Phe Ser Leu Ser Tyr Cys Gly Ser Asn Met Val His Gln Phe Phe
      165              170              175
Cys Asp Ile Pro Gln Leu Leu Ala Ile Ser Cys Ser Glu Asn Leu Ile
      180              185              190
Arg Glu Ile Ala Leu Ile Leu Ile Asn Val Val Leu Asp Phe Cys Cys
      195              200              205
Phe Ile Val Ile Ile Ile Thr Tyr Val His Val Phe Ser Thr Val Lys
      210              215              220
Lys Ile Pro Ser Thr Glu Gly Gln Ser Lys Ala Tyr Ser Ile Cys Leu
225              230              235              240
Pro His Leu Leu Val Val Leu Phe Leu Ser Thr Gly Phe Ile Ala Tyr
      245              250              255
Leu Lys Pro Ala Ser Glu Ser Pro Ser Ile Leu Asp Ala Val Ile Ser
      260              265              270
Val Phe Tyr Thr Met Leu Pro Pro Thr Phe Asn Pro Ile Ile Tyr Ser
      275              280              285
Leu Arg Asn Lys Ala Ile Lys Val Ala Leu Gly Met Leu Ile Lys Gly
      290              295              300
Lys Leu Thr Lys Lys
305

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<210> 2136

<211> 313

<212> PRT

<213> Homo sapien (7283250-5-1-3004)

<400> 2136

```

Met Glu Lys Arg Asn Leu Thr Val Val Arg Glu Phe Val Leu Leu Gly
1      5      10      15
Leu Pro Ser Ser Ala Glu Gln Gln His Leu Leu Ser Val Leu Phe Leu
      20      25      30
Cys Met Tyr Leu Ala Thr Thr Leu Gly Asn Met Leu Ile Ile Ala Thr
      35      40      45
Ile Gly Phe Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ala Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Gln
65      70      75      80
Met Val Val Asn Ile Leu Thr Gly Thr Lys Thr Ile Ser Phe Ala Gly
      85      90      95
Cys Leu Thr Gln Leu Phe Phe Phe Val Ser Phe Val Asn Met Asp Ser
      100      105      110
Leu Leu Leu Cys Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115      120      125
Pro Leu His Tyr Thr Ala Arg Met Asn Leu Cys Leu Cys Val Gln Leu
130      135      140
Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His Ala Leu Leu His Thr
145      150      155      160
Val Leu Ile Ala Gln Leu Ser Phe Cys Ala Ser Asn Ile Ile His His

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          165          170          175
Phe Phe Cys Asp Leu Asn Pro Leu Leu Gln Leu Ser Cys Ser Asp Val
          180          185          190
Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly Gly Leu Leu Ala Leu
          195          200          205
Thr Pro Leu Val Cys Il Leu Val Ser Tyr Gly Leu Ile Phe Ser Thr
          210          215          220
Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln Arg Ala Val Ser Thr
          225          230          235
Cys Ser Cys His Leu Ser Val Val Val Leu Phe Tyr Gly Thr Ala Ile
          245          250          255
Ala Val Tyr Phe Ser Pro Ser Ser Pro His Met Pro Glu Ser Asp Thr
          260          265          270
Leu Ser Thr Ile Met Tyr Ser Met Val Ala Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Thr Leu Arg Asn Arg Asp Met Lys Arg Gly Leu Gln Lys Met
          290          295          300
Leu Leu Lys Cys Thr Val Phe Gln Gln
          305          310

```

<210> 2137

<211> 310

<212> PRT

<213> Homo sapien (7283250-6-1-1725)

<220>

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 2137

```

Met Val Asn Phe Thr His Val Ser Glu Phe Val Leu Leu Gly Phe Gln
  1          5          10          15
Gly Gly Pro Gly Met Gln Ala Met Leu Phe Leu Ile Phe Leu Ile Leu
          20          25          30
Tyr Gly Ile Ala Val Val Gly Asn Leu Gly Met Ile Val Ile Ile Trp
          35          40          45
Val Asp Ala His Leu His Thr Pro Met Tyr Ala Phe Leu Gln Ser Leu
          50          55          60
Ser Leu Leu Asp Ile Cys Tyr Ser Ser Thr Ile Ala Pro Arg Ala Leu
          65          70          75          80
Ala Asn Ser Met Gln Glu Asp His Thr Ile Ser Phe Gly Gly Cys Ala
          85          90          95
Ala Gln Phe Phe Phe Leu Ser Leu Phe Gly Ile Thr Glu Ala Phe Leu
          100          105          110
Leu Ala Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu
          115          120          125
Leu Tyr Ser Val Ser Met Ser His Gln Val Cys Val Leu Leu Ile Ser
          130          135          140
Gly Ser Tyr Leu Trp Gly Val Val Asn Ala Ile Ala Gln Thr Thr Met
          145          150          155          160
Thr Phe Arg Leu Pro Phe Cys Gly Ser Asn Glu Ile Asn Asp Phe Phe
          165          170          175
Cys Asp Val Pro Pro Leu Leu Ser Leu Ser Cys Ser Asp Thr Phe Ile
          180          185          190
Asn Gln Leu Val Leu Leu Gly Leu Cys Gly Ser Ile Ile Val Ser Thr
          195          200          205
Phe Leu Ile Val Leu Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu
          210          215          220
Arg Ile Pro Thr Met Gln Gly Arg Xaa Lys Ala Phe Ser Thr Cys Ala
          225          230          235          240

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S r His Leu Thr Gly Val Cys Leu Phe Phe Gly Thr Val Phe Phe Met
 245 250 255
 Tyr Ala Gln Pro Ser Ala Ile Phe Phe Met Glu Gln Ser Lys Ile Val
 260 265 270
 Ser Ile Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Glu Val Lys Gln Ala Leu Arg Arg Ser Met Gln
 290 295 300
 Lys Leu Ser Leu Xaa Ser
 305 310

<210> 2138

<211> 320

<212> PRT

<213> Homo sapien (7321521-20-4435-9278)

<220>

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 2138

Met Ser Ser Arg Leu Met Asn Val Phe Ser Met Glu Thr Ile Asn Phe
 1 5 10 15
 Val Ser Cys Leu Ile Leu Met Gly Phe Pro Ser Ser Pro Glu Met Gln
 20 25 30
 Leu Leu Tyr Phe Gly Leu Phe Ser Val Ala Tyr Thr Leu Thr Pro Met
 35 40 45
 Gly Asn Ala Ala Ile Val Cys Ala Val Trp Xaa Asp Gln His Leu His
 50 55 60
 Thr Pro Met Tyr Thr Leu Gly Asn Phe Ser Leu Leu Glu Ile Trp
 65 70 75 80
 Tyr Val Thr Ala Thr Lys Leu Leu Ala Asn Phe Leu Ser Thr Ser Lys
 85 90 95
 Ser Ile Ser Phe Met Ser Cys Phe Ala Gln Phe Tyr Phe Phe Ser Leu
 100 105 110
 Gly Tyr Asp Glu Gly Phe Phe Leu Cys Ile Thr Ala Phe Asp Arg Tyr
 115 120 125
 Leu Ala Ile Cys Arg Pro Leu Arg Tyr Pro Cys Ile Met Thr Lys Gln
 130 135 140
 Val Cys Thr Gly Leu Ile Ile Phe Ala Trp Ser Cys Val Phe Val Ile
 145 150 155 160
 Phe Leu Thr Leu Val Ile Leu Ile Ser Gln Leu Ser Tyr Cys Gly Pro
 165 170 175
 Asn Ile Ile Asn His Phe Ile Cys Asp Pro Val Pro Leu Lys Met Leu
 180 185 190
 Ser Cys Ser Glu Asp Ile Ile Ile Thr Gln Leu Ile Tyr Ser Thr Phe
 195 200 205
 Asn Ser Val Phe Ile Ile Gly Thr Phe Leu Phe Ile Leu Cys Ser Tyr
 210 215 220
 Ala Leu Val Ile Leu Ala Ile Ile Arg Met Pro Ser Glu Ala Gly Lys
 225 230 235 240
 Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Leu
 245 250 255
 Phe Tyr Gly Ser Ile Met Val Met Tyr Val Ser Pro Gly Ser Ala His
 260 265 270
 Pro Ala Lys Asn Glu Lys Ile Ile Thr Leu Phe Phe Ser Val Ile Thr
 275 280 285
 Pro Leu Cys Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys
 290 295 300
 Asp Tyr Leu Arg Lys Ile Phe Arg Thr Gly Lys Asp Val Asn Lys Ile

305

310

315

320

<210> 2139

<211> 331

<212> PRT

<213> Homo sapien (7321521-21-4479-8486)

<220>

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 2139

```

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Arg
 1           5           10           15
Leu Thr Gln Phe Arg Asp Ile Xaa Leu Val Phe Val Leu Val Leu
      20           25           30
Ile Phe Tyr Phe Phe Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
      35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Lys
65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
      85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
      100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Thr Ile Cys Leu
      115          120          125
Pro Leu Gln Tyr Ser Thr Val Met Asn Ser Arg Ala Cys Tyr Ala Met
      130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
145          150          155          160
Val Leu Ile Ile Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
      165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
      180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
      195          200          205
Met Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
      210          215          220
Ile Arg Ala Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys
225          230          235          240
Thr Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe
      245          250          255
Ile Tyr Thr Cys Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser
      260          265          270
Leu Phe His Thr Val Ile Leu Pro Leu Leu Asn Pro Val Ile Tyr Thr
      275          280          285
Leu His Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys
      290          295          300
His Ile Ala Xaa Lys Arg Ala Lys Lys Lys Arg Ile Lys Ile Asp Cys
305          310          315          320
Lys Phe Tyr Leu Lys Leu Ile Cys Leu Phe Pro
      325          330

```

<210> 2140

<211> 313

<212> PRT

<213> Homo sapien (7321521-22-8611-12801)

<400> 2140

```

Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly
 1          5          10          15
Leu Ser Gln Thr Pro Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu
 20          25          30
Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr
 35          40          45
Ile Ser Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala
 50          55          60
Asn Leu Ala Phe Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Glu
 65          70          75          80
Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Asp Gly
 85          90          95
Cys Ile Ala Gln Leu Phe Phe Leu His Phe Ala Gly Ala Ser Glu Met
 100          105          110
Phe Leu Leu Thr Val Met Ala Phe Asp Leu Tyr Thr Ala Ile Cys Arg
 115          120          125
Pro Leu His Tyr Ala Thr Ile Met Asn Gln Arg Leu Cys Cys Ile Leu
 130          135          140
Val Ala Leu Ser Trp Arg Gly Gly Phe Ile His Ser Ile Ile Gln Val
 145          150          155          160
Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser
 165          170          175
Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr
 180          185          190
Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val
 195          200          205
Val Trp Leu Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu
 210          215          220
Phe Lys Lys Leu Ser Gly Ser Gly Glu Asn Thr Asn Arg Ala Met Ser
 225          230          235          240
Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser
 245          250          255
Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val
 260          265          270
Val Ser Val Phe Asn Thr Leu Ile Phe Pro Leu Arg Asn Pro Ile Ile
 275          280          285
Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Leu Val
 290          295          300
Thr Lys Tyr Ile Leu Cys Lys Glu Lys
 305          310

```

<210> 2141

<211> 134

<212> PRT

<213> Homo sapien (7321637-16-2663-3767)

<220>

<221> VARIANT

<222> (1)...(134)

<223> Xaa = Any Amino Acid

<400> 2141

```

His Met Val Asp Ile Leu Asn Arg Gln Thr Leu Leu Tyr Leu Val Leu
 1          5          10          15
Gly Leu Trp Leu Glu His Val Leu Pro Ser Ser Phe Gly Thr Val Met
 20          25          30
Val Pro Leu Cys Gly Pro Arg Met Thr Ala Arg Leu Leu Phe Leu Pro
 35          40          45
Val Pro Leu Ser Ala Glu Asn Glu Leu Arg Arg Ala Leu Leu Ser Thr
 50          55          60

```

Glu Ala His Thr Ile Ser Leu Val Gly Gln Arg Leu Ala Ile Pro Cys
 65 70 75 80
 Asn Asn Ile Ser Xaa Phe Ile Tyr Leu Ile Lys Asn Arg Asn Leu Gly
 85 90 95
 Gln Gln Pro Ala Tyr Ser Thr Cys Trp Asp His Xaa Leu Leu Val Ser
 100 105 110
 Leu Phe Tyr Phe Lys Thr Phe His Ile Xaa Thr His Gly Ser Thr Ser
 115 120 125
 Phe Thr Phe Ile Lys Leu
 130

<210> 2142

<211> 315

<212> PRT

<213> Homo sapien (7327747-39-1-1406)

<400> 2142

Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1 5 10 15
 Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val
 20 25 30
 Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
 35 40 45
 Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
 65 70 75 80
 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
 85 90 95
 Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
 100 105 110
 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
 115 120 125
 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
 130 135 140
 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
 145 150 155 160
 Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
 165 170 175
 His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp
 180 185 190
 Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
 195 200 205
 Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala Arg Ile Leu Gly
 210 215 220
 Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
 225 230 235 240
 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
 245 250 255
 Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
 260 265 270
 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys
 290 295 300
 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
 305 310 315

<210> 2143

<211> 308

<212> PRT

<213> Homo sapien (7328761-32-2018-4643)

<220>

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 2143

```

Met Lys Ile Asn Asp Ser Ser Gly Glu Asp Phe Ile Leu Val Gly Phe
 1           5           10           15
Ser Glu Tyr Pro Gln Ala Glu Phe Ile Leu Ser Leu Phe Val Ser Gly
          20           25           30
Phe Tyr Thr Met Thr Phe Thr Gly Asn Thr Ala Ile Ile Leu Val Ser
 35           40           45
Leu Leu Asp Tyr Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Arg Lys
 50           55           60
Leu Ser Phe Leu Asp Met Cys Phe Thr Thr Cys Ile Val Leu Gln Met
 65           70           75           80
Leu Val Asn Ile Trp Gly Glu Ser Lys Lys Val Ser Tyr Val Gly Cys
          85           90           95
Met Val Gln Tyr Ser Val Ala Leu Ala Leu Gly Ser Thr Glu Cys Val
          100          105          110
Leu Leu Ala Ile Met Ala Val Asp Arg Tyr Val Ala Val Arg Trp Pro
          115          120          125
Leu His Tyr Val Thr Ile Met His Gln Gln Ile Cys His Phe Leu Ala
          130          135          140
Ala Leu Ser Trp Phe Ser Gly Leu Ala Asn Ser Leu Phe His Ser Ser
          145          150          155          160
Leu Thr Thr Ile Leu Pro Leu Cys Gly His Arg Arg Val Asp His Phe
          165          170          175
Phe Cys Glu Val Leu Leu Ile Val Lys Leu Ser Cys Val Asp Thr Gly
          180          185          190
Pro Thr Glu Leu Lys Met Leu Ile Ala Arg Val Ile Ile Leu Ala Leu
          195          200          205
Pro Val Cys Thr Ile Leu Thr Ser Tyr Ala Cys Ile Ala Arg Ala Val
          210          215          220
Leu Arg Leu Gln Ser Ala Glu Gly Gln Gln Lys Ala Phe Gly Thr Cys
          225          230          235          240
Ala Ser His Leu Met Val Val Leu Leu Phe Tyr Gly Thr Ile Met Phe
          245          250          255
Met Cys Leu Gln Leu Lys Ser Asn Tyr Ser Gln Ile Gln Gly Lys Leu
          260          265          270
Leu Pro Leu Val Tyr Thr Ile Ala Ala Pro Thr Xaa Asn Pro Leu Ile
          275          280          285
Tyr Ala Leu Arg Asn Lys Val Val Lys Arg Ala Ile Gly Lys Leu Ile
          290          295          300
Trp Lys Asp Ser
305

```

<210> 2144

<211> 101

<212> PRT

<213> Homo sapien (7341899-1-693-1026)

<220>

<221> VARIANT

<222> (1)...(101)

<223> Xaa = Any Amino Acid

<400> 2144

```

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val

```

```

1           5           10           15
Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr
20           25           30
Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr
35           40           45
Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Ile Leu
50           55           60
Glu Gly Xaa Phe Ile His Phe Trp His His Val Tyr Ser Ile Leu Lys
65           70           75           80
Ile Pro Arg Met Lys Lys Lys Asn Leu Gln Ile Ile Pro Leu Ile Gly
85           90           95
Cys Cys Leu Ala Glu
100

```

<210> 2145

<211> 326

<212> PRT

<213> Homo sapien (7341899-24-747-1936)

<400> 2145

```

Met Glu Arg Ala Asn Asp Ser Thr Phe Ser Gly Phe Ile Leu Leu Gly
1           5           10           15
Phe Ser Asn Arg Pro Gln Leu Glu Thr Ala Leu Phe Val Val Ile Leu
20           25           30
Ile Ile Tyr Phe Leu Ser Phe Leu Gly Asn Gly Thr Ile Ile Leu Leu
35           40           45
Ser Ile Val Asp Pro Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50           55           60
Asn Leu Ser Phe Met Asp Leu Cys Leu Thr Thr Cys Thr Val Pro Gln
65           70           75           80
Thr Leu Val Asn Phe Lys Gly Lys Asp Lys Thr Ile Thr Tyr Gly Gly
85           90           95
Cys Val Thr Gln Leu Phe Ile Ala Leu Gly Leu Gly Gly Ser Glu Cys
100           105           110
Val Leu Leu Ser Ala Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Arg
115           120           125
Ser Leu His Tyr Met Val Ser Met His Pro Gln Leu Cys Leu Gln Leu
130           135           140
Val Val Thr Thr Trp Leu Thr Gly Phe Gly Asn Ser Val Ile Gln Thr
145           150           155           160
Ala Leu Thr Met Thr Leu Pro Leu Cys Asp Lys Asn Gln Val Asp His
165           170           175
Phe Phe Cys Glu Val Pro Val Met Leu Lys Leu Ser Cys Thr Asn Thr
180           185           190
Ser Ile Asn Glu Ala Glu Ile Phe Ala Val Ser Val Phe Phe Leu Val
195           200           205
Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Gly His Ile Thr His Ala
210           215           220
Val Leu Lys Ile Lys Ser Ala Gln Gly Arg Gln Lys Ala Phe Gly Thr
225           230           235           240
Cys Gly Ser His Leu Leu Val Val Ile Ile Phe Phe Gly Thr Leu Ile
245           250           255
Ser Met Tyr Leu Gln Pro Pro Ser Ser Tyr Ser Gln Asp Val Asn Lys
260           265           270
Ser Ile Ala Leu Phe Tyr Thr Leu Val Thr Pro Leu Leu Asn Pro Leu
275           280           285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Thr Lys Lys Thr
290           295           300
Ser Gly Glu Asp Ile Ala Cys Met Arg Lys Leu Thr Gln Gly Leu Gln
305           310           315           320
Phe Gln Thr Phe Val His

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325

<210> 2146
 <211> 155
 <212> PRT
 <213> Homo sapien (7341899-6-1-567)

<220>
 <221> VARIANT
 <222> (1)...(155)
 <223> Xaa = Any Amino Acid

<400> 2146
 Met Lys Lys Lys Asn Leu Gln Asp Asn Ser Leu His Val Leu Leu Ala
 1 5 10 15
 Met Leu Lys Thr Val Phe Leu Asp Ala Thr Ile Glu Glu Met Ser Val
 20 25 30
 Phe Val Leu Asn Asn Val Asn Val Leu Ile Cys Leu Ile Ser Asn Phe
 35 40 45
 Thr Cys Tyr Gly Tyr Ile Ala Gly Ala Leu Arg Met Asn Thr Ser Asn
 50 55 60
 Xaa Ile Arg Ser Lys Leu Arg Asn Gln Tyr His His His His Arg
 65 70 75 80
 Cys His Phe Ile Ile Asp Ser Ile Phe Tyr Gly Ile Ile Val Xaa Met
 85 90 95
 Leu Leu Gln Asp Gly Asn Asn Ser Ser Gln Asp Gln Glu Arg Phe Phe
 100 105 110
 Ile Leu Phe Tyr Thr Ile Leu Thr Pro Ser Leu Lys Leu Leu Val Tyr
 115 120 125
 Leu Leu Arg Asn Lys Asp Ile Lys Asp Ile Ser Arg Arg Ile Leu Arg
 130 135 140
 Phe Gly Arg Glu Ser Ser Lys Met Lys Gly Asn
 145 150 155

<210> 2147
 <211> 318
 <212> PRT
 <213> Homo sapien (7341900-14-7037-9080)

<220>
 <221> VARIANT
 <222> (1)...(318)
 <223> Xaa = Any Amino Acid

<400> 2147
 Met Ala Glu Ser Gly Thr Thr Val Thr Glu Phe Phe Leu Arg Gly Phe
 1 5 10 15
 Arg Leu Lys Ala Glu Leu Gln Ile Gly Leu Phe Phe Val Phe Leu Val
 20 25 30
 Ile Phe Leu Ile Thr Met Gly Gly Asn Leu Gly Met Ile Val Leu Met
 35 40 45
 Leu Ile Gln Thr Asp Pro Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser His Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val Ile Gly Pro
 65 70 75 80
 Gln Leu Leu Glu Thr Leu Ala Thr Asp Lys Met Ile Ile Thr Tyr Glu
 85 90 95
 Arg Cys Ala Ser Gln Phe Phe Phe Phe Thr Leu Cys Ala Ser Ile Glu
 100 105 110
 Cys Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
 115 120 125

Asn Pro Leu Leu Tyr Ala Ile Val Met Thr Pro Lys Thr Arg Leu Ala
 130 135 140
 Leu Leu Ala Gly Ala Tyr Ser Gly Ala Ile Val Asn Ser Val Ile Cys
 145 150 155 160
 Thr Gly Cys Thr Phe Ser Ile Ser Phe Ser Lys Ser Asn His Val Asp
 165 170 175
 Phe Phe Phe Cys Asp Leu Pro Pro Leu Lys Leu Ala Cys Ser Glu
 180 185 190
 Thr Arg Pro Arg Glu Trp Val Ile Tyr Leu Ser Ala Phe Leu Val Ile
 195 200 205
 Thr Thr Ser Ile Ser Val Ile Leu Thr Ser Tyr Leu Phe Ile Ile Gln
 210 215 220
 Ser Val Leu Lys Ile Arg Thr Ala Gly Gly Arg Ala Lys Thr Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Met Thr Ala Leu Thr Leu Phe Phe Gly Thr Leu
 245 250 255
 Ile Phe Ile Tyr Leu Lys Gly Asn Met Gly Glu Ser Leu Glu Glu Asp
 260 265 270
 Lys Ile Val Ser Ile Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Met Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Leu Lys Lys
 290 295 300
 Val Phe Asn Arg Ile Arg Val Ser Gln Ala Glu Xaa Leu Leu
 305 310 315

<210> 2148

<211> 317

<212> PRT

<213> Homo sapien (7341900-15-17952-19084)

<400> 2148

Met Gln Pro Tyr Thr Lys Asn Trp Thr Gln Val Thr Glu Phe Val Met
 1 5 10 15
 Met Gly Phe Ala Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu
 20 25 30
 Phe Leu Thr Met Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile
 35 40 45
 Leu Val Val Gly Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe
 50 55 60
 Leu Thr His Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val
 65 70 75 80
 Pro Lys Met Leu Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile
 85 90 95
 Ser Tyr Ala Gly Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly
 100 105 110
 Ala Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Met Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr
 130 135 140
 Cys Ile Arg Leu Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro
 145 150 155 160
 Ile Leu Pro Ile Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn
 165 170 175
 Val Ile Asp His Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser
 180 185 190
 Cys Ser Asp Val Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu
 195 200 205
 Ala Val Leu Leu Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn
 210 215 220
 Ile Val Trp Thr Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys
 225 230 235 240

<210> 2149
<211> 314
<212> PRT
<213> Homo sapien (7341900-16-17098-20843)

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<210> 2150
<211> 311
<212> PRT
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<213> Homo sapien (7341900-6-1691-2778)

<220>

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 2150

Glu	Lys	Asn	Leu	Ile	Ser	Met	Asn	Gly	Phe	Met	Asn	Phe	Thr	Asp	Tyr	1	5	10	15
Pro	Glu	Leu	Glu	Met	Pro	Leu	Phe	Leu	Val	Phe	Leu	Ser	Cys	Phe	Leu	20	25	30	
Ala	Ile	Ile	Leu	Arg	Asn	Met	Glu	Trp	Val	Ile	Leu	Thr	Gln	Val	Asn	35	40	45	
Val	His	Leu	Phe	Thr	Pro	Ile	Tyr	Phe	Phe	Leu	Thr	Asn	Val	Thr	Leu	50	55	60	
Trp	Asp	Thr	Ser	Val	Ile	Met	Pro	Gln	Ile	Leu	Ala	Ile	Leu	Ala	Thr	65	70	75	80
Gly	Lys	Thr	Thr	Ile	Ser	Tyr	Val	Pro	Leu	Ile	Lys	Ala	Met	Arg	Ser	85	90	95	
Phe	Phe	Phe	Ile	Cys	Val	Gly	Thr	Xaa	Cys	Phe	Leu	Pro	Thr	Ala	Met	100	105	110	
Thr	Ile	Ser	Ser	His	Cys	Pro	Thr	Leu	Gln	Ala	Met	Asn	Phe	Lys	Thr	115	120	125	
Cys	Trp	Gly	Phe	Phe	Leu	Val	Gly	Ile	Cys	Cys	Cys	Thr	Cys	Trp	Val	130	135	140	
Leu	Met	Val	Asn	Val	Val	Asn	Ala	Tyr	Thr	Xaa	Gly	Leu	Ser	Gly	Ala	145	150	155	160
Thr	Phe	Asn	Thr	Ile	Cys	Thr	Phe	Ala	Arg	Phe	Phe	Cys	Asp	Asp	Asn	165	170	175	
Xaa	Ile	Lys	Phe	Cys	His	Ile	Leu	Pro	Leu	Leu	Lys	Leu	Ile	Xaa	Asn	180	185	190	
Thr	Ser	Gly	Asn	Ser	Lys	Ile	Ile	Val	Ile	Leu	Thr	Ala	Phe	Met		195	200	205	
Ile	Ile	Ala	Gly	Thr	Arg	Val	Ile	Leu	Ile	Ser	Tyr	Leu	Leu	Ile	Ile	210	215	220	
Arg	Ala	Leu	Arg	Met	Lys	Ser	Ser	Ser	Gly	Arg	Ser	Gln	Xaa	Phe	Tyr	225	230	235	240
Pro	Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Ala	Met	Thr	Phe	Phe	Gly	Ile	245	250	255	
Pro	Ile	Phe	Arg	His	Val	Lys	Tyr	Leu	Arg	Xaa	Ile	Thr	Asp	Arg	Arg	260	265	270	
Gln	Val	Gly	Ile	Met	Thr	Cys	Thr	Ile	Phe	Ile	Pro	Met	Leu	Glu	Leu	275	280	285	
Leu	Ile	Gln	Ser	Leu	Lys	Lys	Asp	Ile	Gln	Val	Ala	Phe	Lys	Lys	Ala	290	295	300	
Ile	Gly	Asn	Phe	Trp	Val	Phe										305	310		

<210> 2151

<211> 306

<212> PRT

<213> Homo sapien (7406632-1-90980-93013)

<400> 2151

Met	Glu	Gly	Lys	Asn	Gln	Thr	Asn	Ile	Ser	Glu	Phe	Leu	Leu	Leu	Gly	1	5	10	15
Phe	Ser	Ser	Trp	Gln	Gln	Gln	Gln	Val	Leu	Leu	Phe	Ala	Leu	Phe	Leu	20	25	30	
Cys	Leu	Tyr	Leu	Thr	Gly	Leu	Phe	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Ala	35	40	45	

Ile Gly Ser Asp His Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Leu Cys Leu Pro Ser Ala Thr Val Pro Lys
 65 70 75 80
 Met Leu Leu Asn Ile Gln Thr Gln Thr Gln Thr Ile Ser Tyr Pro Gly
 85 90 95
 Cys Leu Ala Gln Met Tyr Phe Cys Met Met Phe Ala Asn Met Asp Asn
 100 105 110
 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg Leu Cys Ala Ser Leu
 130 135 140
 Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn Pro Leu Leu His Thr
 145 150 155 160
 Leu Met Met Ala His Leu His Phe Cys Ser Asp Asn Val Ile His His
 165 170 175
 Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu Ser Cys Ser Asp Thr
 180 185 190
 Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val Gly Leu Ile Phe Val
 195 200 205
 Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Val Ser Ala
 210 215 220
 Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe Tyr Gly Ala Ile Thr
 245 250 255
 Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser Thr Glu Lys Asp Ser
 260 265 270
 Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr
 290 295 300
 Leu Ser
 305

<210> 2152

<211> 314

<212> PRT

<213> Homo sapien (7407927-19-1-4216)

<400> 2152

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser
 20 25 30
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
 35 40 45
 Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser
 50 55 60
 Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
 65 70 75 80
 Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly Cys
 85 90 95
 Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
 100 105 110
 Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
 115 120 125
 Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
 130 135 140
 Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
 145 150 155 160

Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
 180 185 190
 Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu
 195 200 205
 Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile
 210 215 220
 Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser
 260 265 270
 Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Lys Leu Asn Ile
 290 295 300
 Gln Tyr Phe Ser Leu Gly Lys Thr Ala Pro
 305 310

<210> 2153
 <211> 117
 <212> PRT
 <213> Homo sapien (7407927-23-3086-3824)

<220>
 <221> VARIANT
 <222> (1)...(117)
 <223> Xaa = Any Amino Acid

<400> 2153
 Ser Ile Thr Glu Ala Leu Cys Leu Lys Tyr Val His Leu Asn Asn Lys
 1 5 10 15
 Glu Met Tyr Phe Met Tyr Leu Gly Lys Asn Arg Ser Arg Ile Ile Asn
 20 25 30
 Val Cys Ser Leu Val Leu Gln Ile Ile Thr Thr Ile Ile Leu Ile Leu
 35 40 45
 Pro Ser Pro Trp Leu Ser Leu Ile Ile Ser Gly Thr Phe Trp Ile Ile
 50 55 60
 Xaa Pro Leu His Ser Phe Pro His Gln Ile Ile Xaa Asn Ile Asn Thr
 65 70 75 80
 Ala Thr Glu Cys Thr Ile Ser Lys Leu Leu Leu Tyr His Leu Gly Ser
 85 90 95
 Lys Leu Phe Asn Val Lys Ala Gln Phe Ser Thr Xaa Leu Leu Pro Asn
 100 105 110
 Glu Leu Tyr Val Leu
 115

<210> 2154
 <211> 338
 <212> PRT
 <213> Homo sapien (7407958-12-642-1844)

<220>
 <221> VARIANT
 <222> (1)...(338)
 <223> Xaa = Any Amino Acid

<400> 2154
 Met Ile Ser Phe Leu Val Pro Gly Leu Met Glu Glu Glu Asn Gln Arg

```

1           5           10           15
Gly Val Val His Phe His Phe His Phe Phe Ser Thr Asp Leu Val Val
20           25           30
Ala Ser Phe Ile Ile Val Ala Leu Met Leu His Leu Arg Ser Leu Val
35           40           45
Gly His Phe Thr Phe Gly Pro Thr Val Trp Gln Asp Pro Phe Leu His
50           55           60
Ile Pro Met Tyr Leu Phe Leu Phe Ser Leu Ala Leu Thr Met Leu Glu
65           70           75           80
Ile Gly Tyr Ser Thr Asn Ile Ser Pro Pro Thr Leu Ala Thr Val Leu
85           90           95
Tyr Met Gly Lys Met Leu Ile Ser Leu Pro Gly Tyr Gly Thr Gln Met
100          105          110
Leu Phe Val Ile Leu Leu Arg Gly Ser Glu Cys Val Leu Leu Ala Val
115          120          125
Met Ala Tyr Asp Arg Tyr Ile Thr Ile Cys His Pro Phe Asn Tyr Asn
130          135          140
Leu Ile Met Ser Gly Xaa Leu Cys Gly Gln Met Thr Leu Gly Ser Leu
145          150          155          160
Arg Leu Gly Phe Leu Leu Ser Leu Phe Leu Thr Met Leu Ile Xaa His
165          170          175
Pro Pro Phe Cys Gly Leu Asp Glu Thr Tyr His Phe Phe Cys Asp Met
180          185          190
Pro Thr Ala Ser Arg Leu Val Cys Ala Asp Thr Thr Val His Glu Ser
195          200          205
Ala Leu Xaa Leu Pro Cys Gly His His His His Pro Leu Pro Ser Ser
210          215          220
Leu Ile Cys Leu Pro Tyr Gly Cys Leu Ala Ala Thr Ile Leu Arg Met
225          230          235          240
His Ser Ala Lys Arg Lys His Xaa Ala Phe Ser Thr Ser Ser Ser His
245          250          255
Leu Ile Val Val Leu Leu Lys Tyr Trp Cys Cys Ile Leu Ile Cys Leu
260          265          270
Cys Pro Ser Ser Ser Tyr Ser Pro Glu Glu Gly Trp Glu Val Ser Leu
275          280          285
Val His Met Phe Ile Leu Pro Val Trp Asn Pro Leu Ile Tyr Ser Val
290          295          300
Trp Asn Gln Asp Val Thr Asp Ala Val Glu Arg Leu Val Ala Arg Met
305          310          315          320
Ser Leu Xaa Leu Thr Ala Arg Asn Ile Pro Ser Xaa Lys Ile Phe Pro
325          330          335
Xaa Leu

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<210> 2155

<211> 314

<212> PRT

<213> Homo sapien (7467565-10-15924-18962)

<400> 2155

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Met Ser Asn Glu Asp Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu
1           5           10           15
Phe Val Leu Thr Gly Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu
20           25           30
Phe Leu Val Phe Leu Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu
35           40           45
Gly Leu Ile Ala Leu Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met
50           55           60
Tyr Phe Phe Leu Gly Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser
65           70           75           80
Thr Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met

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      85              90              95
Ile Ser Leu Ser Glu Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly
      100              105              110
Gly Thr Thr Glu Cys Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr
      115              120              125
Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser
      130              135              140
Leu Cys Ile Arg Leu Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His
145      150      155      160
Ala Leu Ile His Glu Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser
      165              170              175
Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile
      180              185              190
Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser
      195              200              205
Gly Ser Ile Gln Val Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr
      210              215              220
Phe Ala Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg
225      230      235      240
Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
      245              250              255
Tyr Gly Pro Leu Ile Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala
      260              265              270
Asp Asp Gln Asp Met Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro
      275              280              285
Leu Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp
      290              295              300
Ser Phe Thr Lys Met Val Lys Arg Asn Val
305              310

```

<210> 2156

<211> 320

<212> PRT

<213> Homo sapien (7533967-9-17699-19044)

<220>

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 2156

```

Gly Val Gly Leu Xaa Lys Leu Xaa Trp Gln Ile Ile Phe Ser Gly Asp
1      5      10      15
Ser Phe Ser Thr Trp Glu Met Phe Ser Leu Ser Ile Leu Gln Leu Pro
      20      25      30
Xaa Met Tyr Thr Val Ala Leu Ser Gly Thr Ser Ile Leu Ile Phe Leu
      35      40      45
Ile Xaa Thr Asp Phe Xaa Val His Thr Ser Leu Tyr Ser Phe Xaa Val
      50      55      60
Leu Ile Asp Ile Ala Ile Ser Val Val Lys Ile Gly Ile Glu Val Phe
65      70      75      80
Ser Gly Lys Ile Asn Phe Ser His Thr Gly Cys Gly Thr Gln Ile Phe
      85      90      95
Phe Phe Leu Thr Ala Gly Ile Phe Lys Tyr Val Leu Leu Thr Tyr Met
      100      105      110
Ala Tyr Asp His Asn Val Ala Ile Cys Asp Leu Arg Xaa Pro Thr Phe
      115      120      125
Met Ser Asp Gln Val Phe Xaa Gln Trp Ala Val Glu Ser Trp Ile Gly
      130      135      140
Gly Lys Leu Ser Ser Leu Ala His Thr Ile Tyr Ile Phe His Leu Phe
145      150      155      160

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Ser Tyr Lys Ala Lys Glu Ile Ser His Leu Trp Pro Lys Leu Phe Xaa
 165 170 175
 Ser Ser Ser Val Gly Ile Pro Tyr Ile Gln Asn Asp Val Phe Phe Thr
 180 185 190
 Ile Ile Thr Phe Leu Phe Thr Leu Leu Pro Leu Thr Leu Thr Leu Ser
 195 200 205
 Ser Lys Leu Ile Val Phe Thr Ile Leu His Met Asn Ser Ser Asn Gly
 210 215 220
 Gly Ala Lys Ser Trp His Thr Tyr Cys Phe His Leu Ser Val Leu Ile
 225 230 235 240
 Pro Cys Cys Gly Gln Ala Ile Phe Val Tyr Met Thr Ser Ser Ser Phe
 245 250 255
 Xaa Thr Val Asn Lys Tyr Gln Thr Met Ser Val Leu Thr Ala Xaa Leu
 260 265 270
 Tyr Pro Leu Leu Lys Pro Leu Ile Asp Ile Leu Lys Asn Ala Glu Val
 275 280 285
 Ala Gly Ala Trp Ser Lys Phe Leu Xaa Lys Lys Ala Leu Lys Ser Gln
 290 295 300
 His Leu Ile Thr Arg Ser Cys Glu Asn Lys Xaa Thr Thr Glu Gln Ser
 305 310 315 320

<210> 2157

<211> 196

<212> PRT

<213> Homo sapien (7534025-1-1-1622)

<400> 2157

Met Gly Tyr Asp Arg Tyr Met Ala Ile Cys Asn Pro Leu Arg Tyr Ser
 1 5 10 15
 Val Leu Met Gly His Gly Val Cys Met Gly Leu Met Ala Ala Ala Cys
 20 25 30
 Ala Cys Gly Phe Thr Val Ser Leu Val Thr Thr Ser Leu Val Phe His
 35 40 45
 Leu Pro Phe His Ser Ser Asn Gln Leu His His Phe Phe Cys Asp Ile
 50 55 60
 Ser Pro Val Leu Lys Leu Ala Ser Gln His Ser Gly Phe Ser Gln Leu
 65 70 75 80
 Val Ile Phe Met Leu Gly Val Phe Ala Leu Val Ile Pro Leu Leu Leu
 85 90 95
 Ile Leu Val Ser Tyr Ile Arg Ile Ile Ser Ala Ile Leu Lys Ile Pro
 100 105 110
 Ser Ser Val Gly Arg Tyr Lys Thr Phe Ser Thr Cys Ala Ser His Leu
 115 120 125
 Ile Val Val Thr Val His Tyr Ser Cys Ala Ser Phe Ile Tyr Leu Arg
 130 135 140
 Pro Lys Thr Asn Tyr Thr Ser Ser Gln Asp Thr Leu Ile Ser Val Ser
 145 150 155 160
 Tyr Thr Ile Leu Thr Pro Leu Phe Asn Pro Met Ile Tyr Ser Leu Arg
 165 170 175
 Asn Lys Glu Phe Lys Ser Ala Leu Arg Arg Thr Ile Gly Gln Thr Phe
 180 185 190
 Tyr Pro Leu Ser
 195

<210> 2158

<211> 307

<212> PRT

<213> Homo sapien (7534025-11-6732-9742)

<220>

<221> VARIANT

<222> (1)...(307)

<223> Xaa = Any Amino Acid

<400> 2158

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Met Ile Thr Glu Phe Ile Leu Ile Gly Phe Ser Asn Leu Gly Asp Leu
 1           5           10           15
Gln Ile Leu Leu Phe Phe Ile Phe Leu Leu Val Tyr Leu Thr Thr Leu
      20           25           30
Met Ala Asn Thr Thr Ile Met Thr Val Ile His Leu Asp Arg Ala Leu
      35           40           45
His Thr Pro Met Tyr Phe Phe Leu Phe Val Leu Ser Cys Ser Glu Thr
 50           55           60
Cys Tyr Thr Leu Val Ile Val Pro Lys Met Leu Thr Asn Leu Leu Ser
 65           70           75           80
Ala Ile Pro Thr Ile Ser Phe Ser Gly Cys Val Val Gln Leu Tyr Leu
      85           90           95
Phe Val Gly Leu Ala Cys Thr Asn Cys Phe Leu Ile Ala Val Met Gly
      100           105           110
Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Asn Tyr Thr Leu Ile
      115           120           125
Val Ser Xaa Ala Thr Cys Met Gln Leu Val Leu Ala Ser Ser Phe Cys
      130           135           140
Gly Phe Leu Thr Ser Val Ile Val Asn Ile Leu Val Phe Ser Val Leu
      145           150           155           160
Leu Cys Ala Ser Asn Arg Ile Asn His Phe Phe Cys Asp Ile Ser Pro
      165           170           175
Val Ile Lys Leu Gly Cys Thr Asp Thr Asn Leu Lys Glu Met Val Ile
      180           185           190
Phe Phe Leu Ser Ile Leu Val Leu Leu Val Pro Leu Val Leu Ile Phe
      195           200           205
Ile Ser Tyr Ile Phe Ile Val Ser Thr Ile Leu Lys Ile Ser Ser Val
      210           215           220
Glu Gly Gln Cys Lys Ala Phe Ala Thr Cys Ala Ser His Leu Thr Val
      225           230           235           240
Val Val Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr
      245           250           255
Ser Leu Tyr Ser Ser Asp Lys Asp Arg Leu Val Ala Val Thr Tyr Thr
      260           265           270
Val Ile Thr Pro Leu Leu Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys
      275           280           285
Glu Val Lys Met Ala Leu Arg Lys Val Leu Gly Arg Cys Leu Asn Ser
      290           295           300
Lys Thr Val
305

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<210> 2159

<211> 321

<212> PRT

<213> Homo sapien (7534025-12-11728-15143)

<220>

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 2159

```

Gly Thr Lys Ser Ile Lys Leu Thr Ser Leu Ser Glu Phe Leu Leu Leu
 1           5           10           15
Glu Phe Ser Ser Leu Glu Glu Ile Gln Gln Ile Leu Phe Leu Val Cys
      20           25           30
Leu Trp Leu Tyr Leu Ile Val Leu Ser Gly Asn Ile Thr Thr Val Thr

```



```

      35      40      45
Val Ile Arg Leu Asp Gln Ser Leu His Ile Pro Val Tyr Leu Phe Leu
  50      55      60
Gly Ile Leu Ser Ile Ser Gly Thr Cys Tyr Thr Phe Val Ile Leu Pro
  65      70      75      80
Lys Met Leu Ile Asp Leu Leu Ser Leu Leu Arg Thr Ile Ser Phe Ile
      85      90      95
Asn Cys Ala Leu Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn
      100      105      110
Phe Met Phe Leu Gly Met Thr Val Tyr Asp Ser Tyr Val Ala Ile Cys
      115      120      125
His Pro Leu His Tyr Pro Val Leu Thr Ser Trp Gln Ile Cys Lys Gln
      130      135      140
Leu Ala Ala Thr Cys Ala Val Ile Val Phe Phe Cys Leu Phe Val Phe
  145      150      155      160
Thr Asp Arg Leu Leu Leu Arg Phe Ser Leu Leu Phe Cys Gly Pro Asn
      165      170      175
Lys Ile Asn His Tyr Phe Cys Asp Ile Ser Leu Leu Ile Gln Leu Ala
      180      185      190
Cys Thr Asp Thr Tyr Ile Arg Glu Leu Val Ile Phe Ile Gly Gly Ile
      195      200      205
Leu Ala Leu Thr Val Pro Leu Met Phe Ile Cys Ile Ser Tyr Gly Phe
      210      215      220
Ile Val His Thr Ile Leu Arg Ile Pro Ser Cys Glu Ser Lys Gln Lys
  225      230      235      240
Ala Ile Ser Thr Cys Ala Ser His Leu Ile Met Val Val Val His Tyr
      245      250      255
Gly Cys Ala Ser Phe Val Asn Leu Xaa Pro Ser Ala Lys Xaa Ser Ser
      260      265      270
Ser Lys Xaa Pro Ser Ser Lys Asn Arg Leu Val Thr Val Thr Tyr Thr
      275      280      285
Val Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Phe Lys Asn Lys
      290      295      300
Asn Val Gln Met Ala Ile Trp Lys Val Ile Cys Gln Gly Gly Phe Pro
  305      310      315      320
Pro

```

<210> 2160

<211> 324

<212> PRT

<213> Homo sapien (7534025-3-4346-5996)

<400> 2160

```

Met Thr Thr Ile Ile Leu Glu Val Asp Asn His Thr Val Thr Thr Arg
  1      5      10      15
Phe Ile Leu Leu Gly Phe Pro Thr Arg Pro Ala Phe Gln Leu Leu Phe
      20      25      30
Phe Ser Ile Phe Leu Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu
      35      40      45
Leu Ile Ile Leu Ala Ile His Ser Asp Gly Gln Leu His Lys Pro Met
      50      55      60
Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr
  65      70      75      80
Val Ile Ser Pro Lys Met Leu Val Asp Phe Leu Ser His Asp Lys Ser
      85      90      95
Ile Ser Phe Asn Gly Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe
      100      105      110
Val Cys Thr Glu Tyr Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr
      115      120      125
Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln

```

```

      130              135              140
Leu Cys Gly Thr Leu Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr
145              150              155              160
Ala Met Ile Lys Met Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met
      165              170              175
Pro Gln Ile Asn His Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val
      180              185              190
Ser Cys Glu Asp Ala Ser Gln Ala Glu Met Val Asp Phe Phe Leu Ala
      195              200              205
Leu Met Val Ile Ala Ile Pro Leu Cys Val Val Val Ala Ser Tyr Ala
      210              215              220
Ala Ile Leu Ala Thr Ile Leu Arg Ile Pro Ser Ala Gln Gly Arg Gln
225              230              235              240
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Leu Phe
      245              250              255
Tyr Ser Met Thr Leu Phe Thr Tyr Ala Arg Pro Lys Leu Met Tyr Ala
      260              265              270
Tyr Asn Ser Asn Lys Val Val Ser Val Leu Tyr Thr Val Ile Val Pro
      275              280              285
Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn His Glu Val Lys Ala
      290              295              300
Ala Leu Arg Lys Thr Ile His Cys Arg Gly Ser Gly Pro Gln Gly Asn
305              310              315              320
Gly Ala Phe Ser

```

<210> 2161

<211> 305

<212> PRT

<213> Homo sapien (7534103-14-4211-5521)

<400> 2161

```

Met Val Ala Thr Asn Asn Val Thr Glu Ile Ile Phe Val Gly Phe Ser
1      5      10      15
Gln Asn Trp Ser Glu Gln Arg Val Ile Ser Val Met Phe Leu Leu Met
      20      25      30
Tyr Thr Ala Val Val Leu Gly Asn Gly Leu Ile Val Val Thr Ile Leu
      35      40      45
Ala Ser Lys Val Leu Thr Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu
      50      55      60
Ser Phe Val Glu Ile Cys Tyr Cys Ser Val Met Ala Pro Lys Leu Ile
65      70      75      80
Phe Asp Ser Phe Ile Lys Arg Lys Val Ile Ser Leu Lys Gly Cys Leu
      85      90      95
Thr Gln Met Phe Ser Leu His Phe Phe Gly Gly Thr Glu Ala Phe Leu
      100      105      110
Leu Met Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
      115      120      125
His Tyr Met Ala Ile Met Asn Gln Arg Met Cys Gly Leu Leu Val Arg
130      135      140
Ile Ala Trp Gly Gly Gly Leu Leu His Ser Val Gly Gln Thr Phe Leu
145      150      155      160
Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Ile Met Asp His Tyr Phe
      165      170      175
Cys Asp Val His Pro Val Leu Glu Leu Ala Cys Ala Asp Thr Phe Phe
      180      185      190
Ile Ser Leu Leu Ile Ile Thr Asn Gly Gly Ser Ile Ser Val Val Ser
      195      200      205
Phe Phe Val Leu Met Ala Ser Tyr Leu Ile Ile Leu His Phe Leu Arg
210      215      220
Ser His Asn Leu Glu Gly Gln His Lys Ala Leu Ser Thr Cys Ala Ser

```

```

225          230          235          240
His Val Thr Val Val Asp Leu Phe Phe Ile Pro Cys Ser Leu Val Tyr
          245          250          255
Ile Arg Pro Cys Val Thr Leu Pro Ala Asp Lys Ile Val Ala Val Phe
          260          265          270
Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val Ile Tyr Ser Phe Arg
          275          280          285
Asn Ala Glu Val Lys Asn Ala Met Arg Arg Phe Ile Gly Gly Lys Val
          290          295          300
Ile
305

```

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<210> 2162
<211> 301
<212> PRT
<213> Homo sapien (7534103-16-19899-21252)

```

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<220>
<221> VARIANT
<222> (1)...(301)
<223> Xaa = Any Amino Acid

```

```

<400> 2162
Met Ala Ser Thr Asn Asn Val Thr Glu Ser Met Ile Thr Ser Leu Phe
1          5          10          15
Gln Asp Pro Ala Val Gln Arg Val Cys Phe Val Val Phe Leu Pro Val
          20          25          30
Tyr Leu Ala Met Glu Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser
          35          40          45
Ile Ser Lys Ser Leu His Ser Pro Val Tyr Phe Phe Leu Ser Tyr Leu
          50          55          60
Ser Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr
          65          70          75          80
Asp Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala
          85          90          95
Gln Ile Phe Leu His Phe Phe Gly Ile Pro Trp Ile Phe Leu Leu Pro
          100          105          110
Leu Met Thr Asn Asp Gln Tyr Met Ala Asn Cys Lys Leu Tyr Tyr Tyr
          115          120          125
Thr Thr Ile Met Ser Cys Arg Val Cys His Leu Leu Val Ala Gly Phe
          130          135          140
Trp Leu Arg Gly Ile Ile His Ser Met Val Gln Ile Leu Val Ser Val
          145          150          155          160
Gln Leu Phe Phe Cys Gly Pro Asn Met Ile Asp His Ser Phe Cys Asp
          165          170          175
Leu Gln Val Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Val Glu Gly
          180          185          190
Val Ile Val Leu Ala Asn Ser Glu Leu Val Ser Val Phe Phe Leu Ile
          195          200          205
Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Asn Leu Arg Asn His Ser
          210          215          220
Ala Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ala Ser Tyr Leu Val
          225          230          235          240
Phe Xaa Thr Cys Ile Phe Leu Tyr Val Xaa Leu Ser Ser Thr Phe Thr
          245          250          255
Lys Asp Lys Leu Val Ala Val Phe Tyr Val Val Ile Thr Pro Met Leu
          260          265          270
Asn Pro Phe Ile Tyr Thr Leu Gly Asn Ala Glu Met Lys Ile Thr Met
          275          280          285
Arg Arg Leu Leu Gly Arg Thr Val Asn Ser Gly Met Glu
          290          295          300

```

<210> 2163
 <211> 134
 <212> PRT
 <213> Homo sapien (7534103-16-5480-6475)

<220>
 <221> VARIANT
 <222> (1)...(134)
 <223> Xaa = Any Amino Acid

<400> 2163
 Cys Phe Cys Gly Phe Ala Val Leu Thr Ser Cys Leu Phe Cys Leu Thr
 1 5 10 15
 Pro Glu Arg Xaa His Asn Thr Leu Arg Met Ala Leu Gly Ser His Arg
 20 25 30
 Phe Pro Ser Xaa Pro Ile Lys Lys Asn Tyr Lys Trp Pro His Tyr Gln
 35 40 45
 Pro Glu Leu Leu Pro His Trp Ser Ser Lys Thr Glu Arg Ile Cys Ser
 50 55 60
 Pro Ala Pro Ser Gly Leu Glu Met Leu Arg Asn Ala Lys Pro Leu Gly
 65 70 75 80
 Phe Gln Leu Tyr Leu Ile Xaa Asn Glu Gln Ser Arg Leu Ala Pro Gln
 85 90 95
 Gly Val Pro Gln Lys Thr Xaa Ser Leu Cys Ser Ser Ala Leu Ser Ser
 100 105 110
 Tyr Cys Leu Lys Asp Thr Gly Gly Gly Lys Xaa Ser Gly Glu Arg
 115 120 125
 Ser Ser Phe Pro Arg Glu
 130

<210> 2164
 <211> 307
 <212> PRT
 <213> Homo sapien (7547121-7-14093-14713)

<220>
 <221> VARIANT
 <222> (1)...(307)
 <223> Xaa = Any Amino Acid

<400> 2164
 Leu Ile Leu Ile Ser Leu Xaa Val Leu Ile Ser Xaa Gln Lys Leu Leu
 1 5 10 15
 Phe Val Thr Cys Leu Val Val Tyr Leu Val Thr Leu Leu Gly Asn Arg
 20 25 30
 Ile Gln Ile Ile Pro Thr Leu Leu Val Ser His Leu Tyr Leu Cys His
 35 40 45
 Gly Asn Pro Ser Phe Leu Asp Ile Gly Leu Thr Ser Ser Phe Thr Pro
 50 55 60
 Ser Ile Leu Ile Asn Phe Leu Ser Glu Gly Lys Lys Leu Ser Phe Thr
 65 70 75 80
 Asp Cys Ile Ile Gln Met Ser Ile Phe Tyr Ser Met Gly Ser Thr Glu
 85 90 95
 Cys Val Leu Leu Ala Val Met Ala Tyr Asp Asn Cys Val Val Ile Ser
 100 105 110
 Lys Phe Leu Arg Tyr Pro Leu Ile Ile Asn Lys Val Asn Lys Ile Lys
 115 120 125
 Lys Val Leu Cys Val Phe Met Ala Thr Val Ser Tyr Glu Leu Gly Phe
 130 135 140
 Leu Asn Arg Gln Asn Val Leu Ile Val Thr Tyr Ala Met His Phe Cys

```

145          150          155          160
Gly Lys His Ile Ile Asn His Phe Tyr Lys Ile Leu Gln Leu Met Pro
          165          170          175
Leu Ala Cys Ile Asp Ile Ser Leu Asn Glu Asn Ile Ile Ile Leu Gly
          180          185          190
Lys Val Asn Phe Ser Phe Thr Leu Leu Pro Phe Gln Phe Phe Ile
          195          200          205
Phe Ser Phe Leu Tyr Phe His Leu Cys Cys Ile Glu Ile Asn Ser
          210          215          220
Ala Glu Gly Arg Lys Lys Val Ser Ser Thr Cys Ser Ala His Ile Thr
225          230          235          240
Val Val Ile Val Phe His Arg Thr Ile Leu Phe Met Tyr Ile Lys Ser
          245          250          255
Thr Ser Asn Gly Thr Thr Ser Glu Lys Leu Val Asp Leu Phe Cys Gly
          260          265          270
Val Val Met Leu Met Leu Asn Leu Ile Ile Tyr Ser Leu Gly Asn Met
          275          280          285
Glu Val Leu Gly Val Met Lys Lys Leu Ile Ser Met Ser Arg Pro Trp
          290          295          300
Cys Trp Lys
305

```

```

<210> 2165
<211> 214
<212> PRT
<213> Homo sapien (7622326-1-2092-6993)

```

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<220>
<221> VARIANT
<222> (1)...(214)
<223> Xaa = Any Amino Acid

```

```

<400> 2165
Cys Leu Leu Xaa Leu Tyr Gln Val Cys Leu Leu Thr Arg Asp Pro Ile
1      5      10      15
Leu Gln Asp Leu His Xaa Lys Pro Arg Ile Tyr Cys Ser Pro Cys Leu
20     25     30
Xaa Val Tyr Ser Leu Gly Leu Asp Arg Xaa Xaa Val Phe Leu Thr Met
35     40     45
Thr Gln Ser Val Leu Trp Asn Glu Pro Val Cys Phe Met Phe Ser Xaa
50     55     60
Met Pro Phe Cys Leu Ser Xaa Ile Leu Pro Xaa Thr Tyr Tyr Glu Gln
65     70     75     80
Val Val Met Leu Asn Leu Val Cys Ala Asp Ile Thr Tyr Ile Val His
85     90     95
Thr Cys Gly Leu Phe Met Ala Phe Ser Val Asp Gly Phe Asp Ile Phe
100    105    110
Gly Ile Ile Ile His Arg Tyr Gln Thr Leu Gln Ala Val Leu Xaa Leu
115    120    125
Pro Ala Lys Glu Ser Val Pro Lys Val Phe Ser Ile Tyr Ala Phe His
130    135    140
Ile Cys Val Thr Leu Tyr Leu Leu Met Ile Gly Phe Tyr Ser Phe Phe
145    150    155    160
Ser Cys Cys Phe Ser Tyr His Thr Leu Thr Val Ile Pro Ile Ser Phe
165    170    175
Ser Ser Phe Tyr Ser Leu Val Pro Ser Met Phe Asn Thr Ile Thr Cys
180    185    190
Gly Val Lys Ser Lys His Ile Gln Glu Asn Met Val Gln Arg Phe Cys
195    200    205
Gly Lys Ile Ser Cys His
210

```

<210> 2166
 <211> 321
 <212> PRT
 <213> Homo sapien (7622326-2-5218-6423)

<400> 2166
 Met Thr Ile Leu Leu Asn Ser Ser Leu Gln Arg Ala Thr Phe Phe Leu
 1 5 10 15
 Thr Gly Phe Gln Gly Leu Glu Gly Leu His Gly Trp Ile Ser Ile Pro
 20 25 30
 Phe Cys Phe Ile Tyr Leu Thr Val Ile Leu Gly Asn Leu Thr Ile Leu
 35 40 45
 His Val Ile Cys Thr Asp Ala Thr Leu His Gly Pro Met Tyr Tyr Phe
 50 55 60
 Leu Gly Met Leu Ala Val Thr Asp Leu Gly Leu Cys Leu Ser Thr Leu
 65 70 75 80
 Pro Thr Val Leu Gly Ile Phe Trp Phe Asp Thr Arg Glu Ile Gly Ile
 85 90 95
 Pro Ala Cys Phe Thr Gln Leu Phe Phe Ile His Thr Leu Ser Ser Met
 100 105 110
 Glu Ser Ser Val Leu Leu Ser Met Ser Ile Asp Arg Ser Val Ala Val
 115 120 125
 Cys Asn Pro Leu His Asp Ser Thr Val Leu Thr Pro Ala Cys Ile Val
 130 135 140
 Lys Met Gly Leu Ser Ser Val Leu Arg Ser Ala Leu Leu Ile Leu Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Lys Arg Phe Gln Tyr Cys His Ser His Val Leu
 165 170 175
 Ala His Ala Tyr Cys Leu His Leu Glu Ile Met Lys Leu Ala Cys Ser
 180 185 190
 Ser Ile Ile Val Asn His Ile Tyr Gly Leu Phe Val Val Ala Cys Thr
 195 200 205
 Val Gly Val Asp Ser Leu Leu Ile Phe Leu Ser Tyr Ala Leu Ile Leu
 210 215 220
 Arg Thr Val Leu Ser Ile Ala Ser His Gln Glu Arg Leu Arg Ala Leu
 225 230 235 240
 Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Leu Phe Tyr Ile Pro
 245 250 255
 Met Ile Gly Leu Ser Leu Val His Arg Phe Gly Glu His Leu Pro Arg
 260 265 270
 Val Val His Leu Phe Met Ser Tyr Val Tyr Leu Leu Val Pro Pro Leu
 275 280 285
 Met Asn Pro Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Arg Gln Arg
 290 295 300
 Ile Ile Lys Lys Phe Gln Phe Ile Lys Ser Leu Arg Cys Phe Trp Lys
 305 310 315 320
 Asp

<210> 2167
 <211> 345
 <212> PRT
 <213> Homo sapien (7622326-3-3672-5330)

<220>
 <221> VARIANT
 <222> (1)...(345)
 <223> Xaa = Any Amino Acid

<400> 2167

```

Met His Leu Pro Asn Ser Ser Glu Ile Ala Ile Thr Thr Phe Phe Leu
 1          5          10          15
Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Val Pro
          20          25          30
Ile Cys Leu Met Tyr Leu Val Ala Ile Leu Gly Asn Cys Thr Ile Leu
          35          40          45
Phe Val Ile Arg Thr Glu Pro Ser Leu His Ala Pro Met Tyr Tyr Phe
          50          55          60
Leu Ser Met Leu Ala Val Ser Asp Leu Gly Leu Ser Leu Ser Tyr Leu
65          70          75          80
Pro Thr Met Leu Arg Ile Phe Val Phe Asn Ala Thr Gly Ile Ser Ser
          85          90          95
Asn Ala Arg Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
          100          105          110
Glu Ser Ser Val Leu Leu Val Met Ser Phe Asp Arg Phe Leu Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ile Ser Glu Val Leu Val Ser Cys Ile Leu
          130          135          140
Thr Ser Ala Arg Val Ala Lys Met Gly Leu Leu Phe Leu Ile Lys Arg
145          150          155          160
Glu Thr Thr Leu Asn Ser Leu Lys Glu Thr Thr Asn Ser Val Leu Leu
          165          170          175
Val Leu Pro Phe Pro Phe Thr Leu Thr Arg Leu Thr Tyr Cys Arg Lys
          180          185          190
Ser Leu Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Arg Lys Leu
          195          200          205
Ala Cys Ser Asp Asn Thr Val Asn Phe Phe Tyr Gly Phe Phe Leu Ala
          210          215          220
Leu Cys Met Met Ser Glu Ser Val Phe Ile Thr Val Ser Tyr Val Leu
225          230          235          240
Ile Leu Lys Thr Ile Met Gly Ile Gly Ser His Arg Glu Arg Leu Lys
          245          250          255
Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe Tyr
          260          265          270
Ala Pro Val Ile Ala Leu Ala Ser Met His Cys Phe Ala Ser Met Asn
          275          280          285
Cys Phe Gly Lys His Arg Ser Pro Leu Ala Met Ile Leu Ile Ala Asp
          290          295          300
Val Phe Leu Leu Val Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val
305          310          315          320
Lys Thr Gln Gln Ile His Glu Lys Val Leu Gly Lys Leu Gly Leu Gln
          325          330          335
Gln Arg Cys Gln Xaa Thr Trp Tyr Lys
          340          345

```

<210> 2168

<211> 325

<212> PRT

<213> Homo sapien (7622326-4-1-4013)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2168

```

Leu Thr Met Pro His Leu Ser Asn Thr Thr Ser Glu Phe Pro Ile Phe
 1          5          10          15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Phe His Ile Trp Ile Ser
          20          25          30
Ile Pro Phe Phe Leu Leu Ser Thr Val Ala Leu Leu Gly Asn Ser Met

```

```

      35      40      45
Ile Leu Leu Val Val Ile Leu Glu Pro Asn Leu His Glu Pro Met Tyr
  50      55      60
Cys Phe Leu Phe Met Leu Ser Ala Ala Asp Leu Gly Leu Thr Leu Ser
65      70      75      80
Thr Met Pro Thr Thr Leu Ser Val Leu Trp Phe Ser Ala Arg Glu Ile
      85      90      95
Ile Leu Asn Ala Cys Ile Ile Gln Leu Phe Phe Leu His Ser Ser Gly
      100      105      110
Phe Met Glu Ser Ser Val Leu Met Ala Met Ala Phe Asp Arg Phe Val
      115      120      125
Ala Ile Cys Arg Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Ser Arg
      130      135      140
Ile Leu Lys Ile Gly Val Ala Ile Val Leu Arg Thr Leu Ile Ser Leu
145      150      155      160
Ser Pro Ser Leu Phe Leu Ile Lys Arg Leu Ser Phe Cys Lys Val Asn
      165      170      175
Val Leu Ser His Ser Tyr Cys Phe His Pro Asp Ala Leu Lys Val Ala
      180      185      190
Cys Ser Asp Ser Arg Met Asn Ser Tyr Gly Gly Leu Ala Val Leu Ile
      195      200      205
Leu Val Thr Gly Val Gly Thr Pro Cys Val Ala Leu Ser Tyr Ile Leu
      210      215      220
Ile Ile His Ser Val Leu Asn Ile Ile Ser Ser Glu Gly Arg Arg Lys
225      230      235      240
Ala Phe Asp Thr Cys Gly Ser His Ile Gly Ala Val Ala Val Phe Tyr
      245      250      255
Ile Pro Trp Val Val Leu Ser Val Val His Arg Phe Phe His Lys Ala
      260      265      270
Ser Pro Tyr Val His Pro Leu Leu Ser Asn Ile Tyr Phe Leu Gly Pro
      275      280      285
Ser Arg Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg
      290      295      300
Arg Ala Ile Leu Lys Leu Phe Gln Thr Lys Ser Lys Glu Met Xaa Trp
305      310      315      320
Gly Leu Phe Phe Leu
      325

```

<210> 2169

<211> 319

<212> PRT

<213> Homo sapien (7622326-7-11006-13674)

<220>

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 2169

```

Met Ser Pro Leu Asn Asp Thr Lys Met Glu Val Leu Arg Phe Leu Leu
  1      5      10      15
Ile Gly Ile Thr Gly Leu Glu Lys Ser Arg Thr Trp Ile Ser Ile Pro
      20      25      30
Phe Leu Ser Val Tyr Leu Leu Ser Trp Met Gly Asn Phe Thr Val Leu
      35      40      45
Phe Phe Ile Lys Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Leu
      50      55      60
Leu Ser Met Leu Ser Ile Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
65      70      75      80
Pro Ile Thr Leu Gly Leu Phe Leu Phe Asp Val His Glu Ile His Ala
      85      90      95

```


Ala Pro Cys Phe Ala Xaa Glu Phe Phe Ile His Leu Phe Thr Val Ser
 100 105 110
 Glu Ala Ser Val Leu Ser Val Met Ala Phe Asp Trp Tyr Val Ala Ile
 115 120 125
 His Ser Pro Leu Arg Tyr Ser Thr Ile Leu Thr Ser Pro Arg Ala Ile
 130 135 140
 Lys Thr Gly Val Leu Leu Thr Ser Lys Asn Val Leu Leu Ile Leu Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Gln Arg Leu Arg Tyr Cys His Gln Asn Leu Leu
 165 170 175
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Met Cys Ser
 180 185 190
 Asp Asn Thr Val Asn Val Val Tyr Gly Leu Cys Ala Gly Leu Ser Thr
 195 200 205
 Met Leu Asp Leu Val Phe Ile Thr Phe Ser Xaa Ile Met Ile Leu Arg
 210 215 220
 Ala Val Leu Gly Ile Ala Thr Pro Arg Gln Gln Phe Lys Ala Leu Asn
 225 230 235 240
 Thr Cys Ile Ser His Ile Cys Ala Val Leu Ile Phe Tyr Val Pro Met
 245 250 255
 Leu Ser Ala Ala Met Leu His Gln Phe Ala Arg Asp Val Ser Pro Met
 260 265 270
 Ile His Val Leu Met Ala Asp Ile Phe Leu Leu Val Pro Pro Leu Leu
 275 280 285
 Asn Pro Ile Val Tyr Cys Val Lys Thr His Gln Ile Arg Glu Lys Val
 290 295 300
 Val Gly Lys Leu Cys Pro Lys Val Ser Xaa Ser Lys Glu Xaa Glu
 305 310 315

<210> 2170

<211> 323

<212> PRT

<213> Homo sapien (7622326-8-11210-13439)

<400> 2170

Met Ser Thr Leu Pro Thr Gln Ile Ala Pro Asn Ser Ser Thr Ser Met
 1 5 10 15
 Ala Pro Thr Phe Leu Leu Val Gly Met Pro Gly Leu Ser Gly Ala Pro
 20 25 30
 Ser Trp Trp Thr Leu Pro Leu Ile Ala Val Tyr Leu Leu Ser Ala Leu
 35 40 45
 Gly Asn Gly Thr Ile Leu Trp Ile Ile Ala Leu Gln Pro Ala Leu His
 50 55 60
 Arg Pro Met His Phe Phe Leu Phe Leu Leu Ser Val Ser Asp Ile Gly
 65 70 75 80
 Leu Val Thr Ala Leu Met Pro Thr Leu Leu Gly Ile Ala Leu Ala Gly
 85 90 95
 Ala His Thr Val Pro Ala Ser Ala Cys Leu Leu Gln Met Val Phe Ile
 100 105 110
 His Val Phe Ser Val Met Glu Ser Ser Val Leu Leu Ala Met Ser Ile
 115 120 125
 Asp Arg Ala Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Ala Leu Leu
 130 135 140
 Thr Asn Gly Val Ile Ser Lys Ile Ser Leu Ala Ile Ser Phe Arg Cys
 145 150 155 160
 Leu Gly Leu His Leu Pro Leu Pro Phe Leu Leu Ala Tyr Met Pro Tyr
 165 170 175
 Cys Leu Pro Gln Val Leu Thr His Ser Tyr Cys Leu His Pro Asp Val
 180 185 190
 Ala Arg Leu Ala Cys Pro Glu Ala Trp Gly Ala Ala Tyr Ser Leu Phe
 195 200 205

Val Val Leu Ser Ala Met Gly Leu Asp Pro Leu Leu Ile Phe Phe Ser
 210 215 220
 Tyr Gly Leu Ile Gly Lys Val Leu Gln Gly Val Glu Ser Arg Glu Asp
 225 230 235 240
 Arg Trp Lys Ala Gly Gln Thr Cys Ala Ala His Leu Ser Ala Val Leu
 245 250 255
 Leu Phe Tyr Ile Pro Met Ile Leu Leu Ala Leu Ile Asn His Pro Glu
 260 265 270
 Leu Pro Ile Thr Gln His Thr His Thr Leu Leu Ser Tyr Val His Phe
 275 280 285
 Leu Leu Pro Pro Leu Ile Asn Pro Ile Leu Tyr Ser Val Lys Met Lys
 290 295 300
 Glu Ile Arg Lys Arg Ile Leu Asn Arg Leu Gln Pro Arg Lys Val Gly
 305 310 315 320
 Gly Ala Gln

<210> 2171
 <211> 328
 <212> PRT
 <213> Homo sapien (7631097-4-2553-4836)

<220>
 <221> VARIANT
 <222> (1)...(328)
 <223> Xaa = Any Amino Acid

<400> 2171
 Met Leu Pro Ser Gln Thr Tyr Val Asn Ile Ser Phe Phe Gln Pro Pro
 1 5 10 15
 Ala Leu Leu Met Ile Gly Ile Pro Gly Leu Glu Ala Val His Gly Trp
 20 25 30
 Leu Ala Ile Pro Phe Ser Ser Met Tyr Thr Val Ala Leu Pro Gly Asn
 35 40 45
 Cys Leu Ile Leu Leu Ala Val Lys Arg Asn Pro Ser Leu His Gln Pro
 50 55 60
 Met Cys Tyr Phe Leu Ser Met Leu Ala Leu Pro Lys Ala Gly Leu Thr
 65 70 75 80
 Leu Ser Thr Leu Pro Ile Thr Leu Ala Val Leu Trp Phe Asp His Arg
 85 90 95
 Leu Met Gly Phe Asn Ala Cys Leu Val Gln Met Phe Phe Leu His Ser
 100 105 110
 Ser Val Val Glu Ser Ser Val Leu Leu Ala Ile Ser Phe Asp His Phe
 115 120 125
 Val Ala Ile Ser Asn Pro Leu His Tyr Ala Ala Val Leu Thr Asn Ser
 130 135 140
 Val Ile Ile Arg Ile Gly Leu Ala Ile Val Ala Arg Ser Tyr Leu Val
 145 150 155 160
 Pro Leu Pro Val Pro Phe Pro Val Lys Ser Leu Asn Phe Cys Pro Gly
 165 170 175
 Asp Asn Ile Pro Ser His Ser Phe Cys Phe His Pro Asp Val Met Arg
 180 185 190
 Arg Ala Cys Ala Asp Ile Thr Ile Asn Ile Cys Tyr Gly Val Tyr Val
 195 200 205
 Val Val Ser Thr Gly Gly Leu Asp Ser Leu Leu Ile Phe Leu Ser Tyr
 210 215 220
 Thr Phe Ile Leu His Thr Val Met Gly Leu Ala Ala Pro Arg Glu Arg
 225 230 235 240
 Ile Trp Ala Leu Asn Thr Cys Val Ser His Ile Pro Ala Val Phe Val
 245 250 255
 Phe Phe Ile Pro Gly Ile Thr Val Ser Met Ile His His Phe Gly Arg

260 265 270
 His Leu Pro His Ile Val His Ala Leu Val Thr Tyr Val Tyr Leu Val
 275 280 285
 Met Pro Ser Val Leu His Pro Ile Ile Tyr Ser Met Lys Ser Lys Pro
 290 295 300
 Ile Arg Glu Ala Ile Leu Arg Met Leu Met Gly Arg Ser Gln Gly Xaa
 305 310 315 320
 Xaa Asn Tyr Lys Ile Leu Xaa Gly
 325

<210> 2172

<211> 278

<212> PRT

<213> Homo sapien (7631097-7-11130-14291)

<400> 2172

Met Tyr Ala Leu Ala Thr Leu Gly Asn Leu Thr Ile Val Leu Ile Ile
 1 5 10 15
 Arg Val Glu Arg Arg Leu His Glu Pro Met Tyr Leu Phe Leu Ala Met
 20 25 30
 Leu Ser Thr Ile Asp Leu Val Leu Ser Ser Ile Thr Met Pro Lys Met
 35 40 45
 Ala Ser Leu Phe Leu Met Gly Ile Gln Glu Ile Glu Phe Asn Ile Cys
 50 55 60
 Leu Ala Gln Met Phe Leu Ile His Ala Leu Ser Ala Val Glu Ser Ala
 65 70 75 80
 Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro
 85 90 95
 Leu Arg His Ala Ser Val Leu Thr Gly Cys Thr Val Ala Lys Ile Gly
 100 105 110
 Leu Ser Ala Leu Thr Arg Gly Phe Val Phe Phe Phe Pro Leu Pro Phe
 115 120 125
 Ile Leu Lys Trp Leu Ser Tyr Cys Gln Thr His Thr Val Thr His Ser
 130 135 140
 Phe Cys Leu His Gln Asp Ile Met Lys Leu Ser Cys Thr Asp Thr Arg
 145 150 155 160
 Val Asn Val Val Tyr Gly Leu Phe Ile Ile Leu Ser Val Met Gly Val
 165 170 175
 Asp Ser Leu Phe Ile Gly Phe Ser Tyr Ile Leu Ile Leu Trp Ala Val
 180 185 190
 Leu Glu Leu Ser Ser Arg Arg Ala Leu Lys Ala Phe Asn Thr Cys
 195 200 205
 Ile Ser His Leu Cys Ala Val Leu Val Phe Tyr Val Pro Leu Ile Gly
 210 215 220
 Leu Ser Val Val His Arg Leu Gly Gly Pro Thr Ser Leu Leu His Val
 225 230 235 240
 Val Met Ala Asn Thr Tyr Leu Leu Leu Pro Pro Val Val Asn Pro Leu
 245 250 255
 Val Tyr Gly Ala Lys Thr Lys Glu Ile Cys Ser Arg Val Leu Cys Met
 260 265 270
 Phe Ser Gln Gly Gly Lys
 275

<210> 2173

<211> 319

<212> PRT

<213> Homo sapien (7631097-8-20107-27103)

<400> 2173

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe
 1 5 10 15

Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala
 20 25 30
 Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Leu
 35 40 45
 Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr
 50 55 60
 Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser
 65 70 75 80
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile
 85 90 95
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr
 100 105 110
 Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val
 130 135 140
 Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met
 145 150 155 160
 Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn
 165 170 175
 Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala
 180 185 190
 Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser
 195 200 205
 Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu
 210 215 220
 Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys
 225 230 235 240
 Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr
 245 250 255
 Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile
 260 265 270
 Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile
 275 280 285
 Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu
 290 295 300
 Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His
 305 310 315

<210> 2174

<211> 311

<212> PRT

<213> Homo sapien (7637231-2-1-2470)

<220>

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 2174

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu
 1 5 10 15
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro
 20 25 30
 Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu
 35 40 45
 Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe
 50 55 60
 Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile
 65 70 75 80
 Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu

```

      85              90              95
Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val
      100              105              110
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
      115              120              125
Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly
      130              135              140
Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro
      145              150              155              160
Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val
      165              170              175
Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys
      180              185              190
Gly Asp Ser Lys Val Asn Asn Val Tyr Gly Met Ser Ile Gly Phe Leu
      195              200              205
Val Leu Ile Met Glu Ser Val Asp Ser Asp Ala Ser Xaa Val Arg Ser
      210              215              220
Ile Arg Ala Val Met Gly Leu Ala Asn His Glu Asp Arg Ile Lys Thr
      225              230              235              240
Met Gly Thr Gly Glu Tyr His Ile Cys Ala Ile Met Ile Phe Arg Ile
      245              250              255
Pro Val Met Tyr Ile Pro Xaa Asp His Arg Asp Gly Gln Cys Val His
      260              265              270
His Pro Val His Asn Met Met Ala Arg Ile Tyr Ile Ile Ser His Pro
      275              280              285
Ser Ile Lys Pro Ser Val Xaa Asp Asp Arg Thr Lys Gln Ser Arg Glu
      290              295              300
Ser Tyr Ile Gln Arg Ala Arg
      305              310

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<210> 2175

<211> 117

<212> PRT

<213> Homo sapien (7637231-7-1-1398)

<400> 2175

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Asn Ile Lys Gly Ile Ala Val Pro Met Phe Ile Glu Val Leu Asp Leu
  1              5              10              15
Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln Ala Val Leu Gln
      20              25              30
Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser
      35              40              45
His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser
      50              55              60
Val Met His Arg Val Ala Arg Cys Ala Ala Pro His Val His Ile Leu
      65              70              75              80
Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile
      85              90              95
Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val Leu Gly Val Phe
      100              105              110
Pro Arg Lys Asp Val
      115

```

<210> 2176

<211> 227

<212> PRT

<213> Homo sapien (7637775-10-2645-3375)

<220>

<221> VARIANT

<222> (1)...(227)

<223> Xaa = Any Amino Acid

<400> 2176

```

Gly Lys Glu Arg Glu Thr Arg Val Trp Arg Pro Arg Ala Gln Asp Arg
 1           5           10           15
Gly Val Ser Thr Arg His Ala Ala Arg Val Thr Ser Tyr Gln Glu Cys
          20           25           30
Gly Val Arg Gly Gly Gly Val Leu Cys Gly Ala Val Arg Pro Ser Pro
          35           40           45
Leu Asp Ala Gln Leu His Asn Val Ile Ala Tyr Arg Arg Thr Cys Phe
          50           55           60
Lys Asp Val Glu Ile Pro Asn Phe Val Trp Asp Pro Ser Gln Leu Pro
65           70           75           80
Arg Leu Ala Cys Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe
          85           90           95
Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser
          100          105          110
Tyr Asp Lys Ile Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly Gly
          115          120          125
Lys His Lys Ala Phe Ser Thr Arg Gly Ser His Leu Ser Val Val Cys
          130          135          140
Xaa Phe Tyr Gly Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser
145          150          155          160
Ser Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ala
          165          170          175
Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile
          180          185          190
Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Ser Ser Gln Tyr
          195          200          205
Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser
          210          215          220
Lys Val Lys
225

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<210> 2177

<211> 316

<212> PRT

<213> Homo sapien (7655430-8-26100-29590)

<220>

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 2177

```

Ile Ser Met Phe Ser Cys Asn Thr Ser Thr Ser Gly Gln Ser Thr Phe
 1           5           10           15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Ser His His Trp Val Ser
          20           25           30
Ile Pro Ile Asn Leu Phe Cys Val Val Ser Ile Leu Gly Asn Asn Ile
          35           40           45
Ile Leu Phe Leu Ile His Thr Asp Pro Ala Leu His Glu Pro Met Tyr
          50           55           60
Ile Phe Leu Ser Met Leu Ala Ala Ser Asp Leu Gly Leu Cys Ala Ser
65           70           75           80
Thr Phe Pro Thr Met Val Arg Leu Phe Trp Leu Gly Ala Arg Glu Leu
          85           90           95
Pro Phe Asp Leu Cys Ala Ala Gln Met Phe Phe Ile His Thr Phe Thr
          100          105          110
Tyr Val Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Ile
          115          120          125

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Ala Ile Arg Asp Pro Leu His Tyr Ala Ile Ile Ile Thr Cys Ser Val
 130 135 140
 Thr Ala Glu Val Gly Thr Ala Ile Leu Val Arg Ala Val Leu Leu Asn
 145 150 155 160
 Leu Pro Gly Pro Ile Leu Leu Gln Gln Leu Leu Phe Pro Lys Ile Ser
 165 170 175
 Ala Leu Cys His Cys Tyr Cys Leu His Cys Asp Leu Val Gly Leu Ala
 180 185 190
 Cys Ser Asp Thr Gln Ile Asn Ser Leu Val Gly Leu Val Ser Ile Leu
 195 200 205
 Phe Ser Leu Cys Leu Asp Ser Phe Leu Ile Met Leu Ser Tyr Ala Leu
 210 215 220
 Ile Leu Xaa Thr Val Leu Gly Ile Ala Ser Pro Gly Glu Arg Leu Lys
 225 230 235 240
 Ala Leu Asn Thr Cys Val Ser His Leu Cys Ile Val Leu Ile Phe Tyr
 245 250 255
 Leu Pro Ile Ile Gly Leu Ser Val Leu His Arg Val Lys Lys His Asp
 260 265 270
 Tyr Pro Ala Leu Ala Val Leu Met Ala Asn Leu His Phe Leu Val Pro
 275 280 285
 Pro Phe Met Asn Pro Ile Val Tyr Cys Ile Lys Ser Arg Gln Ile Arg
 290 295 300
 Gln Ser Leu Leu Lys His Phe Gln Gln Lys Arg Ile
 305 310 315

<210> 2178

<211> 154

<212> PRT

<213> Homo sapien (7657777-15-1-798)

<220>

<221> VARIANT

<222> (1)...(154)

<223> Xaa = Any Amino Acid

<400> 2178

Cys Thr Met Cys Val Trp Leu Leu Ala Xaa Asp Arg Gln Ile His Ile
 1 5 10 15
 His Ser His Ser Asn Lys Pro Lys Gln Val Thr His Pro Met Cys Phe
 20 25 30
 Trp Asp Lys Asp Val His Ser Ser Trp Ala Trp Gly Cys Gly Tyr Arg
 35 40 45
 Lys Gly Asn Lys Phe Phe Leu Ser Tyr Asp Thr Leu Cys Pro Pro Lys
 50 55 60
 Val Ile His Pro Phe Arg Xaa Gln Leu Phe Leu Ser Ser Ser Asp Ile
 65 70 75 80
 Ile Asn Asp Pro His Ile Asp Lys His Asp Ser Thr Leu Ile Thr Leu
 85 90 95
 Xaa Ala Phe Tyr Thr Ile Phe Tyr Lys Pro Thr Met Leu His Leu Phe
 100 105 110
 Ser Glu Ile Leu Ser Met Ile Tyr Phe Met Gly Thr Lys Lys Asn Glu
 115 120 125
 Xaa Lys Pro Arg Lys Lys Asp Cys Glu Ser His Xaa Lys Gly Leu Glu
 130 135 140
 Xaa Met Gly Gln Ile Ile Ile Leu Phe Tyr
 145 150

<210> 2179

<211> 170

<212> PRT

<213> Homo sapien (7657777-22-544-1713)

<220>
 <221> VARIANT
 <222> (1)...(170)
 <223> Xaa = Any Amino Acid

<400> 2179
 His Thr Gln Pro Arg Gly Leu Thr Arg Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Gln Asp Pro Gln Leu Gln Pro Val Leu Ser Gly Leu Ser
 20 25 30
 Leu Cys Met Cys Leu Gly Thr Gln Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Gly Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Ser Phe Leu
 50 55 60
 Ser Asn Leu Ser Gly Ala Asp Ile Ser Phe Thr Ser Thr Thr Gly Pro
 65 70 75 80
 Lys Leu Ile Val Asp Ile His Ser Tyr Thr Arg Asp Ile Ser Tyr Ala
 85 90 95
 Arg Cys Leu Thr His Thr Pro Leu Phe Ala Ile Phe Gly Gly Val Glu
 100 105 110
 Arg Asp Met Leu Leu Arg Val Met Gly Tyr Asp Arg Val Val Asp Ile
 115 120 125
 Cys Asp Pro Leu Tyr His Ser His Ala Met Asn Pro Cys Val Cys Gly
 130 135 140
 Ser Leu Asp Leu Trp Ser Leu Phe Phe Leu Thr Leu Leu Tyr Thr His
 145 150 155 160
 Leu His Asn Ser Ile Ala Leu His Met Thr
 165 170

<210> 2180
 <211> 198
 <212> PRT
 <213> Homo sapien (7657777-42-1-597)

<220>
 <221> VARIANT
 <222> (1)...(198)
 <223> Xaa = Any Amino Acid

<400> 2180
 Met Asn Pro Cys Leu Cys Gly Phe Arg Val Val Val Ser Phe Phe Phe
 1 5 10 15
 His Ser Leu Leu Gly Ala Gln Val His Asn Leu Ser Ala Ser Gln Met
 20 25 30
 Thr Cys Phe Glu Tyr Val Glu Ile His Asn Phe Leu Trp Ala Leu Ser
 35 40 45
 Gln Leu Pro His Arg Ala Trp Cys Asp Thr Phe Pro Asn Asn Ile Ile
 50 55 60
 Val Tyr Phe Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ala Gly Thr
 65 70 75 80
 Leu Phe Ser Xaa Tyr Glu Ser Val Ser Ser Ile Glu Arg Val Ser Ser
 85 90 95
 Xaa Gly Gly Glu Tyr Lys Ala Phe Pro Thr Cys Gly Ser His Leu Ser
 100 105 110
 Val Val Cys Xaa Leu Tyr Gly Thr Gly Val Gly Gly His Leu Ser Ser
 115 120 125
 Asp Val Ser Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met Tyr
 130 135 140
 Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Met Arg Asn
 145 150 155 160

Arg Asp Thr Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Xaa
 165 170 175
 Phe Xaa Tyr Leu Leu Ile Cys Pro Ile Pro Phe Val Val Trp Val Lys
 180 185 190
 Lys Gly Arg Lys Val Lys
 195

<210> 2181
 <211> 199
 <212> PRT
 <213> Homo sapien (7657788-15-11714-13012)

<220>
 <221> VARIANT
 <222> (1)...(199)
 <223> Xaa = Any Amino Acid

<400> 2181
 Leu Glu Met Xaa Leu Lys Ile Leu Tyr Leu Lys Asn Cys Ser Phe Xaa
 1 5 10 15
 Cys Asn Arg Pro Glu His Tyr Asn Xaa Lys Asn Cys Gly Xaa Phe Cys
 20 25 30
 Leu Leu Ile Thr Ile Ile Thr Phe Arg Ser Gly Ile Ile Asp Ile Cys
 35 40 45
 Leu His His His Lys Thr Ile Phe Ile Phe Lys Lys His Ser Gly Phe
 50 55 60
 Glu Gly Xaa Leu Trp Leu Arg Ile Xaa Asn Gln Ser Pro Lys Ser Trp
 65 70 75 80
 Ile Ser Ile Ala Cys Asp Cys Cys Val Ala Xaa Asn Met Lys Gln Val
 85 90 95
 Ala Ile Ser Cys His Ser Phe Ser Ser Val Lys Xaa Ser Pro Tyr Val
 100 105 110
 Ile Trp Lys Tyr Phe Cys Lys Xaa Tyr Lys His Ile Lys Asn Gly Arg
 115 120 125
 Asp Xaa Ile Xaa Leu Leu Thr Leu Lys Xaa Ile Lys His Leu Phe Val
 130 135 140
 Val Cys Ile Ile Tyr Thr Pro Cys Met Phe His Pro Phe Gln Asn Lys
 145 150 155 160
 Tyr Met Val Thr Glu Ser Leu Ile Xaa Ser Tyr Xaa Val Asp Pro Val
 165 170 175
 Ser Asn Pro Ala Leu Ile Thr Ala Arg Ser His Xaa Asn His Leu Val
 180 185 190
 Ile Ser Gln His Asn Asn Asn
 195

<210> 2182
 <211> 324
 <212> PRT
 <213> Homo sapien (7658481-16-11475-15098)

<220>
 <221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 2182
 Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe
 1 5 10 15
 Leu Thr Gly Ile Pro Gly Leu Glu Ala Ala His Phe Trp Ile Ala Ile
 20 25 30
 Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu

```

      35              40              45
Ile Leu Val Ile Ala Met Asp Asn Ala Leu His Ala Pro Met Tyr Leu
  50              55              60
Phe Leu Cys Leu Leu Ser Leu Thr Asp Leu Ala Leu Ser Ser Thr Thr
  65              70              75              80
Val Pro Lys Met Leu Ala Ile Leu Trp Leu His Ala Gly Glu Ile Ser
      85              90              95
Phe Gly Gly Cys Leu Ala Gln Met Phe Cys Val His Ser Ile Tyr Ala
  100              105              110
Leu Glu Ser Ser Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
  115              120              125
Ile Cys Asn Pro Leu Arg Tyr Thr Thr Ile Leu Asn His Ala Val Ile
  130              135              140
Gly Arg Ile Gly Phe Val Gly Leu Phe Arg Ser Val Ala Ile Val Ser
  145              150              155              160
Pro Phe Ile Phe Leu Arg Arg Leu Pro Tyr Cys Gly His Arg Val
      165              170              175
Met Thr His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys
  180              185              190
Ala Asn Ile Thr Val Asn Ile Val Tyr Gly Leu Thr Val Ala Leu Leu
  195              200              205
Ala Met Gly Leu Asp Ser Ile Leu Ile Ala Ile Ser Tyr Gly Phe Ile
  210              215              220
Leu His Ala Val Phe His Leu Pro Ser His Asp Ala Gln His Lys Ala
  225              230              235              240
Leu Ser Thr Cys Gly Ser His Ile Gly Ile Ile Leu Val Phe Tyr Ile
      245              250              255
Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Glu Val
  260              265              270
Pro Lys His Val His Ile Phe Leu Ala Asn Leu Tyr Val Leu Val Pro
  275              280              285
Pro Val Leu Asn Pro Ile Leu Tyr Gly Ala Arg Thr Lys Glu Ile Arg
  290              295              300
Ser Arg Leu Leu Lys Leu Leu His Leu Gly Lys Thr Ser Ile Xaa Met
  305              310              315              320
Leu Ser Arg Ser

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<210> 2183

<211> 317

<212> PRT

<213> Homo sapien (7658481-18-4217-6941)

<400> 2183

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Met Ser Gln Val Thr Asn Thr Thr Gln Glu Gly Ile Tyr Phe Ile Leu
  1              5              10              15
Thr Asp Ile Pro Gly Phe Glu Ala Ser His Ile Trp Ile Ser Ile Pro
  20              25              30
Val Cys Cys Leu Tyr Thr Ile Ser Ile Met Gly Asn Thr Thr Ile Leu
  35              40              45
Thr Val Ile Arg Thr Glu Pro Ser Val His Gln Arg Met Tyr Leu Phe
  50              55              60
Leu Ser Met Leu Ala Leu Thr Asp Leu Gly Leu Thr Leu Thr Thr Leu
  65              70              75              80
Pro Thr Val Met Gln Leu Leu Trp Phe Asn Val Arg Arg Ile Ser Ser
      85              90              95
Glu Ala Cys Phe Ala Gln Phe Phe Phe Leu His Gly Phe Ser Phe Met
  100              105              110
Glu Ser Ser Val Leu Leu Ala Met Ser Val Asp Cys Tyr Val Ala Ile
  115              120              125
Cys Cys Pro Leu His Tyr Ala Ser Ile Leu Thr Asn Glu Val Ile Gly

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      130              135              140
Arg Thr Gly Leu Ala Ile Ile Cys Cys Cys Val Leu Ala Val Leu Pro
145              150              155              160
Ser Leu Phe Leu Leu Lys Arg Leu Pro Phe Cys His Ser His Leu Leu
      165              170              175
Ser Arg Ser Tyr Cys Leu His Gln Asp Met Ile Arg Leu Val Cys Ala
      180              185              190
Asp Ile Arg Leu Asn Ser Trp Tyr Gly Phe Ala Leu Ala Leu Ile
      195              200              205
Ile Ile Val Asp Pro Leu Leu Ile Val Ile Ser Tyr Thr Leu Ile Leu
      210              215              220
Lys Asn Ile Leu Gly Thr Ala Thr Trp Ala Glu Arg Leu Arg Ala Leu
225              230              235              240
Asn Asn Cys Leu Ser His Ile Leu Ala Val Leu Val Leu Tyr Ile Pro
      245              250              255
Met Val Gly Val Ser Met Thr His Arg Phe Ala Lys His Ala Ser Pro
      260              265              270
Leu Val His Val Ile Met Ala Asn Ile Tyr Leu Leu Ala Pro Pro Val
      275              280              285
Met Asn Pro Ile Ile Tyr Ser Val Lys Asn Lys Gln Ile Gln Trp Gly
      290              295              300
Met Leu Asn Phe Leu Ser Leu Lys Asn Met His Ser Arg
305              310              315

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<210> 2184

<211> 315

<212> PRT

<213> Homo sapien (7658481-19-24037-28136)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 2184

```

Phe Ser Gln Asn Leu Leu Ile Ser Gly Ser Gly Ser Phe Val Leu Leu
1      5      10      15
Gly Met Pro Gly Leu Glu Ala Leu His Ala Trp Leu Ser Val Leu Val
      20      25      30
Cys Leu Leu Tyr Met Ala Ala Leu Val Gly Asn Ala Leu Leu Val Gly
      35      40      45
Leu Val Val Thr Asp Lys Ala Leu Trp Ala Pro Met Tyr Gln Leu Leu
      50      55      60
Trp Leu Leu Ala Ala Ala Asp Phe Val Leu Ala Thr Ser Thr Val Pro
65      70      75      80
Lys Ala Leu Ala Val Leu Trp Gly Leu Ser Ser Glu Ile Ser Phe Gly
      85      90      95
Gly Cys Leu Ala Gln Leu Phe Val Ala His Ser Val Asn His Cys His
      100      105      110
Ile Ala Glu Ser Ser Val Leu Leu Ser Thr Ala Val Asp Cys Gln Pro
      115      120      125
Leu Arg Tyr Gly Ala Leu Leu Ala Gln Phe Val Val Gly Leu Val Ala
130      135      140
Leu Thr Thr Met Thr Arg Asp Val Cys Val Met Tyr Thr Leu Xaa Phe
145      150      155      160
Leu Phe Lys Lys Leu Pro Tyr Cys Gly Gln Trp Ala Leu Thr His Thr
      165      170      175
Tyr Cys Glu His Met Gly Val Ala Cys Leu Ala Cys Gly Asp Thr Cys
      180      185      190
Pro Ile Ile Arg Tyr Gly Leu Ala Thr Thr Leu Leu Ser Pro Ala Leu
195      200      205

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Asp Leu Gly Leu Ile Gly Ala Ser Tyr Ala Leu Ile Phe Arg Ala Val
 210 215 220
 Cys Arg Leu Pro Ser His Val Ala Cys His Lys Ala Leu Gly Asn Cys
 225 230 235 240
 Gly Thr Tyr Ala Ser Ile Ile Gly Leu Phe Tyr Thr Pro Ala Leu Phe
 245 250 255
 Ser Phe Leu Ala His Cys Phe Gly Cys His Thr Val Pro Asn His Ile
 260 265 270
 His Ile Leu Leu Ala Asn Leu Tyr Ala Val Val Phe Pro Ala Phe Asn
 275 280 285
 Pro Val Val Tyr Gly Val Gln Thr Gln Gln Ser Ser Glu Ala Gln Glu
 290 295 300
 Leu Ala Ser Thr Phe Leu Gly Arg Ser Ser Glu
 305 310 315

<210> 2185

<211> 320

<212> PRT

<213> Homo sapien (7658481-19-6742-9039)

<400> 2185

Met Pro Ser Ala Ser Ala Met Ile Ile Phe Asn Leu Ser Ser Tyr Asn
 1 5 10 15
 Pro Gly Pro Phe Ile Leu Val Gly Ile Pro Gly Leu Glu Gln Phe His
 20 25 30
 Val Trp Ile Gly Ile Pro Phe Cys Ile Ile Tyr Ile Val Ala Val Val
 35 40 45
 Gly Asn Cys Ile Leu Leu Tyr Leu Ile Val Val Glu His Ser Leu His
 50 55 60
 Glu Pro Met Phe Phe Phe Leu Ser Met Leu Ala Met Thr Asp Leu Ile
 65 70 75 80
 Leu Ser Thr Ala Gly Val Pro Lys Ala Leu Ser Ile Phe Trp Leu Gly
 85 90 95
 Ala Arg Glu Ile Thr Phe Pro Gly Cys Leu Thr Gln Met Phe Phe Leu
 100 105 110
 His Tyr Asn Phe Val Leu Asp Ser Ala Ile Leu Met Ala Met Ala Phe
 115 120 125
 Asp His Tyr Val Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr Ile Leu
 130 135 140
 Thr Pro Lys Thr Ile Ile Lys Ser Ala Met Gly Ile Ser Phe Arg Ser
 145 150 155 160
 Phe Cys Ile Ile Leu Pro Asp Val Phe Leu Leu Thr Cys Leu Pro Phe
 165 170 175
 Cys Arg Thr Arg Ile Ile Pro His Thr Tyr Cys Glu His Ile Gly Val
 180 185 190
 Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Phe Trp Tyr Gly Phe
 195 200 205
 Cys Val Pro Ile Met Thr Val Ile Ser Asp Val Ile Leu Ile Ala Val
 210 215 220
 Ser Tyr Ala His Ile Leu Cys Ala Val Phe Gly Leu Pro Ser Gln Asp
 225 230 235 240
 Ala Cys Gln Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys Val Ile
 245 250 255
 Leu Met Phe Tyr Thr Pro Ala Phe Phe Ser Ile Leu Ala His Arg Phe
 260 265 270
 Gly His Asn Val Ser Arg Thr Phe His Ile Met Phe Ala Asn Leu Tyr
 275 280 285
 Ile Val Ile Pro Pro Ala Leu Asn Pro Met Val Tyr Gly Val Lys Thr
 290 295 300
 Lys Gln Ile Arg Asp Lys Val Ile Leu Leu Phe Ser Lys Gly Thr Gly
 305 310 315 320

<210> 2186
 <211> 315
 <212> PRT
 <213> Homo sapien (7658481-2-1-1440)

<220>
 <221> VARIANT
 <222> (1)...(315)
 <223> Xaa = Any Amino Acid

<400> 2186
 Met Gly Gly Phe Gly Thr Asn Ile Ser Ser Thr Thr Ser Phe Thr Leu
 1 5 10 15
 Thr Gly Phe Pro Glu Met Lys Gly Leu Glu His Trp Leu Ala Ala Leu
 20 25 30
 Leu Leu Leu Leu Cys Ala Ile Ser Phe Leu Gly Asn Ile Leu Ile Leu
 35 40 45
 Phe Ile Ile Lys Glu Glu Gln Ser Leu His Gln Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Leu Phe Ser Val Asn Asp Leu Gly Val Ser Phe Ser Thr Leu
 65 70 75 80
 Pro Thr Val Leu Ala Ala Val Cys Phe His Ala Pro Glu Thr Thr Phe
 85 90 95
 Asp Ala Cys Leu Ala Gln Thr Phe Phe Ile His Phe Ser Ser Trp Thr
 100 105 110
 Glu Phe Gly Ile Leu Leu Ala Met Ser Phe Asp His Tyr Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Arg Tyr Ala Thr Val Leu Thr Asp Val Arg Val Ala
 130 135 140
 His Asn Gly Ile Ser Ile Val Ile Arg Ser Phe Cys Met Val Phe Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Lys Arg Leu Pro Phe Cys Lys Ala Ser Val Val
 165 170 175
 Leu Ser His Ser Tyr Cys Leu His Ala Asp Leu Ile Arg Leu Pro Cys
 180 185 190
 Gly Asp Thr Thr Ile Asn Ser Met Tyr Gly Leu Phe Ile Val Ile Ser
 195 200 205
 Ala Phe Gly Val Asp Ser Leu Leu Ile Leu Leu Ser Tyr Val Leu Ile
 210 215 220
 Leu His Ser Val Leu Ala Ile Ala Ser Arg Gly Glu Arg Leu Lys Thr
 225 230 235 240
 Leu Asn Thr Cys Val Ser His Ile Tyr Ala Val Leu Ile Phe Tyr Val
 245 250 255
 Pro Met Val Ser Val Ser Met Val His Arg Phe Gly Arg His Ala Pro
 260 265 270
 Glu Tyr Val His Lys Phe Met Ser Ser Leu Tyr Leu Pro Met Leu Tyr
 275 280 285
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile Arg Arg Arg Leu His
 290 295 300
 Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Lys
 305 310 315

<210> 2187
 <211> 124
 <212> PRT
 <213> Homo sapien (7658497-19-2333-3610)

<220>
 <221> VARIANT
 <222> (1)...(124)

<223> Xaa = Any Amino Acid

<400> 2187

```

Leu Ile Leu Ser Ala Gln Ile Cys Arg Ala Leu Xaa Leu Ser Ile Phe
 1           5           10           15
Leu Val Arg Leu His Phe Lys Lys Leu Gly Pro Lys Ser Leu Asp Leu
           20           25           30
Tyr Phe Pro Gly Leu Gly Leu Lys Tyr Lys Ile Asn Ser Thr Asn Asn
           35           40           45
Tyr Arg Thr Ala Leu Glu Phe Xaa Val Phe Arg Gln Ala Val Xaa Leu
           50           55           60
Xaa Phe Thr Phe Phe Leu Phe Lys Tyr Ser Cys Leu Ser Lys Pro Gln
65           70           75           80
Xaa Glu Xaa Gly Ser Ser Asp Xaa Val Pro Cys Gln Tyr Ser Arg Cys
           85           90           95
Ser Glu His Asn Val Ala Leu Leu Ser Pro Gly Phe Ile Val Met Xaa
           100          105          110
Val Leu Val Gln Leu Pro Leu Phe Ser Phe Thr Ser
           115          120

```

<210> 2188

<211> 278

<212> PRT

<213> Homo sapien (7670214-14-2036-3224)

<400> 2188

```

Met Leu Leu Gly Asn Leu Ala Ile Ile Ser Phe Ile Cys Leu Asp Ser
 1           5           10           15
Arg Leu His Ser Pro Met Tyr Phe Phe Leu Cys Asn Phe Ser Leu Met
           20           25           30
Glu Met Val Val Thr Ser Thr Val Val His Arg Met Leu Ala Asp Leu
           35           40           45
Leu Ser Thr His Lys Thr Met Ser Leu Ala Lys Cys Leu Thr Gln Ser
           50           55           60
Phe Phe Tyr Phe Ser Leu Gly Ser Ala Asn Phe Leu Ile Leu Met Val
65           70           75           80
Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro
           85           90           95
Thr Ile Thr Asn Gly Pro Val Cys Val Lys Leu Val Val Ala Cys Trp
           100          105          110
Val Val Gly Phe Leu Ser Ile Val Ser Pro Thr Leu Gln Lys Thr Arg
           115          120          125
Leu Trp Phe Cys Gly Pro Asn Ile Ile Gly His Tyr Phe Cys Asp Ser
           130          135          140
Ala Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg His Ile Glu Arg
145           150          155          160
Met Asp Leu Phe Leu Ser Leu Leu Phe Val Leu Thr Thr Met Leu Leu
           165          170          175
Ile Ile Leu Ser Tyr Ile Leu Ile Val Ala Ala Val Leu His Ile Pro
           180          185          190
Ser Ser Ser Gly Cys Gln Lys Ala Phe Ser Thr Cys Ala Ser His Leu
           195          200          205
Thr Val Val Val Leu Gly Tyr Gly Ser Ala Ile Phe Ile Tyr Val Arg
           210          215          220
Pro Gly Lys Gly His Ser Thr Tyr Leu Asn Lys Ala Val Ala Met Val
225           230          235          240
Thr Ala Met Val Thr Pro Phe Leu Asn Pro Phe Ile Phe Thr Phe Arg
           245          250          255
Asn Glu Lys Val Lys Glu Val Ile Glu Asp Val Thr Lys Arg Ile Phe
           260          265          270
Leu Gly Asp Pro Ala Ala

```

275

<210> 2189
 <211> 203
 <212> PRT
 <213> Homo sapien (7670214-23-12266-12905)

<220>
 <221> VARIANT
 <222> (1)...(203)
 <223> Xaa = Any Amino Acid

<400> 2189
 Pro Leu Ile Xaa Pro Asp Pro Phe Ile Phe Thr Gln Leu Cys Ser Phe
 1 5 10 15
 Leu Asn Lys Tyr Val Ala Ser Thr Arg Leu Asn Asp His Asn Ile Asp
 20 25 30
 Gln Ala Pro Xaa Ser Arg Ser Ile Ile Leu Asn Leu Cys Leu Ile Ser
 35 40 45
 Phe Gly Ile Lys Gly Met Trp Ser Asn Val Asn Ser Cys Phe Leu Ser
 50 55 60
 Ser Leu Pro Arg Glu Lys Glu Leu Gly Leu Lys Ser Glu Gly Asn Tyr
 65 70 75 80
 Ser Ser Ala Thr Gln Phe Cys Leu Leu Gly Phe Pro Gly Phe Glu Glu
 85 90 95
 Leu Pro His Phe Leu Leu Val Asn Phe Phe Phe His Leu Met Arg Leu
 100 105 110
 Met Gly Asn Ala Val Ile Tyr Met Val Arg Ile Asp Xaa Ser Leu Gln
 115 120 125
 Ser Pro Gly Asp Phe Phe Leu Ser Gln Leu Phe Ile Phe Ser His Ser
 130 135 140
 Leu Leu Met Asp Ile Ser Ile Val Ile Ala Ser Leu Ile Gln Ile Asp
 145 150 155 160
 Ser Tyr Ser Ser Ile Pro Ser Ala Ser Gly Gln Lys Lys Ser Phe Ser
 165 170 175
 Thr His Ala Ser His Phe Thr Cys Val Gly Ile Asp Tyr Asp Ser Cys
 180 185 190
 Leu Phe Leu Tyr Val Lys Pro Lys Gln Ile Trp
 195 200

<210> 2190
 <211> 321
 <212> PRT
 <213> Homo sapien (7671636-1-417-2747)

<220>
 <221> VARIANT
 <222> (1)...(321)
 <223> Xaa = Any Amino Acid

<400> 2190
 Phe Lys Arg Ser Ile Thr Phe Thr Pro Thr Thr Phe Thr Leu Val Gly
 1 5 10 15
 Ile Pro Gly Leu Glu Ala Glu His Tyr Trp Ile Ser Ile Pro Phe Cys
 20 25 30
 Leu Ile Tyr Thr Ile Ile Phe Pro Gly Asn Gly Ile Ile Leu His Ile
 35 40 45
 Ile Arg Ile Asp Ser Ser Leu His Gln Pro Met Tyr Tyr Phe Leu Ala
 50 55 60
 Met Pro Ala Phe Val Glu Leu Gly Val Ser Ala Ser Thr Met Pro Thr
 65 70 75 80

Val Leu Ser Ile Phe Leu Phe Gly Ile Asn Asp Val Ser Phe Gly Gly
 85 90 95
 Cys Leu Leu Gln Met Phe Ser Met His Ser Phe Thr Leu Met Glu Ser
 100 105 110
 Gly Val Leu Leu Ala Met Ser Val Asp Arg Phe Val Ala Ile Tyr Ser
 115 120 125
 Pro Leu Arg Tyr Thr Thr Ile Leu Thr Ile Ala Cys Ile Ser Gly Met
 130 135 140
 Gly Ala Ala Ile Ala Leu Arg Ser Val Met Leu Met Leu Pro Leu Leu
 145 150 155 160
 Phe Leu Leu Arg Arg Leu Pro Phe Cys Gly His Asn Thr Leu Thr His
 165 170 175
 Ser Tyr Cys Leu His Ser Asp Leu Ile Lys Leu Pro Cys Gly Asp Thr
 180 185 190
 Arg Pro Asn Ser Ile Leu Ala Leu Phe Val Ile Thr Phe Thr Phe Gly
 195 200 205
 Leu Asp Leu Leu Phe Ile Val Val Ser Tyr Val Leu Ile Leu His Thr
 210 215 220
 Val Leu Glu Ile Ala Ser Arg Ser Arg Ala Trp Gln Ala Leu Asn Thr
 225 230 235 240
 Cys Val Ser His Ile Cys Ala Val Leu Val Tyr Tyr Val Pro Met Ile
 245 250 255
 Ser Leu Ser Xaa Val His Arg Phe Gly Arg His Leu Pro Pro Leu Phe
 260 265 270
 Gln Thr Val Thr Ala Asn Ala Tyr Leu Phe Phe Pro Pro Val Val Asn
 275 280 285
 Pro Ile Val Tyr Ser Ile Lys Ile Lys Glu Ile Arg Asn Ser Val Val
 290 295 300
 Leu Thr Leu Ser Arg Lys Arg Gly Glu Phe Xaa Trp Arg Pro Lys Ile
 305 310 315 320
 Pro

<210> 2191

<211> 295

<212> PRT

<213> Homo sapien (7690091-1-489-1697)

<220>

<221> VARIANT

<222> (1)...(295)

<223> Xaa = Any Amino Acid

<400> 2191

Ile Gln Cys Lys Gly Xaa Xaa Lys Xaa Ile Lys Thr Phe Ser Val Thr
 1 5 10 15
 Pro Ile Leu Asn Gly Asn Arg Glu Ile Ala Arg Phe Leu Ser Asn Leu
 20 25 30
 Ser Leu Ala Gly Ile Gly Phe Pro Ser Thr Ile Val Ser Lys Met Ile
 35 40 45
 Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu
 50 55 60
 Thr Gln Val Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu
 65 70 75 80
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Asp Ile Cys His Pro Leu
 85 90 95
 Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 100 105 110
 Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile
 115 120 125
 Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe

130	135	140
Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr		
145	150	155
Asn Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro		160
	165	170
Ile Ser Gly Thr Phe Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu		175
	180	185
Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly		190
	195	200
Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Gly Phe Gly Gly		205
	210	215
Asp Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala		220
225	230	235
Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr		240
	245	250
Ser Arg Asn Arg Glu Ile Lys Ser Ala Leu Arg Gln Leu His Cys Arg		255
	260	265
Ile Val Xaa Ser His Phe Leu Ile Ile Cys Ser Ile Pro Ser Val Val		270
	275	280
Xaa Val Arg Lys Gly Ser Lys		285
	290	295

<210> 2192

<211> 197

<212> PRT

<213> Homo sapien (7705148-11-94-972)

<220>

<221> VARIANT

<222> (1)...(197)

<223> Xaa = Any Amino Acid

<400> 2192

Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn Pro Leu Leu	
1	5
Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu Ala Ile Gly	10
	20
Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr Thr Asn Thr	25
	30
Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr Thr Asn Thr	35
	40
Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe Phe Cys Asp	45
	50
Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr Met His Asp	55
65	60
Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile Cys Leu Leu	65
	70
Ser Val Leu Leu Ser Tyr Val Phe Ile Met Ala Ala Ile Leu Arg Thr	75
	80
Gly Ser Val Glu Gly Arg Arg Arg Gly Phe Ser Thr Cys Ala Ser His	85
	90
Leu Thr Val Val Thr Met Tyr His Gly Thr Leu Ile Phe Ile Tyr Leu	95
	100
Arg Pro Ser Thr Gly His Ser Leu Asp Ile Asp Lys Val Thr Ser Val	105
145	110
Phe Tyr Thr Leu Ile Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu	115
	120
Arg Asn Lys Asp Val Lys Asn Ala Phe Arg Lys Val Ile Gly Arg Lys	125
	130
Leu Leu Pro Xaa Gly	135
	140
	145
	150
	155
	160
	165
	170
	175
	180
	185
	190
	195

<210> 2193

<211> 128
 <212> PRT
 <213> Homo sapien (7705148-13-12855-13510)

<220>
 <221> VARIANT
 <222> (1)...(128)
 <223> Xaa = Any Amino Acid

<400> 2193
 Ser Arg Ser Asp Thr Gln Val Asn Glu Leu Val Leu Phe Thr Val Phe
 1 5 10 15
 Gly Phe Ile Glu Leu Ser Thr Ile Ser Gly Val Phe Ile Ser Tyr Cys
 20 25 30
 Tyr Ile Ile Leu Ser Val Leu Glu Ile His Ser Ala Glu Gly Arg Phe
 35 40 45
 Lys Ala Leu Ser Thr Cys Thr Ser His Leu Ser Ala Val Ala Ile Phe
 50 55 60
 Gln Gly Thr Leu Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser
 65 70 75 80
 Leu Asp Gln Asp Lys Met Thr Ser Leu Phe Tyr Thr Leu Val Val Pro
 85 90 95
 Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu
 100 105 110
 Ala Leu Lys Lys Leu Lys Asn Lys Ile Leu Phe Xaa Gly Asn Ser Lys
 115 120 125

<210> 2194
 <211> 208
 <212> PRT
 <213> Homo sapien (7705148-18-30183-31440)

<220>
 <221> VARIANT
 <222> (1)...(208)
 <223> Xaa = Any Amino Acid

<400> 2194
 Met Glu Leu Glu Asn Gly Thr Val Lys Thr Gly Phe Phe Leu Leu Gly
 1 5 10 15
 Phe Ser Asp His Leu Glu Leu Gln Ser Leu Leu Phe Ala Glu Phe Phe
 20 25 30
 Ser Ile Tyr Ser Val Thr Leu Met Gly Asn Leu Gly Met Ile Leu Leu
 35 40 45
 Ile Thr Ile Ser Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50 55 60
 Val Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Ile Ala Pro Lys
 65 70 75 80
 Leu Leu Val Asn Leu Val Ser Glu Lys Lys Thr Ile Ser Tyr Asn Gly
 85 90 95
 Cys Val Ala Gln Leu Tyr Phe Phe Cys Ser Leu Val Asp Thr Glu Ser
 100 105 110
 Phe Leu Leu Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu
 130 135 140
 Ala Ile Gly Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr
 145 150 155 160
 Thr Asn Thr Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe
 165 170 175
 Phe Cys Asp Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr

	180		185		190
Met	His	Asp	Ile	Ile	Leu
	195		200		205

<210> 2195

<211> 188

<212> PRT

<213> Homo sapien (7705148-8-1-2633)

<400> 2195

Met	Asp	Trp	Glu	Asn	Cys	Ser	Ser	Leu	Thr	Asp	Phe	Phe	Leu	Leu	Gly
1				5					10					15	
Ile	Thr	Asn	Asn	Pro	Glu	Met	Lys	Val	Thr	Leu	Phe	Ala	Val	Phe	Leu
		20						25					30		
Ala	Val	Tyr	Ile	Ile	Asn	Phe	Ser	Ala	Asn	Leu	Gly	Met	Ile	Val	Leu
	35					40					45				
Ile	Arg	Met	Asp	Tyr	Gln	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
	50				55					60					
His	Leu	Ser	Phe	Cys	Asp	Leu	Cys	Tyr	Ser	Thr	Ala	Thr	Gly	Pro	Lys
65				70				75						80	
Met	Leu	Val	Asp	Leu	Ala	Lys	Asn	Lys	Ser	Ile	Pro	Phe	Tyr	Gly	
		85					90						95		
Cys	Ala	Leu	Gln	Phe	Leu	Val	Phe	Cys	Ile	Phe	Ala	Asp	Ser	Glu	Cys
		100					105					110			
Leu	Leu	Leu	Ser	Val	Met	Ala	Phe	Asp	Arg	Tyr	Lys	Ala	Ile	Ile	Asn
	115					120					125				
Pro	Leu	Leu	Tyr	Thr	Val	Asn	Met	Ser	Ser	Arg	Val	Cys	Tyr	Leu	Leu
	130				135					140					
Leu	Thr	Gly	Val	Tyr	Leu	Val	Gly	Ile	Ala	Asp	Ala	Leu	Ile	His	Met
145					150				155					160	
Thr	Leu	Ala	Phe	Arg	Leu	Cys	Phe	Cys	Gly	Ser	Asn	Glu	Ile	Asn	His
			165					170					175		
Phe	Phe	Cys	Asp	Ile	Pro	Pro	Leu	Leu	Leu	Ser					
		180					185								

<210> 2196

<211> 210

<212> PRT

<213> Homo sapien (7705159-18-2705-3893)

<220>

<221> VARIANT

<222> (1)...(210)

<223> Xaa = Any Amino Acid

<400> 2196

Cys	His	Pro	Pro	Leu	Arg	Trp	Gly	Ser	Xaa	Glu	Pro	Ala	Glu	Glu	Glu
1				5					10					15	
Gly	Leu	Ala	Leu	Ser	Ser	Arg	Xaa	Phe	Phe	Phe	Phe	Leu	Ser	Val	Leu
		20					25					30			
Asp	Ala	Gln	Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Gln
	35					40					45				
Asp	Ala	Glu	Ile	Pro	Asn	Phe	Trp	Asp	Pro	Ser	Gln	Leu	Pro	His	
	50				55					60					
Leu	Ala	Cys	Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Met	Tyr	Phe	Pro
65				70					75					80	
Ala	Val	Ile	Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Leu	Phe	Ser	Tyr
			85					90					95		
Tyr	Lys	Ile	Val	Ser	Ser	Ile	Leu	Ser	Val	Ser	Ser	Ser	Arg	Gly	Gln
		100					105					110			
Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Cys	Xaa

```

      115      120      125
Phe Tyr Gly Thr Gly Val Gly Gly Tyr Phe Ser Ser Asp Val Ser Ser
 130      135      140
Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr
145      150      155      160
Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg His Ile Lys
      165      170      175
Ser Val Leu Arg Arg Pro His Ser Ser Thr Val Gln Ser Pro Cys Leu
      180      185      190
Leu Asn Cys Ser Ile Pro Phe Val Val Trp Val Asn Lys Gly Ser Lys
      195      200      205
Val Lys
 210

```

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<210> 2197
<211> 186
<212> PRT
<213> Homo sapien (7708872-11-1-1518)

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<220>
<221> VARIANT
<222> (1)...(186)
<223> Xaa = Any Amino Acid

```

```

<400> 2197
Pro Ala His Pro Arg Ser Pro His His Pro Leu Phe Pro Pro Tyr Ile
 1      5      10      15
Tyr Leu Lys Asn Phe Phe Pro Thr Ile Phe Pro Gln Asn Leu Leu Ser
      20      25      30
Leu Leu Phe Thr Thr Val Phe Pro Pro Pro Pro Thr Pro Asn Ile Phe
      35      40      45
Ser Pro Pro Ser Phe Pro His Cys Leu Phe Cys Asn Thr Phe Ser Cys
      50      55      60
Ser Leu Ile Leu Tyr Phe Pro Leu Ala Leu Thr Thr Leu Phe Thr Pro
65      70      75      80
Pro Ser Thr Pro Lys Leu Phe Ser Pro Ser Tyr Arg Ser Ser His Thr
      85      90      95
Ala Val Ser Val Ala Ala Thr Asn Arg Ser Glu Ala Ser Cys Ala Cys
      100      105      110
Arg Ser His Ser Leu Gln His Ala Ala Val Ala Ser Pro Cys Pro Gly
      115      120      125
Pro Leu Ser Arg Glu Arg Ser Ser Pro Ala Arg Arg His Ala Xaa Ala
      130      135      140
Xaa Asn Gly Leu Thr Pro Leu Leu Ala Pro Phe Ile Tyr Xaa Gly Tyr
145      150      155      160
Ala Tyr Glu Val Pro Gly Leu Leu Phe Gln Asp Trp Val Arg Glu Asn
      165      170      175
Ala Glu Ala Tyr Ser Asp Trp Thr Leu Leu
      180      185

```

```

<210> 2198
<211> 323
<212> PRT
<213> Homo sapien (7708872-16-23686-24654)

```

```

<220>
<221> VARIANT
<222> (1)...(323)
<223> Xaa = Any Amino Acid

```

```

<400> 2198

```

Val Ala Cys Tyr Leu Pro Glu Leu Ser Val Gly Cys Pro Gly Gly Lys
 1 5 10 15
 Glu Asn Glu Thr Gly Val Gly Glu Phe Leu Leu Leu Ser Ile Thr Ser
 20 25 30
 Asp Ser Glu Lys Gln Gln Ala Leu Phe Trp Leu Phe Leu Cys Met His
 35 40 45
 Leu Val Thr Glu Ala Gly Asn Thr Pro Ile Ile Leu Gly Ile Gly Ser
 50 55 60
 Asn Pro Arg Leu His Thr Pro Thr Tyr Phe Phe Thr His Leu Ser Phe
 65 70 75 80
 Val Asn Ile Cys Phe Ile Thr Asn Leu Ile Pro Lys Leu Leu Val Asn
 85 90 95
 His Val Ala Gly Thr Gly Met Ile Thr Ile Ser Ser Pro Gln Cys Leu
 100 105 110
 Thr Gln Met Tyr Phe Leu Ile Ser Phe Ala Asn Val Asp Thr Phe Leu
 115 120 125
 Leu Ala Ile Met Ala Leu Asp His Tyr Val Ala Ile Cys Ser Ala Leu
 130 135 140
 Arg Tyr Cys Ser Ile Ile Thr Pro Glu Leu Cys Gln Gly Leu Ala Val
 145 150 155 160
 Leu Ala Xaa Ala Gly Ser Ser Leu Ile Ser Leu Val His Thr Val Ile
 165 170 175
 Met Ser Arg Leu Ala Phe Cys Ser Ser Ala Gln Ile Ser His Phe Tyr
 180 185 190
 Cys Asp Ala Tyr Leu Leu Met Lys Ile Ala Cys Ser His Thr Val Asn
 195 200 205
 Gln His Val Phe Leu Gly Ala Val Val Leu Phe Leu Ala Pro Cys Ala
 210 215 220
 Leu Ile Leu Val Ser Tyr Ile Arg Ile Ala Ala Ile Leu Arg Ile
 225 230 235 240
 Pro Ser Pro Thr Arg Arg Arg Lys Ala Cys Ser Ile Cys Ser Ser His
 245 250 255
 Leu Ser Leu Val Thr Leu Phe Tyr Gly Thr Val Leu Gly Ile Cys Ile
 260 265 270
 Xaa Pro Pro Asp Ser Phe Ser Ala Gln Asp Thr Ile Ala Thr Ile Met
 275 280 285
 Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe Ile Tyr Ser Leu Met
 290 295 300
 Asn Lys Glu Val Gln Glu Ala Val Arg Arg Leu Phe Ser Arg Gly Ser
 305 310 315 320
 His Ser Ser

<210> 2199

<211> 328

<212> PRT

<213> Homo sapien (7715624-11-1-3301)

<220>

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 2199

Leu Ser Ile Cys Phe Phe Leu Cys Ile Phe Ser Ala Asp Ile Xaa Ser
 1 5 10 15
 Met Leu Ala Met Glu Gln Asn Asn Gly Thr Glu Val Thr Glu Phe Ile
 20 25 30
 Leu Leu Gly Phe Ala Gly Gln His Lys Ser Trp His Ile Leu Ser Ile
 35 40 45
 Ala Phe Leu Ala Ile Tyr Val Val Thr Pro Val Gly Asn Ile Gly Met

```

      50              55              60
Ile Leu Leu Ile Lys Ile Asp Ala Ser Leu His Ile Pro Met Xaa Ile
65              70              75              80
Phe Leu Gln His Leu Ala Phe Val Asp Leu Cys Tyr Thr Ser Ala Ile
      85              90              95
Thr Pro Lys Met Leu Lys Asn Phe Val Glu Thr Lys Lys Ser Ile Ser
      100              105              110
Cys Ile Gly Cys Met Val Gln Leu Leu Val Tyr Gly Thr Phe Ala Thr
      115              120              125
Ser Asp Cys Tyr Ile Leu Ala Ala Met Ala Val Asp Arg Tyr Val Ala
      130              135              140
Phe Cys Asn Pro Leu His Tyr Pro Gly Val Met Ser Gln Arg Leu Cys
145              150              155              160
Ile Lys Leu Leu Val Ser Ser Tyr Val Met Gly Phe Leu Asn Ala Ser
      165              170              175
Ile Asn Ile Ser Phe Thr Phe Ser Leu Asn Phe Cys Lys Ser Lys Thr
      180              185              190
Ile Asn His Phe Phe Cys Asp Glu Pro Pro Ile Ile Ala Leu Pro Cys
      195              200              205
Ser Asn Ile Asp Leu Asn Ile Met Leu Leu Thr Val Phe Val Gly Leu
      210              215              220
Asn Leu Met Cys Thr Val Met Val Val Ile Ile Ser Cys Ile Tyr Val
225              230              235              240
Leu Val Ala Ile Leu Arg Ile Ser Ser Ala Ala Gly Lys Lys Lys Ser
      245              250              255
Leu Ser Thr Cys Ala Ser His Leu Thr Ala Val Thr Ile Phe Tyr Gly
      260              265              270
Val Leu Ser Tyr Met Tyr Leu Cys His Arg Ile Asn Glu Ser Gln Lys
      275              280              285
Gln Glu Lys Val Ala Ser Val Phe Tyr Gly Ile Ile Ile Pro Met Leu
      290              295              300
Asn Pro Leu Ile Tyr Ser Gln Arg Asn Gln Asp Val Ile Glu Ala Ile
305              310              315              320
Lys Leu Thr Glu Lys Lys Tyr Phe
      325

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<210> 2200

<211> 193

<212> PRT

<213> Homo sapien (7768677-1-106933-108798)

<220>

<221> VARIANT

<222> (1)...(193)

<223> Xaa = Any Amino Acid

<400> 2200

```

Phe Phe Asn Ile Thr Xaa Phe Val Pro Glu Val Met Lys Ser Leu Ser
1              5              10              15
Arg Ser Lys Asp Ile Ser Phe Asn Phe Cys Phe Xaa Phe Phe Phe
      20              25              30
Ser Cys Gly Cys Thr Gly Leu Thr Glu Asp Ile Phe Val Val Phe Lys
      35              40              45
Ser Phe Val Leu Phe Gly Val Leu Ser Xaa Ala His Leu Pro Val Lys
      50              55              60
Lys Lys Lys Lys Arg Phe Cys Ser Leu Leu Tyr Xaa Thr Thr Ile Leu
65              70              75              80
Ile Cys Lys Trp Pro Lys Thr Ser Pro Phe Phe Thr Glu Phe Leu Ser
      85              90              95
Leu Ser Arg Lys Asn Leu Lys Phe Gln Lys Asn Ile Glu Cys Glu Tyr
      100              105              110

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Met Ile Ser Val Xaa Ala Thr Cys Ile Gly Asn Lys Tyr Leu Asn Cys
 115 120 125
 Glu Ile Tyr Leu Arg Ser Leu Thr Phe Pro Asn Ile Ser Ser Ile Val
 130 135 140
 Phe Phe Leu Leu Gln Ser Lys Tyr Met Phe Thr Phe Xaa Lys Tyr Arg
 145 150 155 160
 Glu Ala Gln Asn Trp Gly Lys Lys Pro Xaa Xaa Ile Pro Pro Ser Arg
 165 170 175
 Lys Lys Ala Ile Asn Leu Xaa Arg Ile Ser Ser Xaa Ser Leu Phe Cys
 180 185 190
 Val

<210> 2201

<211> 291

<212> PRT

<213> Homo sapien (7770649-26-5915-7266)

<400> 2201

Met Val Gly Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly
 1 5 10 15
 Leu Thr Asn Ser Trp Glu Ile Arg Leu Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Met Phe Tyr Met Ala Ser Met Met Gly Asn Ser Leu Ile Leu Leu Thr
 35 40 45
 Val Thr Ser Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Gly Val Ser Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys His Glu Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu Gln Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Met Phe Phe
 130 135 140
 Leu Val Ala Ala Trp Val Thr Gly Leu Ile His Ser Val Val Gln Leu
 145 150 155 160
 Val Phe Val Val Asn Leu Pro Phe Cys Gly Pro Asn Val Ser Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Thr Asp Ser
 180 185 190
 Tyr Arg Leu Glu Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu
 195 200 205
 Gly Ser Phe Phe Ile Leu Ile Ile Ser Tyr Val Val Ile Ile Leu Thr
 210 215 220
 Val Leu Lys His Ser Ser Ala Gly Leu Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Ser Ala His Val Ser Val Val Val Leu Phe Phe Gly Pro Leu Ile Phe
 245 250 255
 Val Tyr Thr Trp Pro Ser Pro Ser Thr His Leu Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Val Leu Asn Pro Ile Ile Tyr Thr
 275 280 285
 Phe Arg Asn
 290

<210> 2202

<211> 92

<212> PRT

<213> Homo sapien (7939486-13-581-990)

<220>

<221> VARIANT

<222> (1)...(92)

<223> Xaa = Any Amino Acid

<400> 2202

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Cys His Pro Ser His Tyr Phe Ser Ile Leu Ile Arg Phe Leu Cys Leu
 1           5           10           15
Tyr Leu Ser Leu Glu Met Gln Ala Ala Cys Ser Ser Ser Xaa Leu Thr
      20           25           30
His Thr Ile His Phe Met Lys His Lys Pro Val Leu Thr Asn Ser Leu
      35           40           45
Ser Ser Leu Phe Asn Leu Ser Asn Cys Asp Lys Asn His Thr Ala Leu
      50           55           60
Tyr Pro Val Xaa Pro Pro Met Ile Phe Asp Gln Lys Pro Asn Leu Phe
65           70           75           80
Phe Val Val Phe Thr Tyr Gly Gln Leu Gly Ser Thr
      85           90

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<210> 2203

<211> 168

<212> PRT

<213> Homo sapien (7996320-1-1-801)

<400> 2203

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Lys Gln Ser Ser Gly Asp Ser Gly Asn Gln Thr Thr Trp Leu Ile Leu
 1           5           10           15
Val Gly Phe Gly Glu Leu Gln Tyr Leu Gly Phe Leu Pro Phe Thr Leu
      20           25           30
Phe Leu Ala Ile Tyr Val Val Thr Val Val Gly Asn Ala Leu Ile Met
      35           40           45
Leu Ala Val Ala Ser Ser Arg Thr Leu His Pro Pro Met Tyr Phe Phe
      50           55           60
Leu Cys His Phe Ser Leu Leu Glu Ile Gly Tyr Thr Ser Asn Val Ile
65           70           75           80
Leu Trp Leu Leu Gln Ser Phe Leu Glu Gly Lys Glu Val Ile Ser Leu
      85           90           95
Val Ser Cys Leu Ala Gln Phe Tyr Val Phe Ser Ser Leu Ala Ala Ala
      100           105           110
Glu Cys Leu Leu Leu Ser Ala Val Ser Tyr Asp Cys Tyr Leu Ala Ile
      115           120           125
Cys Cys Pro Leu His Tyr Pro Ala Leu Met Ser Thr Trp Phe Cys His
      130           135           140
Cys Leu Ala Ala Gly Ala Trp Phe Ser Gly Phe Phe Ser Ser Ala Phe
145           150           155           160
Thr Met Ala Leu Ala Ala Pro Leu
      165

```

<210> 2204

<211> 167

<212> PRT

<213> Homo sapien (7996320-11-500-1042)

<220>

<221> VARIANT

<222> (1)...(167)

<223> Xaa = Any Amino Acid

<400> 2204

Gly Leu Gly Gly Gly Gln Ser Cys Ala Asn Lys Lys Trp Gly Thr Gly
 1 5 10 15
 Leu Asn Leu Thr Pro Ser Phe His Gly Ser Arg Ser Asn Phe Cys Gly
 20 25 30
 Pro Xaa Ile Ser Ile His Ser Tyr Ser Leu Gln Ser Phe Leu Pro Val
 35 40 45
 Leu Ile Met Asn Leu Tyr Xaa Thr His Cys Ser Xaa Gln Ser Ser Pro
 50 55 60
 Ile Leu His Tyr Pro Val Gln Val Leu Gly Leu Gly Thr Leu Val Leu
 65 70 75 80
 Leu Leu Gly Ser Tyr Ser Cys Ile Ile Met Thr Ala Pro Gly Asp Gln
 85 90 95
 Leu Cys Xaa Gln Gly Arg Ser Lys Ile Leu Ser Thr Cys Ser Ser His
 100 105 110
 Tyr Leu Val Val Thr Ile Phe Tyr Thr Ser Gly Phe Leu Arg Tyr Val
 115 120 125
 Ile Leu Tyr Pro Xaa Ile Xaa Met Arg Asp Ile Pro Tyr Pro Lys Trp
 130 135 140
 Ser Pro Leu Ala Glu Glu Ser Ile Thr Lys Xaa Gln Asp Ile Gln Lys
 145 150 155 160
 Ala Xaa Ala Leu Val Leu Leu
 165

<210> 2205

<211> 294

<212> PRT

<213> Homo sapien (8052042-13-4893-7590)

<400> 2205

Ala Thr Tyr Asn Ser Ser Asn Thr Val Val Thr Glu Phe Val Phe Leu
 1 5 10 15
 Ser Phe Pro Glu Leu His His Leu Gln Gly Leu Leu Phe Val Ser Leu
 20 25 30
 Leu Ile Ile Tyr Val Val Thr Ile Leu Glu Asp Leu Ala Val Val Gly
 35 40 45
 Thr Ile Arg Ala Ser His His Leu His Ile Ser Thr His Leu Phe Leu
 50 55 60
 Ala Gln Leu Ser Val Leu Glu Thr Leu Tyr Thr Ser Val Thr Val Pro
 65 70 75 80
 Lys Leu Leu Ala Gly Leu Pro Ala Glu Arg Arg Pro Ser Ile Ser Phe
 85 90 95
 Ser Gly His Leu Thr Trp Leu Leu Leu Phe Leu Ser Leu Ser Ser
 100 105 110
 Glu Cys Val Leu Pro Ala Asn Met Asp Cys Asp Trp His Pro Val Ile
 115 120 125
 Cys His Leu Leu His Tyr Leu Ser Pro Ser Trp Thr Pro Cys Ser Trp
 130 135 140
 Leu Cys Leu His Leu Ala Ile Ser Ala Gln Leu Ser Ser Phe Pro Ala
 145 150 155 160
 Ser Phe Val Ser Thr Ala Leu Asn Ser Ser Leu Arg Leu Arg Ser Pro
 165 170 175
 Asp Val Leu Asn His Phe Cys Asp Ile Pro Pro Pro Leu Gly Leu Ser
 180 185 190
 Cys Ser Ser Thr Thr Thr Ile Glu Met Arg Thr Gln Ala Ala Gln Val
 195 200 205
 Ile Leu Ala Ala Ser Leu Gln Ala Thr Thr Val Ser Tyr Thr His Ile
 210 215 220
 Leu Ala Arg Ser Leu Arg Ile Pro Glu Arg Pro Ser Lys Leu Lys Ala
 225 230 235 240
 Phe Pro Thr Tyr Ala Ser His Leu Gly Cys Gly Ser Ser Asn Leu Ile
 245 250 255

Lys Leu Val Ser Gly Val Tyr Leu Val Gly Ile Pro Leu Leu Lys Pro
 260 265 270
 Ile Ile Tyr Cys Leu Arg Asn Cys Asn Ile Arg Glu Ala Leu Ala Lys
 275 280 285
 Leu Leu Gln Ala Leu Pro
 290

<210> 2206

<211> 175

<212> PRT

<213> Homo sapien (8052042-5-3342-10968)

<220>

<221> VARIANT

<222> (1)...(175)

<223> Xaa = Any Amino Acid

<400> 2206

Leu Leu Met Ala Ala Asp Asn His Thr Arg Val Glu Ala Phe Val Leu
 1 5 10 15
 Gln Gly Phe Ser Glu Asp Leu Pro Leu Gln Gly Cys Cys Phe Ala Phe
 20 25 30
 Phe Leu Leu Tyr Leu Met Ala Leu Val Gly Asn Ile Leu Met Val Met
 35 40 45
 Ala Ile Ser Leu Asn Pro Gly Leu His Thr Pro Val Tyr Phe Phe Leu
 50 55 60
 Thr Asn Leu Ala Leu Leu Asp Ile Val Cys Thr Ser Met Asp Asn Ser
 65 70 75 80
 Arg Val Val Ala Val Leu Tyr Thr Val Val Ser Pro Thr Leu Asn Pro
 85 90 95
 Ser Pro Thr Pro Cys Gly Thr Arg Thr Tyr Gln Xaa His Xaa Gly Glu
 100 105 110
 Cys Phe Leu Ala Ser Gly Lys Arg Lys Gly Ser Phe Xaa Cys Glu Met
 115 120 125
 Phe Gln Val Leu Thr Asn Xaa Phe Gln His Met Thr Leu Arg Ile Ser
 130 135 140
 Cys Lys Gln Gln Gly Thr Arg Lys Xaa Leu Met Pro His Ile Tyr Lys
 145 150 155 160
 Xaa Cys Ala Pro Ala Arg Gly Cys His His Ser Met Trp Asn Ser
 165 170 175

<210> 2207

<211> 275

<212> PRT

<213> Homo sapien (8072456-16-39461-40850)

<400> 2207

Met Val Gly Asn Leu Leu Ile Trp Val Thr Thr Ile Gly Ser Pro Ser
 1 5 10 15
 Leu Gly Ser Leu Met Tyr Phe Phe Leu Ala Tyr Leu Ser Leu Met Asp
 20 25 30
 Ala Ile Tyr Ser Thr Ala Met Ser Pro Lys Leu Met Ile Asp Leu Leu
 35 40 45
 Cys Asp Lys Ile Ala Ile Ser Leu Ser Ala Cys Met Gly Gln Leu Phe
 50 55 60
 Ile Glu His Leu Leu Gly Gly Ala Glu Val Phe Leu Leu Val Val Met
 65 70 75 80
 Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro Leu His Tyr Leu Asn
 85 90 95
 Ile Met Asn Arg Leu Val Cys Ile Leu Leu Val Val Ala Met Ile
 100 105 110

Gly Gly Phe Val His Ser Val Val Gln Ile Val Phe Leu Tyr Ser Leu
 115 120 125
 Pro Ile Cys Gly Pro Asn Val Ile Asp His Ser Val Cys Asp Met Tyr
 130 135 140
 Pro Leu Leu Glu Leu Leu Cys Leu Asp Thr Tyr Phe Ile Gly Leu Thr
 145 150 155 160
 Val Val Ala Asn Gly Gly Ile Ile Cys Met Val Ile Phe Thr Phe Leu
 165 170 175
 Leu Ile Ser Cys Gly Val Ile Leu Asn Phe Leu Lys Thr Tyr Ser Gln
 180 185 190
 Glu Glu Arg His Lys Ala Leu Pro Thr Cys Ile Ser His Ile Ile Val
 195 200 205
 Val Ala Leu Val Phe Val Pro Cys Ile Phe Met Tyr Val Arg Pro Val
 210 215 220
 Ser Asn Phe Pro Phe Asp Lys Leu Met Thr Val Phe Tyr Ser Ile Ile
 225 230 235 240
 Thr Leu Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Gln Ser Glu Met
 245 250 255
 Lys Asn Ala Met Lys Asn Leu Trp Cys Glu Lys Leu Ser Ile Val Arg
 260 265 270
 Lys Arg Val
 275

<210> 2208

<211> 316

<212> PRT

<213> Homo sapien (8077072-13-9613-11523)

<220>

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 2208

Met Val Ile Leu Ser Trp Glu Asn Gln Thr Met Arg Val Glu Phe Val
 1 5 10 15
 Leu Gln Gly Phe Ser Ser Ile Arg Gln Leu Asn Ile Phe Leu Phe Met
 20 25 30
 Ile Ile Leu Val Phe Tyr Ile Leu Thr Val Ser Gly Asn Ile Leu Ile
 35 40 45
 Val Leu Leu Val Leu Val Arg His His Leu His Thr Pro Met Tyr Phe
 50 55 60
 Leu Leu Val Asn Leu Ser Cys Leu Glu Ile Trp Tyr Thr Ser Asn Ile
 65 70 75 80
 Ile Pro Lys Met Leu Leu Ile Ile Ala Glu Xaa Lys Thr Ile Ser
 85 90 95
 Val Ala Gly Trp Leu Ala Gln Phe Tyr Phe Phe Gly Ser Leu Ala Ala
 100 105 110
 Thr Glu Cys Leu Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala
 115 120 125
 Ile Cys Gln Pro Leu Cys Tyr Arg Val Leu Met Thr Gly Pro Leu Cys
 130 135 140
 Ile Arg Leu Ala Ala Gly Ser Trp Phe Cys Cys Phe Leu Leu Thr Ala
 145 150 155 160
 Ile Thr Met Val Leu Leu Cys Arg Leu Thr Phe Cys Gly Pro Tyr Glu
 165 170 175
 Thr Asp His Phe Phe Cys Asp Phe Thr Pro Leu Val His Leu Ser Cys
 180 185 190
 Met Asp Thr Ser Val Thr Glu Thr Ile Ala Phe Ala Thr Ser Ser Ala
 195 200 205
 Val Thr Leu Ile Pro Phe Leu Leu Ile Val Ala Ser Tyr Ser Cys Val

210	215	220
Leu Ser Ala Ile Leu Arg Ile Pro Ser Cys Thr Gly Gln Lys Lys Ala		
225	230	235
Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Val Phe Tyr Gly		240
	245	250
Thr Leu Ile Ala Thr Tyr Leu Val Pro Ser Ala Asn Ser Ser Gln Leu		255
	260	265
Leu Cys Lys Gly Ser Ser Leu Leu Tyr Ile Ile Leu Thr Pro Met Phe		270
	275	280
Asn Pro Ile Ile Tyr Ser Leu Arg Asn Arg Asp Ile His Glu Ala Leu		285
	290	295
Lys Lys Cys Leu Arg Lys Lys Ser Gly Val Cys Leu		300
305	310	315

<210> 2209

<211> 309

<212> PRT

<213> Homo sapien (8081198-24-6628-8036)

<400> 2209

Met Glu Asn Gln Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr		
1	5	10
Glu Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met		15
	20	25
Tyr Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile		30
	35	40
Thr Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu		45
	50	55
Ser Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile		60
	65	70
Val Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu		75
	85	90
Thr Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu		95
	100	105
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu		110
	115	120
His Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly		125
	130	135
Gly Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe		140
	145	150
Met Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile		155
	165	170
Cys Asp Leu Phe Gln Leu Leu Thr Leu Ala Cys Thr Asp Thr His Ile		175
	180	185
Leu Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile		190
	195	200
Phe Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys		205
	210	215
Ser Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser		220
	225	230
His Leu Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr		235
	245	250
Met Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser		255
	260	265
Asp Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg		270
	275	280
Asn Ala Glu Val Lys Ser Ala Met Lys Lys Leu Trp Met Lys Trp Glu		285
	290	295
Ala Leu Ala Gly Lys		300
305		

<210> 2210
 <211> 270
 <212> PRT
 <213> Homo sapien (8086488-18-2452-4090)

<400> 2210
 Met Glu Val Ser Gly Asn His Thr Ser Val Ala Met Phe Val Leu Leu
 1 5 10 15
 Gly Leu Ser Asp Glu Lys Glu Leu Gln Leu Ile Leu Phe Pro Val Phe
 20 25 30
 Leu Val Ile Tyr Leu Val Thr Leu Ile Trp Asn Met Gly Leu Ile Ile
 35 40 45
 Leu Ile Arg Ile Asp Ser His Leu Asn Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Phe Leu Ser Phe Thr Asp Ile Cys Tyr Ser Ser Thr Ile Ser Pro
 65 70 75 80
 Arg Met Leu Ser Asp Phe Leu Lys Asp Lys Lys Thr Ile Ser Phe Leu
 85 90 95
 Ala Cys Ala Thr Gln Tyr Phe Leu Gly Ala Trp Met Ser Leu Ala Glu
 100 105 110
 Cys Cys Leu Val Ile Met Ala Cys Asp Arg Tyr Val Ala Ile Gly
 115 120 125
 Ser Pro Leu Gln Tyr Ser Ala Ile Met Val Pro Ser Ile Cys Trp Lys
 130 135 140
 Met Val Ala Gly Val Cys Gly Gly Gly Phe Leu Ser Ser Leu Val His
 145 150 155 160
 Thr Val Pro Cys Phe Asn Leu Tyr Tyr Cys Gly Pro Asn Ile Ile Gln
 165 170 175
 His Phe Phe Cys Asn Thr Leu Gln Ile Ile Ser Leu Ser Cys Ser Asn
 180 185 190
 Pro Phe Ile Ser Gln Met Ile Leu Phe Leu Glu Ala Ile Phe Val Gly
 195 200 205
 Leu Gly Ser Leu Leu Val Ile Leu Leu Ser Tyr Gly Phe Ile Val Ala
 210 215 220
 Ser Ile Leu Lys Ile Ser Ser Thr Lys Cys Cys Ala Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Ala Ser His Leu Ala Ala Val Ala Leu Phe Tyr Gly Thr Ala
 245 250 255
 Leu Ser Val Tyr Met His Pro Ser Ser Ser His Ser Met Lys
 260 265 270

<210> 2211
 <211> 161
 <212> PRT
 <213> Homo sapien (8096828-10-670-2127)

<220>
 <221> VARIANT
 <222> (1)...(161)
 <223> Xaa = Any Amino Acid

<400> 2211
 Gly Trp Lys Ser Ser Thr Phe Asn Ile Ser Cys Thr Lys Phe Phe Leu
 1 5 10 15
 Val Gly Phe Pro Gly Leu Arg Glu Trp Trp Pro Leu Leu Val Leu Pro
 20 25 30
 Leu Val Phe Leu Phe Val Thr Ile Ile Ser Ala Asn Ala Leu Val Ile
 35 40 45
 His Thr Val Val Ala Arg Gln Asn Leu His Gln Pro Thr Cys Met Leu
 50 55 60
 Ile Thr Val Leu Leu Ala Val Asn Ile Arg Ala Ala Thr Ala Val Met

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65          70          75          80
Pro Lys Met Leu Glu Gly Phe Val Tyr Tyr Ala Asn Pro Ile Ser Leu
          85          90          95
His Gly Arg Leu Ala Xaa Val Phe Phe Ile Tyr Phe Thr Leu Leu Leu
          100          105          110
Asp Tyr Asn Phe Leu Trp Pro Trp Pro Trp Thr Gly Tyr Phe Ala Ile
          115          120          125
Cys His Pro Leu Cys Phe Ser Asp Leu Met Thr Ser Gln Leu Leu Gly
          130          135          140
Leu Leu Ala Ile Leu Ala Phe Glu Gln Ser Pro Gly Ser Asp Pro Ala
145          150          155          160
Pro

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<210> 2212
 <211> 198
 <212> PRT
 <213> Homo sapien (8096828-22-1-1563)

<220>
 <221> VARIANT
 <222> (1)...(198)
 <223> Xaa = Any Amino Acid

```

<400> 2212
Val Ala Ile Cys His Pro Leu Cys Phe Gln Thr Glu Xaa Leu Pro Ser
1          5          10          15
Trp Leu Gly Leu Leu Ala Ile Leu Ala Leu Thr Gln Ser Trp Gly Val
          20          25          30
Thr Val Pro Leu Val Val Leu Thr Ala Lys Ala Asp Phe Cys Arg Thr
          35          40          45
Ala Val Ile Arg His Phe Thr Cys Glu Cys Ile Ala Leu Leu Ser Ile
          50          55          60
Ala Cys Gly Asp Leu Thr Phe Asn Asn Trp Leu Gly Leu Ala Met Cys
65          70          75          80
Leu Val Thr Val Ile Ser Asp Met Ala Leu Leu Gly Thr Ser Tyr Thr
          85          90          95
His Ile Ile Tyr Ala Ala Phe Arg Ile Ser Ser Trp Gly Ala Gln Ala
          100          105          110
Lys Ala Leu His Thr Cys Gly Ser His Leu Leu Val Ile Leu Ser Ile
          115          120          125
Tyr Val Ser Gly Leu Ser Thr Ser Ile Thr Phe Xaa Val Ala Lys Thr
          130          135          140
Val Ser Gln Asn Val Gln Asn Leu Leu Ser Ala Ile Tyr Leu Leu Leu
145          150          155          160
Pro Gly Ala Leu Asn Pro Val Ile Tyr Gly Val Arg Thr Arg Glu Ile
          165          170          175
Gln Gln His Val Glu Lys Met Leu Cys Glu Lys Glu Thr Ala Gln Lys
          180          185          190
Ala Gly Glu Lys Pro Lys
          195

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<210> 2213
 <211> 323
 <212> PRT
 <213> Homo sapien (8096945-19-338-2509)

<220>
 <221> VARIANT
 <222> (1)...(323)
 <223> Xaa = Any Amino Acid

<400> 2213

Gly Thr Leu Asn Leu Ser Ser Phe Asn Pro Gly Leu Phe Ile Leu Leu
 1 5 10 15
 Gly Ile Pro Gly Leu Glu Trp Phe Cys Ile Trp Met Gly Ile Leu Ser
 20 25 30
 Phe Thr Ser Tyr Leu Val Ser Leu Ala Gly Asn Val Ile Leu Leu Tyr
 35 40 45
 Leu Ile Thr Val Glu His Asn Leu His Lys Pro Met Phe Ser Phe Leu
 50 55 60
 Ser Ile Pro Ala Ser Ala Asn Leu Ile Leu Cys Ile Thr Tyr Phe Pro
 65 70 75 80
 Lys Thr Phe Gly Ile Phe Xaa Leu Lys Ala Gln Lys Ile Ile Phe Pro
 85 90 95
 Gly Cys Phe Thr Arg Phe Phe Phe Phe Gly Leu Leu His Phe Ser Phe
 100 105 110
 Phe Leu Asp Leu Ala Ile Leu Leu Gly Leu Ala Phe Asp His Tyr Met
 115 120 125
 Thr Ile Gly Phe Leu Leu Arg Tyr Thr Ser Gly Leu Thr Pro Arg Thr
 130 135 140
 Leu Gly Lys Ile Val Val Ser Ile Asp Xaa Arg Phe Asn Asn Ile Leu
 145 150 155 160
 Pro Ile Asp Phe Leu Gly Lys His Leu Pro Phe Cys Arg Thr His Ile
 165 170 175
 Asn Ser Asn Thr Tyr Cys Glu His Ile Gly Val Ala Leu Leu Ser Tyr
 180 185 190
 Ala Asp Ile Ser Ile Asn Ile Trp Tyr Asp Phe Thr Ile Leu Val Met
 195 200 205
 Thr Ile Ile Ser Asp Leu Ile Leu Thr Asp Ile Ser Tyr Thr Leu Thr
 210 215 220
 Leu His Ala Val Phe His Leu Pro Ser Ser Asp Ala Leu Leu Lys Ala
 225 230 235 240
 Leu Ser Thr Cys Gly Ser His Val Ser Val Ile Leu Met Leu Tyr Thr
 245 250 255
 Pro Thr Met Leu Ser Ala Leu Thr His His Phe Gly Gln Ser Ile Ser
 260 265 270
 Cys Thr Phe Tyr Ile Met Phe Val Gly Leu Tyr Arg Ala Ile Pro Pro
 275 280 285
 Val Leu Asn Ser Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gly Asn
 290 295 300
 Lys Val Ile Leu Leu Phe Phe Leu Lys Gly Met Gln Xaa Tyr Glu Asp
 305 310 315 320
 Glu Asn Met

<210> 2214

<211> 130

<212> PRT

<213> Homo sapien (8099799-17-8549-9091)

<220>

<221> VARIANT

<222> (1)...(130)

<223> Xaa = Any Amino Acid

<400> 2214

Phe Xaa Ser Ser Ser Gly Gln Thr Arg His Phe Lys Ala Tyr Glu Xaa
 1 5 10 15
 His Leu Val Thr Gln Cys Ser Met Leu Trp Val Xaa Asp Xaa Tyr Phe
 20 25 30
 Leu Cys Ala Leu Leu Gln Pro Leu His His Gly Ser Lys Ser Xaa Thr

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      35              40              45
Gln Gly Ser Ser Phe Trp Ala Lys Gly Phe Val Leu Glu Val Ile Leu
  50              55              60
Ser Phe Ser Xaa Xaa Val Ala His Ile Cys Ser Xaa Leu Val Leu Ser
65              70              75              80
Ala Phe Ser Cys Leu Xaa Asn Phe Met Ser Leu Thr Ala Phe Phe His
      85              90              95
Phe Val Leu Ser Leu Ser Leu Xaa His Lys Leu Val Val Phe Leu Lys
      100              105              110
Leu Tyr His Phe Xaa Lys Pro Gly Ser Pro Met Tyr Val Met Thr Ile
      115              120              125
His Ile
      130

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<210> 2215
 <211> 188
 <212> PRT
 <213> Homo sapien (8102357-9-3785-4449)

<220>
 <221> VARIANT
 <222> (1)...(188)
 <223> Xaa = Any Amino Acid

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<400> 2215
His Trp Lys Ile Leu Arg Arg Asn Ser Lys Met Ile His Glu Ile Ile
  1              5              10              15
Xaa Thr Leu Cys Gln Ile Leu Tyr Ser Glu Asp Lys Thr Cys Tyr Ile
      20              25              30
Gln Ile Gln Ser Leu Phe Cys Thr Asp Leu Glu Ile Pro Asn Phe Phe
      35              40              45
Cys Glu Leu Asn Xaa Val Val His Leu Ala Cys Ser Asp Thr Phe Leu
      50              55              60
Lys Asp Ile Val Arg Tyr Cys Thr Thr Met Leu Leu Ser Gly Gly Pro
65              70              75              80
Ile Ala Gly Ile Phe Tyr Ser Phe Ser Lys Ile Ile Ser Ser Ile Cys
      85              90              95
Ala Ile Pro Ser Ala Gln Gly Lys His Lys Ala Phe Pro Thr Cys Val
      100              105              110
Ser His Leu Ser Asn Met Ser Leu Phe Tyr Cys Arg Ser Thr Gly Leu
      115              120              125
Tyr Leu Ser Phe Ala Ala Thr His Asn Ser Cys Ser Asn Ala Thr Ala
      130              135              140
Ser Val Arg His Thr Val Val Lys Pro Leu Leu Asn Val Phe Ile Leu
145              150              155              160
Lys Ser Ser Asn Lys Asp Ile Lys Xaa Ala Leu Lys Val Phe Phe Arg
      165              170              175
Gly Lys Gln Trp Lys His His Phe Ser Lys Ser Ala
      180              185

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<210> 2216
 <211> 318
 <212> PRT
 <213> Homo sapien (8102369-26-1-1971)

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<400> 2216
Met Ala Gly Glu Asn His Thr Thr Leu Pro Glu Phe Leu Leu Leu Gly
  1              5              10              15
Phe Ser Asp Leu Lys Ala Leu Gln Gly Pro Leu Phe Trp Val Val Leu
      20              25              30
Leu Val Tyr Leu Val Thr Leu Leu Gly Asn Ser Leu Ile Ile Leu Leu

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      35              40              45
Thr Gln Val Ser Pro Ala Leu His Ser Pro Met Tyr Phe Phe Leu Arg
  50              55              60
Gln Leu Ser Val Val Glu Leu Phe Tyr Thr Thr Asp Ile Val Pro Arg
  65              70              75              80
Thr Leu Ala Asn Leu Gly Ser Pro His Pro Gln Ala Ile Ser Phe Gln
      85              90              95
Gly Cys Ala Ala Gln Met Tyr Val Phe Ile Val Leu Gly Ile Ser Glu
      100              105              110
Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      115              120              125
Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser Pro Arg Ala Cys Met Ala
      130              135              140
Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr Ala Thr Thr His
      145              150              155              160
Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg Ser His Pro Ile Ile Pro
      165              170              175
His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu Ala Ser Ala Gly
      180              185              190
Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr Ile Val Phe Ile
      195              200              205
Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile Arg Ile Leu Gly
      210              215              220
Ala Asn Leu Ala Met Gly Leu Thr Gln Ser Arg Arg Lys Val Phe Ser
      225              230              235              240
Thr Cys Ser Ser His Arg Leu Val Val Ser Leu Phe Phe Gly Thr Ala
      245              250              255
Ser Ile Thr Asn Asn Arg Pro Gln Ala Gly Ser Ser Glu Thr Thr Asp
      260              265              270
Arg Val Ile Ser Leu Phe Asn Thr Val Ile Thr Pro Met Leu Asn Pro
      275              280              285
Ile Ile Asn Thr His Gly Asn Lys Asp Val Arg Arg Ala Leu Arg Tyr
      290              295              300
Leu Val Lys Arg Arg Arg Pro Ser Pro Gly Arg Gly Ser Gly
      305              310              315

```

<210> 2217

<211> 109

<212> PRT

<213> Homo sapien (8102369-32-1554-1892)

<220>

<221> VARIANT

<222> (1)...(109)

<223> Xaa = Any Amino Acid

<400> 2217

```

Tyr Met Val Val Thr Leu Val Leu Val Ile Leu Ser Tyr Ala Phe Ile
  1              5              10              15
Ile Lys Thr Ile Leu Lys Leu Pro Ser Ala Gln Gln Arg Thr Lys Ala
      20              25              30
Phe Pro Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser Tyr Gly
      35              40              45
Ser Cys Met Phe Met Tyr Ile Asn Pro Ser Ala Lys Asp Arg Asp Thr
      50              55              60
Phe Asn Lys Gly Val Ala Leu Leu Ile Thr Ser Val Ala Pro Leu Leu
      65              70              75              80
Asn Pro Phe Ile Tyr Thr Leu Arg Asn Gln Gln Val Arg Gln Pro Phe
      85              90              95
Lys Asp Met Val Lys Lys Leu Leu Asn Leu Xaa Arg Ile
      100              105

```

<210> 2218
 <211> 131
 <212> PRT
 <213> Homo sapien (8102369-33-1-1370)

<400> 2218
 Met Lys Asn Lys Thr Val Leu Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Asp Val Pro Glu Leu Gln Val Ala Val Phe Thr Phe Leu Phe Leu Ala
 20 25 30
 Tyr Leu Leu Ser Ile Leu Gly Asn Leu Thr Ile Leu Ile Leu Thr Leu
 35 40 45
 Leu Asp Ser His Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg Asn Phe
 50 55 60
 Ser Phe Leu Glu Ile Ser Phe Thr Asn Ile Phe Ile Pro Arg Val Leu
 65 70 75 80
 Ile Ser Ile Thr Thr Gly Asn Lys Ser Ile Ser Phe Ala Gly Cys Phe
 85 90 95
 Thr Gln Tyr Phe Phe Ala Met Phe Leu Gly Ala Thr Glu Phe Tyr Leu
 100 105 110
 Leu Ala Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Lys Leu Met
 115 120 125
 Thr Met His
 130

<210> 2219
 <211> 313
 <212> PRT
 <213> Homo sapien (8102369-49-1-1012)

<220>
 <221> VARIANT
 <222> (1)...(313)
 <223> Xaa = Any Amino Acid

<400> 2219
 Met Pro Asn Lys Ile Val Val Thr Glu Phe Phe Leu Thr Arg Pro Asp
 1 5 10 15
 Gly Leu Gln Lys Ser Phe Gln Val Ala Val Phe Leu Leu Pro Asp Ala
 20 25 30
 Cys His Thr Leu Xaa Leu Ser Leu Gly Thr Xaa Ile Ile Ile Thr Met
 35 40 45
 Thr Leu Leu Asp Thr Arg Met Gln Thr Ser Met Tyr Leu Phe Leu Gln
 50 55 60
 Asn Leu Ser Cys Leu Glu Ile Trp Phe Gln Thr Val Ile Val Pro Lys
 65 70 75 80
 Met Leu Leu Asn Ile Ala Met Gly Thr Lys Thr Val Ser Phe Ala Gly
 85 90 95
 Cys Ile Thr Gln Asp Phe Phe His Ile Phe Leu Gly Ala Thr Glu Phe
 100 105 110
 Phe Leu Leu Thr Ala Met Ala Tyr Asp Gln Tyr Ile Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Pro Met Leu Ile Ser Ser Arg Val Cys Thr Gln Leu
 130 135 140
 Ile Leu Thr Cys Trp Leu Leu Gly Phe Ser Phe Ile Ile Met Pro Val
 145 150 155 160
 Ile Leu Thr Ser Gln Leu Pro Phe Cys Asp Thr His Ile Lys His Phe
 165 170 175
 Phe Cys Asp Tyr Thr Pro Leu Met Glu Val Val Cys Ser Gly Pro Lys
 180 185 190

Val Leu Glu Met Val Asp Phe Thr Leu Ala Leu Val Ala Leu Phe Gly
 195 200 205
 Thr Leu Val Leu Ile Thr Leu Ser Tyr Val Gln Ile Ile Gln Thr Ile
 210 215 220
 Val Arg Ile Pro Ala Val Gln Glu Arg Lys Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Val Ile Met Val Thr Met Cys Tyr Asp Ser Cys Phe Phe
 245 250 255
 Met Tyr Val Lys Pro Ser Pro Gly Lys Trp Val Asp Val Asn Lys Gly
 260 265 270
 Val Ser Leu Ile Asn Thr Ile Ile Ala Pro Leu Leu Asn Pro Phe Ile
 275 280 285
 Cys Thr Leu Arg Asn Gln Gln Val Lys Gln Val Met Lys Asp Leu Val
 290 295 300
 Arg Lys Met Thr Leu Ser Glu Asn Lys
 305 310

<210> 2220
 <211> 96
 <212> PRT
 <213> Homo sapien (8117362-7-1589-1951)

<220>
 <221> VARIANT
 <222> (1)...(96)
 <223> Xaa = Any Amino Acid

<400> 2220
 Pro Leu Xaa Leu Met Val Val Ile Phe Ser Gln Val Tyr Thr Leu Ala
 1 5 10 15
 Ala Ile Pro Lys Met Ser Ser Thr Ala Gly Arg Thr Gln Gly Phe Phe
 20 25 30
 Met Xaa Ala Ser His Leu Thr Ala Val Val Ile Phe Tyr Gly Thr Pro
 35 40 45
 Ser Tyr Met Tyr Leu His His Gly Asn Asn Gly Ser Pro Lys Gln Gly
 50 55 60
 Lys Val Ser Ser Val Phe Tyr Gly Ile Val Ile Asp Leu Ser Leu Arg
 65 70 75 80
 Val Gln Asp Ala Arg Glu Ala Leu Lys Glu Lys Gly Lys Lys Gln Phe
 85 90 95

<210> 2221
 <211> 195
 <212> PRT
 <213> Homo sapien (8117365-9-1-1453)

<220>
 <221> VARIANT
 <222> (1)...(195)
 <223> Xaa = Any Amino Acid

<400> 2221
 Arg Met Phe Xaa Thr Xaa Phe Phe Ser Ser Leu Thr Leu Arg Leu Gln
 1 5 10 15
 Leu Ser His Leu Phe Pro Cys Leu Gly Tyr Val Phe Ser Leu Leu Gly
 20 25 30
 Xaa His Asp Lys Arg Tyr Met Ile Gln Leu Asn Pro Ser Leu Ala Val
 35 40 45
 Leu Lys Cys Val Ile Phe Trp Cys Val Cys Val Leu Val Cys Met Ser
 50 55 60
 Tyr Glu Glu Gly Glu Arg Leu Ser Thr Ser Phe Leu Ala Pro Cys Val

```

65          70          75          80
Ser Xaa Leu Trp Val Phe Ile Thr Cys Arg Val Gly Glu Val Phe Gly
      85          90          95
Phe Xaa Gly Phe Xaa Ala Ser Gln Xaa Ser His Lys Ile Asn Tyr Cys
      100         105         110
Val Asn Ile Val Leu Leu Gly Gly Cys Ile Leu Gln His Thr Xaa Asp
      115         120         125
Thr Ser Gln Leu Lys Glu Met Ser Ser Glu Met Leu Ala Arg Arg Lys
      130         135         140
Arg Arg Ile Thr Leu Arg Ser Leu Met Gly His Pro Ser Ile Phe Leu
145         150         155         160
Leu Arg Arg Ser Lys Ala Gly Ser Ile Ser Xaa Thr Asp Lys Ser Arg
      165         170         175
Leu Ser His Arg His Ser Arg Val Arg Leu Tyr Ile Ile Thr Gly Thr
      180         185         190
Asn Met Val
      195

```

<210> 2222

<211> 318

<212> PRT

<213> Homo sapien (8117535-2-10765-15227)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2222

```

Cys Val Asp Ser Ser Leu Lys Xaa Glu Ile Thr Gln Xaa Cys Leu Ser
1          5          10          15
Leu Leu Leu Xaa Met Ala Glu Gly Trp Arg Leu Tyr Phe Ile Ile Leu
      20         25         30
Ile Ile Ser Tyr Lys Phe Cys Thr Leu Leu Gly Asn Val Ile Phe Arg
      35         40         45
Thr Leu Val Cys Ser Leu Gly Phe His Thr Ser Cys Met Tyr Phe Phe
      50         55         60
Pro Xaa Lys Ile Ser Leu Xaa Leu Ala Xaa Val Cys His Ser Ile Ile
65         70         75         80
Ala Leu Pro Ser Thr Gln Lys Xaa Ala Ile Asn Val Gln Gly Ala Ala
      85         90         95
Val His Val Phe Ser Phe Pro Cys Leu Tyr Cys Pro Glu Ile Phe Leu
      100        105        110
His Ser Leu Thr Gln Cys His Pro Phe Ile Ala Ile Gly Tyr Pro Leu
      115        120        125
Gln Gly Met His Thr Ile Thr His Lys Leu Tyr Ile Leu Leu Thr Thr
      130        135        140
Gly Pro Trp Arg Gly Cys Xaa Leu His Val Asn Leu Leu Thr Ala Leu
145        150        155        160
Leu Gly Ser Tyr Pro Asn Pro Val Pro Thr Lys Leu Trp Leu Ser Phe
      165        170        175
Pro Ser Ile Pro Glu Val Lys Leu Xaa Pro Met Gln Ala Tyr Thr Lys
      180        185        190
Pro Tyr Ala Gly Leu Ser Leu Cys Leu Ser Leu Ser Leu Ser Leu Ser
      195        200        205
Phe Ser Leu Phe Ser Ile Ile Ser Ile Ser Tyr Ile Cys Asn Glu Ile
      210        215        220
Asp Ile Pro Lys Ile Ile Ser Ala Asp Ser Val His Gly Ala Phe Ser
225        230        235        240
Thr Cys Leu Ala His Leu Phe Ala Phe Ser Thr Cys Ile Ala Gln Pro
      245        250        255

```

Ala Val Cys Asn Ser Leu Trp Pro Trp Thr Glu Ala Gln Thr Glu Ser
 260 265 270
 Ser Arg Asp Ser Val Ile Gln Arg Pro Asn Leu Cys Val Thr Ile Ser
 275 280 285
 Leu Asn Ser Leu Ile Ser Ser Leu Arg Asn Glu Ser Val Lys Gln Ala
 290 295 300
 Ser His Lys Ile Phe Lys Glu Gln Thr Leu Phe Met Lys Ile
 305 310 315

<210> 2223

<211> 304

<212> PRT

<213> Homo sapien (8117535-5-1968-4011)

<220>

<221> VARIANT

<222> (1)...(304)

<223> Xaa = Any Amino Acid

<400> 2223

Met Arg Asn His Thr Leu Leu Asn Glu Phe Ile Leu Arg Gly Ile Pro
 1 5 10 15
 Gln Thr Glu Gly Leu Glu Ala Val Leu Cys Ala Val Phe Ser Phe Ile
 20 25 30
 Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Ile Ala Ile Phe
 35 40 45
 Leu His Thr Pro Met Tyr Phe Phe Leu Gly Arg Leu Ser Thr Phe Asp
 50 55 60
 Ile Leu Phe Pro Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu Ser
 65 70 75 80
 Gly Gln Ser Pro Val Ile Ser Phe Lys Gly Cys Ala Ser Gln Leu Phe
 85 90 95
 Phe Tyr Gln Leu Leu Gly Ser Ala Glu Gly Cys Leu Tyr Ser Val Met
 100 105 110
 Ser Tyr Asp Arg Phe Val Ala Ile His His Thr Leu Arg Tyr Met Leu
 115 120 125
 Ile Met Lys Pro Gly Val Cys Val Gly Leu Val Val Val Pro Trp Leu
 130 135 140
 Val Gly Cys Leu His Ala Thr Ile Leu Thr Ser Phe Thr Phe Gln Leu
 145 150 155 160
 Ser Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile Pro
 165 170 175
 Ala Val Leu Pro Leu Ala Cys Thr Asp Ser Ala Leu Ala Gln Arg Val
 180 185 190
 Gly Ser Ile Asn Val Gly Phe Leu Ala Leu Thr Leu Leu Ile Ser Val
 195 200 205
 Cys Val Cys Tyr Thr Ser Ile Gly Ile Ala Ile Leu Arg Ile Arg Ser
 210 215 220
 Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala His Leu Val
 225 230 235 240
 Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Ile Ile Tyr Leu Lys Ser
 245 250 255
 Thr Pro Asn Pro Leu Leu Gly Gly Gln Val Gln Ile Leu Asn Asn Val
 260 265 270
 Val Ser Pro Met Leu Asn Ser Leu Ile Tyr Ser Leu Arg Asn Lys Glu
 275 280 285
 Val Lys Arg Ser Leu Lys Arg Val Phe Xaa Asn Val Leu Leu Thr Val
 290 295 300

<210> 2224

<211> 268

<212> PRT

<213> Homo sapien (8117653-5-5695-6912)

<400> 2224

```

Met Met Ala Leu Ile Phe Thr Asp Ser His Leu Gln Ser Pro Met Tyr
1      5      10      15
Phe Phe Leu Asn Val Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Val
20      25      30
Val Thr Pro Lys Leu Leu Val Asn Phe Leu Val Ser Asp Lys Ser Ile
35      40      45
Ser Phe Glu Gly Cys Val Val Gln Leu Ala Phe Phe Val Val His Val
50      55      60
Thr Ala Glu Ser Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Phe Leu
65      70      75      80
Ala Ile Cys Gln Pro Leu His Tyr Gly Ser Ile Met Thr Arg Gly Thr
85      90      95
Cys Leu Gln Leu Val Ala Val Ser Tyr Ala Phe Gly Gly Ala Asn Ser
100     105     110
Ala Ile Gln Thr Gly Asn Val Phe Ala Leu Pro Phe Cys Gly Pro Asn
115     120     125
Gln Leu Thr His Tyr Tyr Cys Asp Ile Pro Pro Leu Leu His Leu Ala
130     135     140
Cys Ala Asn Thr Ala Thr Ala Arg Val Val Leu Tyr Val Phe Ser Ala
145     150     155     160
Leu Val Thr Leu Leu Pro Ala Ala Val Ile Leu Thr Ser Tyr Cys Leu
165     170     175
Val Leu Val Ala Ile Gly Arg Met Arg Ser Val Ala Gly Arg Glu Lys
180     185     190
Asp Leu Ser Thr Cys Ala Ser His Phe Leu Ala Ile Ala Ile Phe Tyr
195     200     205
Gly Thr Val Val Phe Thr Tyr Val Gln Pro His Gly Ser Thr Asn Asn
210     215     220
Thr Asn Gly Gln Val Val Ser Val Phe Tyr Thr Ile Ile Ile Pro Met
225     230     235     240
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala
245     250     255
Leu Gln Arg Lys Leu Gln Val Asn Ile Phe Pro Gly
260     265

```

<210> 2225

<211> 184

<212> PRT

<213> Homo sapien (8117705-18-1061-1646)

<220>

<221> VARIANT

<222> (1)...(184)

<223> Xaa = Any Amino Acid

<400> 2225

```

Leu Val Lys Val Lys Lys Asn Xaa Asn Ile Phe Leu Ser Thr Ala Tyr
1      5      10      15
His Phe Phe Pro Thr Leu Ser Val Asn Asn Asn Lys Phe Leu Xaa Ile
20      25      30
Ile Asn Asn Asn Phe Xaa Val Xaa Phe Asn Leu His Ser Glu Thr Ser
35      40      45
His Ser Xaa Val Tyr Ser Leu Val Leu Ser Ser Lys Val Cys Ile Leu
50      55      60
Leu Ala Ala Gly Val Val Gly Gly Ile Leu Ser Arg Arg Ile Val Cys
65      70      75      80
Gly Pro Thr Val Ser Leu Ser Ser Ser Arg Ser Asn Ala Ile Asn His

```

```

      85              90              95
Phe Phe Cys Asn Lys Ser Leu Gly Leu Gly Leu Ser Cys Tyr Asn Ile
      100              105              110
Tyr Ile Ser Thr Ala Val Pro Ala Phe Val Gly Val Xaa Val Leu His
      115              120              125
Ser Leu Pro Tyr Leu Val Ile Met Phe Ser Trp Thr Tyr Ile Leu Val
      130              135              140
Ala Ile Lys Arg Met Ser Ser Val Gly Arg Lys Glu Leu Ser Ile Cys
145              150              155              160
Val Ser His Leu Lys Thr Ser Thr Ile Phe His Thr Ala Leu Phe Tyr
      165              170              175
Val Tyr Leu Gln Pro Asp Phe Phe
      180

```

<210> 2226

<211> 148

<212> PRT

<213> Homo sapien (8117705-9-1-790)

<220>

<221> VARIANT

<222> (1)...(148)

<223> Xaa = Any Amino Acid

<400> 2226

```

Thr Tyr Asp Val Pro Arg Ser Gly Leu Cys Ile Val Ser Tyr Asn Thr
1      5      10      15
Cys Lys Ser Thr Met Met Ser Ile Lys Ile Gln Leu Lys Tyr Met Xaa
      20      25      30
Xaa Lys Xaa Leu Leu Ile Tyr Ala Gly Val Tyr Leu Asn Val Thr Met
      35      40      45
Leu Ile Val Thr Phe Lys Tyr Thr His Ile Phe His His Pro Glu Leu
      50      55      60
Ala Leu Cys Tyr Val Ser Phe Ser Ala Val Val Phe His Leu Thr Ala
65      70      75      80
Val Thr Ile Phe Phe Gly Ala Leu Ser Tyr Met Asp Leu Gln Pro Glu
      85      90      95
Ser Thr Val Phe Gln Glu Gln Glu Asn Pro Ala Ser Ile Phe Cys Gly
      100      105      110
Ile Met Thr Leu Val Leu Asn Phe Leu Ile Tyr Cys Leu Xaa Asn Xaa
      115      120      125
Glu Val Lys Glu Ala Leu Gln Leu Thr Arg Lys Lys Tyr Xaa Tyr Met
      130      135      140
Xaa Thr Glu Gly
145

```

<210> 2227

<211> 115

<212> PRT

<213> Homo sapien (8118143-13-1464-2322)

<400> 2227

```

Met Phe Val Val Ala Gly Phe Asn Phe Thr Tyr Pro Leu Leu Ile Ile
1      5      10      15
Leu Ile Ser Tyr Leu Tyr Ile Phe Pro Ala Thr Leu Arg Ile Cys Ser
      20      25      30
Thr Glu Gly Arg His Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr
      35      40      45
Ala Val Thr Ile Phe Tyr Ser Ala Leu Phe Phe Met Tyr Leu Arg Arg
      50      55      60
Pro Ser Glu Glu Ser Met Glu Gln Gly Lys Met Val Ala Val Phe Tyr

```

```

65          70          75          80
Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn
          85          90          95
Lys Asp Val Lys Glu Ala Leu Cys Lys Glu Leu Phe Lys Arg Lys Leu
          100          105          110
Phe Ser Lys
          115

```

<210> 2228
 <211> 157
 <212> PRT
 <213> Homo sapien (8118143-4-5591-10363)

<220>
 <221> VARIANT
 <222> (1)...(157)
 <223> Xaa = Any Amino Acid

```

<400> 2228
Ile Cys His Asn Arg Lys Val Ile Pro Ala Ser Met Xaa Asn Met Cys
1          5          10          15
Xaa Phe Leu Leu Lys Val Ala Xaa Asp Asn Phe Leu His Val Leu Phe
          20          25          30
Ile Leu Ala Lys Thr Ala Pro Pro Leu Leu Phe Leu Xaa Glu Ile Pro
          35          40          45
Ser Tyr Phe Ser Ser Pro Ser Xaa Ile Ile Val Leu Xaa Cys Leu Pro
          50          55          60
Xaa Phe Leu Lys Gln Leu Val Ile Leu Phe Val Phe Leu Leu Leu Asn
65          70          75          80
Xaa Ser Tyr Leu Thr Leu Ile Phe Met Leu Leu Thr Met Lys Ile Thr
          85          90          95
Ser Ser Phe Lys Ala Ser Thr Val Ile Ser Cys Leu Gln Phe Pro Ser
          100          105          110
Lys Ala Thr Cys Met His Gly Val Phe Ser Ala Val Cys Ala Gln Met
          115          120          125
Xaa Pro Tyr Tyr Asn Gly Xaa Ile Ile Xaa His Pro Glu Ser Ile Thr
          130          135          140
Glu Ser Lys Xaa Leu Thr Cys Val Asn Pro Xaa Phe Asn
145          150          155

```

<210> 2229
 <211> 320
 <212> PRT
 <213> Homo sapien (8118143-4-617-5265)

<220>
 <221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

```

<400> 2229
Met Leu Val Pro Lys Lys Met Val Arg Gly Asn Ser Thr Leu Val Thr
1          5          10          15
Glu Phe Ile Leu Leu Gly Leu Lys Asp Leu Pro Glu Leu Gln Pro Ile
          20          25          30
Leu Phe Val Leu Phe Leu Leu Ile Tyr Leu Ile Thr Val Gly Gly Asn
          35          40          45
Leu Gly Met Leu Val Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro
          50          55          60
Met Tyr Phe Phe Leu Ala Ser Leu Ser Cys Leu Asp Leu Tyr Tyr Ser
65          70          75          80

```


Thr Asn Val Thr Pro Lys Met Leu Val Asn Phe Phe Ser Asp Lys Lys
 85 90 95
 Ala Ile Ser Tyr Ala Ala Cys Leu Val Gln Cys Tyr Phe Phe Ile Ala
 100 105 110
 Val Val Ile Thr Glu Tyr Tyr Met Leu Ala Val Met Ala Tyr Asp Arg
 115 120 125
 Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Ser Ser Lys Met Ser Lys
 130 135 140
 Gly Leu Cys Ile Arg Leu Ile Ala Gly Pro Tyr Val Tyr Gly Phe Leu
 145 150 155 160
 Ser Gly Leu Met Glu Thr Met Trp Thr Tyr His Leu Thr Phe Cys Gly
 165 170 175
 Ser Asn Ile Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Ile Arg
 180 185 190
 Leu Ser Cys Ser Asp Thr Phe Ile Lys Glu Thr Ser Met Phe Val Val
 195 200 205
 Ala Xaa Phe Asn Leu Ser Ser Ser Leu Ile Ile Ile Leu Ile Ser Tyr
 210 215 220
 Ile Phe Ile Leu Ile Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg
 225 230 235 240
 Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Ala Val Thr Val
 245 250 255
 Phe Tyr Gly Thr Leu Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg
 260 265 270
 Ser Val Glu Gln Ser Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser
 275 280 285
 Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300
 Gln Ala Phe Trp Lys Leu Ile Arg Arg Asn Val Leu Leu Lys Xaa Asn
 305 310 315 320

<210> 2230

<211> 312

<212> PRT

<213> Homo sapien (8118750-5-4885-6910)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 2230

Met Xaa Asn Ser Arg Glu Ala Ser Gln Phe Ile Phe Leu Gly Leu Ser
 1 5 10 15
 Asn Val Pro Glu Leu Gln Val Pro Phe Phe Ile Met Phe Val Leu Ile
 20 25 30
 Tyr Leu Ile Asn Val Val Gly Asn Leu Gly Met Ile Ile Leu Ile Leu
 35 40 45
 Trp Tyr Ser Gln Leu His Asn Pro Met Tyr Phe Phe Phe Ser Asn Leu
 50 55 60
 Ser Leu Val Asp Phe Phe Tyr Ser Ser Val Val Thr Pro Lys Val Met
 65 70 75 80
 Thr Gly Leu Leu Arg Glu Asp Lys Ile Ile Ser Tyr Thr Val Trp Ala
 85 90 95
 Thr Gln Thr Phe Phe Ser Asp Ser Phe Ala Ser Val Val Asn Leu Leu
 100 105 110
 Leu Ala Leu Met Ala Ser Gly His Tyr Ala Ala Val Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Thr Thr Met Met Thr Ser Val Cys Thr Cys Leu Ala Ile
 130 135 140
 Gly Xaa Tyr Val Gly Gly Phe Leu Asn Ala Ser Ile His Thr Gly Glu

145 150 155 160
 Thr Phe Ser Leu Phe Cys Met Ser Ser Glu Val His His Phe Phe Cys
 165 170 175
 Glu Val Pro Ala Val Met Ala Leu Ser Cys Ser Asp Arg His Val Asn
 180 185 190
 Val Val Val Leu Val Tyr Val Thr Ser Phe Asn Ile Leu Phe Ala Leu
 195 200 205
 Leu Val Ile Leu Ile Ser Tyr Leu Leu Met Phe Ile Thr Ile Leu Lys
 210 215 220
 Met His Ser Thr Ala Gly Tyr Gln Lys Ala Leu Ala Ile Cys Ala Ser
 225 230 235 240
 His Leu Thr Ala Val Ala Ile Phe Tyr Gly Thr Ile Ile Phe Met His
 245 250 255
 Ile Gln Pro Ser Ser Ser His Ser Ile Asp Thr Asp Lys Ile Ala Ala
 260 265 270
 Val Phe Tyr Thr Ile Val Phe Pro Met Val Asn His Val Val Xaa Arg
 275 280 285
 Leu Lys Asn Lys Val Lys Ser Thr Phe Lys Lys Ile Val Glu Lys Val
 290 295 300
 Lys Leu Ser Leu Gly Leu Xaa Val
 305 310

<210> 2231

<211> 267

<212> PRT

<213> Homo sapien (8118750-8-1-2827)

<400> 2231

Ile Ile Leu Cys Phe Phe Ile Ile Gly Asn Ser Gln Asp Asn Ser Gln
 1 5 10 15
 Met Thr Leu Met Asp Asn Ile Ser Glu Val Thr Glu Phe Val Leu Val
 20 25 30
 Gly Leu Thr Asp Val Leu Glu Leu Gln Val Pro Leu Phe Ile Ile Phe
 35 40 45
 Thr Val Ile Tyr Leu Thr Thr Leu Val Gly Asn Phe Gly Met Ile Met
 50 55 60
 Leu Ile Leu Leu Asp Ser Arg Leu His Ile Pro Met Tyr Phe Phe Leu
 65 70 75 80
 Gly Lys Leu Ser Leu Val Asp Ser Val Cys Ala Cys Leu Val Thr Gly
 85 90 95
 Ser Tyr Ile Cys Gly Leu Phe Gln Ser Ser Ile His Val Ala Phe Thr
 100 105 110
 Phe His Leu Ser Phe Cys His Ser Asn Val Val Asn His Phe Phe Cys
 115 120 125
 Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Ile Tyr Ala His
 130 135 140
 Glu Ile Val Leu Phe Ile Leu Ala Ala Phe Asn Ile Phe Phe Thr Leu
 145 150 155 160
 Leu Ile Ile Leu Asn Ser Tyr Val Phe Ile Phe Ile Ala Ile Leu Arg
 165 170 175
 Met His Ser Ala Glu Gly Gln Lys Lys Val Phe Ser Thr Cys Ala Tyr
 180 185 190
 His Leu Thr Thr Val Ser Ile Phe Tyr Gly Thr Ile Thr Phe Met Tyr
 195 200 205
 Leu Gln Pro Ser Ser Gly His Ser Met Asp Thr Asp Lys Ile Ser Ser
 210 215 220
 Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Val Tyr Ser
 225 230 235 240
 Leu Arg Asn Lys Glu Val Gln Ser Ala Phe Lys Val Val Ile Gly Lys
 245 250 255
 Ala Lys Ser Ser Leu Gly Leu Ala Tyr Tyr Leu

260

265

<210> 2232
 <211> 309
 <212> PRT
 <213> Homo sapien (8118822-9-5564-7217)

<220>
 <221> VARIANT
 <222> (1)...(309)
 <223> Xaa = Any Amino Acid

<400> 2232
 Glu Xaa Met Gly Thr Ser Asn Asn Val Thr Glu Phe Val Leu Pro Gly
 1 5 10 15
 Leu Ser Gln Asp Pro Asp Val Gln Lys Ala Leu Phe Val Met Phe Leu
 20 25 30
 Leu Thr Tyr Asn Val Thr Met Val Gly Asn Leu Leu Ile Val Val Thr
 35 40 45
 Ile Ile Ala Ile Ala Ser Leu Asp Ser Pro Val Ser Phe Phe Leu Ala
 50 55 60
 Cys Leu Ser Phe Ile Asp Ala Val Tyr Ser Thr Ser Phe Ser Pro Lys
 65 70 75 80
 Leu Met Ile Asp Leu Leu Cys Asp Lys Lys Thr Val Ser Phe Leu Ala
 85 90 95
 Cys Met Gly Gln Leu Phe Ile Asn Tyr Pro Phe Gly Gly Ile Glu Val
 100 105 110
 Phe Leu Leu Val Gly Met Ala Cys Asp His Tyr Val Asp Ile Cys Lys
 115 120 125
 Leu Leu His Tyr Leu Thr Ile Met Asn Trp Gln Val Cys Ile Leu Leu
 130 135 140
 Phe Met Val Ala Val Thr Gly Gly Phe Leu His Ser Met Phe Gln Ile
 145 150 155 160
 Val Val Val Tyr Ser Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His
 165 170 175
 Phe Cys Asp Met Tyr Pro Leu Leu Glu Met Val Cys Thr Asp Thr Tyr
 180 185 190
 Phe Ile Gly Leu Thr Val Ile Ala Asn Gly Gly Ala Val Cys Met Val
 195 200 205
 Ile Phe Ile Leu Leu Leu Ile Ser Tyr Gly Val Ile Leu Asn Ser Leu
 210 215 220
 Lys Thr Tyr Ser Gln Glu Gly Gly His Lys Ala Leu Ser Thr Cys Ser
 225 230 235 240
 Ser Asn Ile Thr Val Val Ser Leu Phe Phe Asp Pro Cys Ile Phe Ile
 245 250 255
 Tyr Val Arg Pro Asp Ser Asn Phe Pro Ile Asp Lys Phe Met Thr Val
 260 265 270
 Phe Tyr Thr Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu
 275 280 285
 Arg Asn Leu Glu Val Arg Ile Ala Val Lys Asn Leu Trp Cys Lys Asn
 290 295 300
 Xaa Thr Ile Val Arg
 305

<210> 2233
 <211> 257
 <212> PRT
 <213> Homo sapien (8118832-14-2647-3682)

<220>
 <221> VARIANT

<222> (1)...(257)

<223> Xaa = Any Amino Acid

<400> 2233

```

Ser Met Tyr Phe Phe Leu Thr Asn Phe Ala Gly Leu Glu Ile Phe Tyr
 1           5           10           15
Phe Phe Thr Ile Ala Pro Leu Thr Leu Ala Asn Val Leu Pro Met Gly
          20           25           30
Arg Asn Leu Ile Ser Leu Pro Gly Cys Gly Gly Gln Met Phe Phe Phe
      35           40           45
Ile Phe Leu Gly Arg Ala Asp Cys Ile Leu Leu Ala Val Met Ala Phe
      50           55           60
Asp Trp Phe Val Ala Ile Cys Cys Pro Leu Cys Tyr Gly Leu Ile Met
65           70           75           80
Ser Trp Arg Leu Cys Val Gln Leu Thr Leu Gly Ser Leu Leu Leu Gly
      85           90           95
Phe Phe Leu Ala Met Gln Leu Thr Val Leu Ile Phe Gln Leu Pro Leu
      100          105          110
Cys Ser Ser Lys Glu Ile Ser Thr Phe Tyr Cys Asp Val Leu Pro Val
      115          120          125
Met Arg Leu Ala Cys Ala Asp Thr Trp Val His Glu Ala Thr Met Ser
      130          135          140
Met Val Ser Thr Thr Phe Leu Thr Val Pro Phe Leu Leu Ile Thr Leu
      145          150          155          160
Ser Tyr Val Ser Ile Met Ala Ala Ile Leu Lys Ile Cys Ser Ala Glu
      165          170          175
Gly Arg His Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val
      180          185          190
Leu Leu Gln Asp Xaa Cys Thr Arg Leu Ala Phe Leu Cys Pro Ser Ser
      195          200          205
Ser Tyr Tyr Pro Glu Arg Gly Gln Ala Val Ser Val Val Tyr Thr Phe
      210          215          220
Ile Thr Pro Val Leu Asn Pro Leu Ile Tyr Ser Met Arg Asn Thr Glu
      225          230          235          240
Leu Lys Asp Ala Leu Lys Arg Ala Met Thr Arg Val Pro Leu Leu Xaa
      245          250          255

```

Thr

<210> 2234

<211> 327

<212> PRT

<213> Homo sapien (8118892-3-16899-18792)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 2234

```

Met Glu Gln Arg Lys Asn Val Thr Glu Phe Val Leu Val Gly Leu Thr
 1           5           10           15
Gln Ser Pro Gln Gly Gln Lys Ile Leu Phe Leu Val Phe Leu Leu Ile
          20           25           30
Tyr Val Val Thr Met Val Gly Asn Ile Phe Ile Val Val Thr Val Val
      35           40           45
Val Ser Pro Thr Leu Gly Cys Pro Met Tyr Phe Phe Leu Gly Tyr Leu
      50           55           60
Ser Phe Met Asp Ala Val His Ser Thr Thr Val Thr Pro Asn Met Ile
      65           70           75           80
Ile Asp Leu Leu Tyr Glu Lys Lys Thr Ile Ser Phe Gln Ala Cys Ile

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      85      90      95
Thr Gln Ile Phe Ile Gly His Leu Phe Gly Gly Ala Glu Ile Leu Leu
      100      105      110
Leu Val Val Met Ala Tyr Asp Gly Tyr Val Thr Ile Cys Lys Pro Leu
      115      120      125
His Tyr Leu Thr Ile Met Asn Gln Arg Val Cys Ile Leu Leu Leu Leu
      130      135      140
Leu Ala Trp Ala Gly Gly Phe Leu His Ala Val Val Gln Leu Leu Phe
145      150      155      160
Val Tyr Asn Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile
      165      170      175
Cys Asp Met Tyr Pro Leu Leu Lys Leu Ala Cys Thr Asp Thr Tyr Val
      180      185      190
Thr Gly Leu Thr Val Val Ala Asn Asp Gly Ala Ile Cys Val Val Ile
      195      200      205
Phe Met Leu Leu Leu Phe Ser Tyr Gly Val Ile Leu His Ser Leu Lys
      210      215      220
Asn Leu Ser Gln Glu Gly Arg His Lys Ala Leu Ser Thr Cys Gly Ser
225      230      235      240
His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
      245      250      255
Val Arg Pro Pro Leu Thr Leu Pro Ile Asp Lys Ser Leu Thr Val Phe
      260      265      270
Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
      275      280      285
Asn Ala Glu Met Lys Asn Ala Met Lys Lys Leu Trp Thr Arg Lys Arg
      290      295      300
Lys Xaa Gly Gly Asp Lys Cys Ile Ile Tyr Phe Gln Xaa Arg Val Ala
305      310      315      320
Pro Ser Arg Lys Ala Ile Cys
      325

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<210> 2235

<211> 125

<212> PRT

<213> Homo sapien (8118970-10-4947-6912)

<400> 2235

```

Leu Ala Cys Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Pro Asp
1      5      10      15
Val Gly Leu Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr
      20      25      30
Thr Arg Ile Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg
      35      40      45
Arg Arg Ala Phe Ser Thr Cys Ser Ala His Leu Ile Ala Ile Leu Cys
      50      55      60
Ala Tyr Gly Pro Ile Ile Thr Val Tyr Leu Gln Pro Thr Pro Asn Pro
65      70      75      80
Met Leu Gly Thr Val Val Gln Ile Leu Met Asn Leu Val Gly Pro Met
      85      90      95
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Thr Ala
      100      105      110
Leu Lys Thr Ile Leu His Arg Thr Gly His Val Pro Glu
      115      120      125

```

<210> 2236

<211> 112

<212> PRT

<213> Homo sapien (8118970-16-561-1769)

<400> 2236

```

Met Glu Val Lys Asn Cys Cys Met Val Thr Glu Phe Ile Leu Leu Gly
 1          5          10          15
Ile Pro His Thr Glu Gly Leu Glu Met Thr Leu Phe Val Leu Phe Leu
          20          25          30
Pro Phe Tyr Ala Cys Thr Leu Leu Gly Asn Val Ser Ile Leu Val Ala
          35          40          45
Val Met Ser Ser Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
          50          55          60
Asn Leu Ser Val Phe Asp Met Gly Phe Ser Ser Val Thr Val Pro Lys
65          70          75          80
Met Leu Leu Tyr Leu Met Gly Leu Ser Arg Leu Ile Ser Tyr Lys Asp
          85          90          95
Cys Val Cys Gln Leu Phe Phe Phe His Phe Leu Gly Ser Ile Glu Cys
          100          105          110

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<210> 2237

<211> 287

<212> PRT

<213> Homo sapien (8119016-6-4856-7402)

<220>

<221> VARIANT

<222> (1)...(287)

<223> Xaa = Any Amino Acid

<400> 2237

```

Val Ile Arg Asn Gln Thr Met Val Thr Glu Phe Thr Leu Val Ser Leu
 1          5          10          15
Pro Ala Val Gln Glu Leu Gln Ile Trp Leu Cys Val Leu Leu Trp Leu
          20          25          30
Val His Met Leu Thr Ile Thr Gly Asn Leu Phe Val Ile Phe Leu Thr
          35          40          45
Trp Thr Asp Asn Cys Leu Gln Thr Pro Met Asp Leu Phe Leu Glu Lys
          50          55          60
Lys Val Ile Ser Phe Ser Gly Cys Ile Thr Gln Ile Tyr Phe Tyr Phe
65          70          75          80
Phe Leu Gly Thr Val Ala Phe Ile Pro Leu Ala Val Thr Ser Phe Lys
          85          90          95
His Cys Met Ala Thr Cys Asp Pro Leu Cys Ser Thr Ile Ile Ala Lys
          100          105          110
Ser Arg Ala Cys Leu Leu Leu Ala Leu Gly Cys Trp Met Gly Thr Phe
          115          120          125
Leu Ala Val Leu Arg Leu Thr Ile Val Val Ser Arg Leu Pro Asp Cys
          130          135          140
Thr Glu Lys Ile Ser Pro Phe Phe Cys Asp Ile Ala Ser Leu Leu Gln
          145          150          155          160
Val Ala Cys Ile Asp Ile His Phe Ile Glu Met Ile Ser Phe Leu Xaa
          165          170          175
Ser Ser Leu Met Val Leu Thr Ser Leu Val Leu Asn Ala Thr Ser Tyr
          180          185          190
Ala Tyr Ile Ile Ser Thr Leu Leu Cys Ile Pro Ser Ala Gln Gly Cys
          195          200          205
Gln Glu Ala Phe Ser Thr Cys Ala Ser His Ile Thr Ile Ile Phe Ile
          210          215          220
Ala Cys Arg Asn Ser Ile Ser Thr Cys Val Arg Pro Asn Pro Arg Tyr
          225          230          235          240
Xaa Leu Asp Phe Asp Lys Val Thr Ala Ile Leu Thr Ile Val Val Thr
          245          250          255
Ser Phe Leu Asn Pro Arg Ile Tyr Ser Leu Arg Xaa Arg Lys Tyr Glu
          260          265          270
Gly Ser Xaa Ile Cys Thr Ile Leu Ser Pro His Ser Lys Gly Thr

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275

280

285

<210> 2238
 <211> 210
 <212> PRT
 <213> Homo sapien (8119057-10-2407-4064)

<220>
 <221> VARIANT
 <222> (1)...(210)
 <223> Xaa = Any Amino Acid

<400> 2238
 Leu Gly Asn Val Ser Thr Glu Thr Thr Phe Ile Phe Val Cys Phe Thr
 1 5 10 15
 Asn Gly Gln Gln Phe Gln Pro Val Cys Phe Ser Ser Phe Xaa Val Leu
 20 25 30
 Gly His Ser Val Leu Gly Leu Ser Ser Leu Leu Asn Ile His Gly Glu
 35 40 45
 Leu Val Phe Ser Leu Phe Ser Phe Val Phe Val Phe Gln Met Ser Tyr
 50 55 60
 Ser Phe Val Ile Leu Ile Lys Met Ile Met Asn Ser Ile Ser Glu Arg
 65 70 75 80
 Tyr Ile Thr Thr Asn Leu Lys Cys Lys Thr Ser Ala Leu Val Phe Ile
 85 90 95
 Cys Phe Ala Ile Ser Glu Thr Leu Ile Leu Leu Ala Trp Gly His Cys
 100 105 110
 Gly Ile Cys Val Pro Gln Val Cys Ser Leu Thr Met Leu Gly Leu His
 115 120 125
 Gly Val Gly Ile Asp Gly Val Met Ala His Pro Glu Ala Met Val Ser
 130 135 140
 Leu Ser Phe Cys Asp Arg Ser Ile Ile Asn His Cys Val Trp His Thr
 145 150 155 160
 Ser Phe His Gln Thr Leu Leu Arg Ala Pro Ala Ser Gln Ala Gly Asp
 165 170 175
 Phe Val Val Ile Ala Xaa Xaa Leu Ile Ile Phe Ile Ser Asp Ile Leu
 180 185 190
 Ile Leu Ser Thr Ile Leu His Phe Leu Phe Pro Glu Ala Asn Ser Lys
 195 200 205
 Ala Phe
 210

<210> 2239
 <211> 228
 <212> PRT
 <213> Homo sapien (8119057-15-786-3116)

<220>
 <221> VARIANT
 <222> (1)...(228)
 <223> Xaa = Any Amino Acid

<400> 2239
 Met Leu Ile Pro Ser Ser Thr Arg Lys Met Ala Ala Glu Ser His Ser
 1 5 10 15
 Thr Val Thr Glu Phe Ile Leu Arg Lys Lys Pro Ala Arg Ala Pro Ala
 20 25 30
 Pro Pro Leu Leu Gly Ile Cys Leu Lys Thr Val Val Gly Ala Leu Ile
 35 40 45
 Leu Ile Thr Leu Val Phe Leu Asn Ser Gln Leu His Pro Pro Met Tyr
 50 55 60

Tyr Val Ile Arg Asn Leu Ser Phe Met Asp His Cys Asn Cys Ser Il
 65 70 75 80
 Ser Thr Pro Lys Ile Leu Val Lys Phe Val Leu Glu Lys Thr Ile Ile
 85 90 95
 Ser Tyr Glu Asp Gly Met Ser Gln Leu Cys Ser Ala Ser Cys Tyr Ile
 100 105 110
 Leu Ser Trp Pro Ser Val Thr Cys Gly Pro Ala Thr Ala Val Ile Thr
 115 120 125
 Phe His Gln Val Ser Ser Leu Leu Val Val Val Val Tyr Tyr Met Glu
 130 135 140
 Leu Thr Gly Thr Thr Ile Glu Phe Cys Leu Val Leu Lys Xaa Tyr Xaa
 145 150 155 160
 Cys Glu Leu Phe Ile Ser His Tyr Phe Cys Ser Cys Thr Ser Ile Tyr
 165 170 175
 Asp Ile Asp Arg Thr Ile Phe Phe Phe Thr Xaa Cys Asn Ile Val Val
 180 185 190
 Thr Arg Leu Thr Val Val Ser Tyr Ser Phe Leu Ser Ser Ile Leu His
 195 200 205
 Ile Ser Phe Thr Arg Ala Ala Leu Gly Phe Ser Arg Arg Ser Asp Ala
 210 215 220
 Phe Met Leu Cys
 225

<210> 2240

<211> 277

<212> PRT

<213> Homo sapien (8119057-2-10436-11711)

<220>

<221> VARIANT

<222> (1)...(277)

<223> Xaa = Any Amino Acid

<400> 2240

His Ser Phe Leu Arg Tyr Ile Phe Ala Lys Leu Thr Gly Glu Pro Glu
 1 5 10 15
 Leu Gln Pro Ser Leu Tyr Ser Val Phe Trp Ser Pro Xaa Leu Gly Xaa
 20 25 30
 Pro His His Thr Ser Met Tyr Pro Leu His Thr Ser Met Tyr Leu Tyr
 35 40 45
 Ile Phe Ser Phe Ser Phe Ile Gly Phe Phe Tyr Ser Ser Val Ile Ser
 50 55 60
 Pro Gln Met Thr Ile Ser Phe Val Thr Glu Lys Asn Ile Ile Thr Tyr
 65 70 75 80
 Val Thr Ser Asn Thr Gln Pro Phe Pro Leu Cys Phe Phe Val Ile Ser
 85 90 95
 Asp Tyr Ser Ile Phe Ile Pro Leu Ala Leu Asp His Tyr Glu Ala Met
 100 105 110
 Thr Leu Pro Val Ser Phe Ile Ser Phe Ile Ser Val Asp Gly Ser Xaa
 115 120 125
 Val Ile Glu Phe Ala Asp Ala Val Val His Gln Gly Ser Met Asp Gln
 130 135 140
 Phe Leu Phe Cys Asp His Ser Cys Met Ser Leu Asn Leu Cys Asn Ile
 145 150 155 160
 Gly Pro Leu Gln Ala Ala Xaa Ile Ser Thr Tyr Val Ser Lys Gln Val
 165 170 175
 Asp Leu Tyr Ser Xaa Glu Pro Ala Val Tyr His Ala Val Leu Ser Phe
 180 185 190
 Ser Tyr Phe Val Phe Ile Leu Phe Asn Ile Phe His Xaa Pro Ser Gly
 195 200 205
 Pro Asn Leu Gln Pro Asp Ser Ile Asn Leu Phe Ile Ser Phe Phe Gly

210 215 220
 Leu Gly Thr Phe Met Tyr Leu Arg Ser Pro Glu Ala Met Gly Xaa Cys
 225 230 235 240
 Lys Phe Thr Val Ser Phe Thr Lys M t Gly Pro Val Met Asn Gly Leu
 245 250 255
 Phe Asn Thr Leu Arg Asn Lys Thr Ile Xaa Leu Ala Ala Met Lys Pro
 260 265 270
 Leu Ser Phe Ser Ser
 275

<210> 2241
 <211> 125
 <212> PRT
 <213> Homo sapien (8119057-22-209-1834)

<220>
 <221> VARIANT
 <222> (1)...(125)
 <223> Xaa = Any Amino Acid

<400> 2241
 Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser Lys
 1 5 10 15
 Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Ser Leu Phe Phe
 20 25 30
 Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu
 35 40 45
 Asp Gln Gly Lys Val Ser Ser Ile Phe Cys Thr Ala Val Val Pro Met
 50 55 60
 Phe Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala
 65 70 75 80
 Leu Arg Arg Thr Phe Cys Arg Lys Leu Val Ser Xaa Lys Xaa Met Arg
 85 90 95
 Lys Gly Ile Gln Thr Phe Val Asn Gln Gly Val Ser Phe Leu Phe Phe
 100 105 110
 Ser Glu Gly Thr Asn Ala Thr Ala Phe Ser Pro Ile Leu
 115 120 125

<210> 2242
 <211> 164
 <212> PRT
 <213> Homo sapien (8119071-15-1-1473)

<220>
 <221> VARIANT
 <222> (1)...(164)
 <223> Xaa = Any Amino Acid

<400> 2242
 Trp Lys Asn His Phe Thr Ser Val Asn Cys Gly Phe Ala Ile Cys Arg
 1 5 10 15
 Ala Glu Cys Xaa Pro Xaa Pro Lys Ile Leu Ser Ile Ile Gly Leu Lys
 20 25 30
 Xaa Asn Ile Asn Glu Thr Leu Xaa Met Leu Asn Tyr Asn Thr Asn His
 35 40 45
 Met Val Ser Val Asp Val Leu Ile Val Pro Asn Ser Leu Ile Thr Leu
 50 55 60
 Ser Tyr Phe Phe Ile Val Ala Ala Ile Leu His Ile Arg Ser Ala Glu
 65 70 75 80
 Gly Arg His Lys Ala Phe Pro Thr Cys Ser Phe His Leu Val Val Ile
 85 90 95

Leu Leu Gln His Asn Ala Thr Ser Leu Thr Tyr Leu Cys Pro Ser Ser
 100 105 110
 Ile Phe Ser Tyr Glu Arg Gly Lys Val Val Ser Thr Val Tyr Thr Cys
 115 120 125
 Ile Thr Pro Val Pro Asn Pro Leu Ile Cys Ser Met Arg Lys Lys Glu
 130 135 140
 Leu Lys His Ala Leu Lys Lys Lys Glu Glu Ile Ala Arg Phe Leu Leu
 145 150 155 160
 Leu Arg Thr His

<210> 2243
 <211> 131
 <212> PRT
 <213> Homo sapien (8131609-2-31657-32554)

<220>
 <221> VARIANT
 <222> (1)...(131)
 <223> Xaa = Any Amino Acid

<400> 2243
 Ile Ile Tyr Leu Leu Cys Xaa Asp Pro Ala Ile Cys Glu Ser Val Ile
 1 5 10 15
 Phe Phe Pro Met Gly Phe Ser Asp Cys Leu Pro Ile Leu Ser Ile Met
 20 25 30
 Ile Thr Tyr Leu Phe Thr Phe Ile Asp Leu Leu Ile Pro Leu Pro His
 35 40 45
 Val Xaa Leu Gln Lys Asp Tyr Tyr Val Cys Ala Ser Asn Leu Thr Val
 50 55 60
 Val Ser Thr Phe Ser Xaa Asp His Leu Phe Ser Cys Leu His Ser Ser
 65 70 75 80
 Asp Ala Ala Leu Leu Trp Thr Gln Thr Lys Leu His Ser Tyr Phe Ala
 85 90 95
 Ile Val Ile Pro Thr Leu Tyr Pro Leu Val His Ser Leu Lys Asn Arg
 100 105 110
 Gly Gly Gln Ser Ala Leu Arg Lys Val Leu Val Lys Ala Lys Ser Gln
 115 120 125
 Leu Ser Leu
 130

<210> 2244
 <211> 312
 <212> PRT
 <213> Homo sapien (8131609-3-27134-29103)

<220>
 <221> VARIANT
 <222> (1)...(312)
 <223> Xaa = Any Amino Acid

<400> 2244
 Thr Thr Ser Ile Asp Asp Asn Thr Glu Val Asn Glu Phe Ile Xaa Leu
 1 5 10 15
 Gly Leu Thr Lys Ala Pro Glu Leu Gln Val His Leu Phe Val Leu Phe
 20 25 30
 Asn Phe Ile Tyr Leu Phe Thr Leu Ser Gly Asn Leu Gly Met Met Leu
 35 40 45
 Leu Ile Leu Leu Asp Ser Arg Leu His Thr Ser Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Val Asp Phe Cys Tyr Ser Glu Thr Val Thr Pro

```

65          70          75          80
Lys Met Met Ala Gly Leu Leu Ile Ala His Lys Val Ile Ser Tyr Asn
      85          90          95
Val Cys Ala Ala Gln Met Phe Phe Phe Ala Val Phe Ala Thr Val Glu
      100          105          110
Ser Tyr Phe Leu Thr Ser Val Ala Tyr Asp Cys Tyr Arg Val Met Cys
      115          120          125
Lys Pro Leu His Tyr Thr Thr Thr Met Thr Thr Asn Val Cys Ala Ser
      130          135          140
Leu Ala Ile Ala Cys Tyr Val Leu Gly Leu Leu Thr Ala Ala Val Asp
145          150          155          160
Ile Gly Asp Ile Cys Met Ser Asn Glu Ile His His Phe Phe Cys Asp
      165          170          175
Ile Leu Ala Val Met Thr Leu Thr Cys Ser Asn Lys His Ile Asn Glu
      180          185          190
Leu Ile Leu Val Leu Leu Gln Ala Ile Phe Phe Thr Leu Leu Val Ile
      195          200          205
Leu Ile Ser Cys Leu Phe Val Phe Val Phe Val Thr Ile Leu Lys Met
      210          215          220
His Leu Phe Lys Ser Tyr Lys Lys Val Leu Ser Thr Tyr Gly Ser His
225          230          235          240
Leu Thr Ala Val Pro Leu Phe Tyr Glu Thr Val Leu Ile Thr Tyr Val
      245          250          255
Gln Pro Ser Ser Ser His Phe Met Asn Thr Glu Lys Ile Val Ser Val
      260          265          270
Phe His Ile Met Val Ile Pro Met Leu Ile Pro Val Val Tyr Ser Leu
      275          280          285
Arg Asn Asn Glu Val Lys Ser Ala Phe Lys Thr Val Val Glu Glu Thr
      290          295          300
Lys Tyr Phe Leu Gly Leu Val Phe
305          310

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<210> 2245

<211> 189

<212> PRT

<213> Homo sapien (8131615-11-1-272)

<220>

<221> VARIANT

<222> (1)...(189)

<223> Xaa = Any Amino Acid

<400> 2245

```

Ala Thr Lys Glu Leu Cys Phe Leu Gly Val Tyr Ile Pro Lys Gly Asp
1          5          10          15
Ala Cys Trp Lys Xaa Leu Xaa Leu Gly Leu His Leu Leu Leu Gly
      20          25          30
Xaa Gln Val Val Ser Met Val Gly Asn Leu Ala Leu Ile Ala Leu Ile
      35          40          45
Gly Xaa Asn Ser Tyr Leu His His Pro Gln Ala Leu Phe Ser Phe Thr
      50          55          60
Gln Ser Phe Pro Asp Leu Tyr Cys Pro Val Cys Thr Pro Arg Met Leu
65          70          75          80
Met Thr Phe Val Ser Lys Lys Asn Ile Phe Tyr Val Arg Cys Met Thr
      85          90          95
Gln Leu Ser Gln Leu Phe Phe Leu Phe Ile Val Leu Ser Ile Lys Tyr
      100          105          110
His Val Leu Met Phe Ile Ala Cys Gly Cys Leu Val Ala Ile Tyr Asn
      115          120          125
Pro Ser Leu His Glu Val Thr Met Ser Pro Gln Val Arg Glu Met Arg
130          135          140

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Glu Ser Gly Phe Ala Gly Thr Thr Ala His Thr Gly His Ile Leu Arg
 145 150 155 160
 Pro Asn Leu Cys Asn Ile Asp Val Ile Asn His His Leu Thr Asp Ser
 165 170 175
 Leu Leu Val Leu Xaa Val Ser Cys Thr Ser Thr Cys Ala
 180 185

<210> 2246

<211> 207

<212> PRT

<213> Homo sapien (8131622-1-12991-13959)

<220>

<221> VARIANT

<222> (1)...(207)

<223> Xaa = Any Amino Acid

<400> 2246

Glu Ile Ile Leu Ile Gly Ile Ser Leu Lys Leu Tyr Leu Val Val Phe
 1 5 10 15
 Thr Ile Ile Lys Ile Lys Xaa His Ser Ile Gly Leu Ser Ser Asn Lys
 20 25 30
 Asn Met Arg Leu Pro Ser Asp Phe Leu Ser Gln Ala Ile Tyr Tyr
 35 40 45
 Xaa Trp Ala Leu Met Cys Val Leu Glu Asn Lys Thr Tyr Ala Ser Val
 50 55 60
 Arg Leu Val Xaa Arg Phe Gly Trp Xaa Lys Leu Ala Asn Xaa Met Ser
 65 70 75 80
 Val Leu Tyr Leu Glu Ala Asn Leu Gly Asn Met Asp Asn Ala Leu Leu
 85 90 95
 Lys Xaa Leu Lys Arg Asn Tyr Phe Val Phe Val Phe Thr Ser Phe Leu
 100 105 110
 Phe Gly Cys Ile Ala Phe Lys Xaa Lys Glu Ile Phe Tyr Pro Tyr Thr
 115 120 125
 Ser Ile Cys Ile Tyr His Leu Leu Met Met Glu Arg Lys Val Ser Cys
 130 135 140
 Leu Thr Leu Ile Cys Leu Ala Xaa Asp Leu Xaa His Phe Xaa Cys Ser
 145 150 155 160
 Leu Val Thr Val Leu Ser Leu Glu Cys Xaa Gln Leu Asp Ile Cys Asn
 165 170 175
 Val Val Thr Tyr Phe Asn Thr Met Val Xaa Ser Thr Thr Gly Ser Asn
 180 185 190
 Ser Xaa Thr Pro Asn His Ser Val Leu Ile Cys Asn Met Leu Lys
 195 200 205

<210> 2247

<211> 311

<212> PRT

<213> Homo sapien (8131622-11-1950-4442)

<400> 2247

Met Thr Gly Gly Gly Asn Ile Thr Glu Ile Thr Tyr Phe Ile Leu Leu
 1 5 10 15
 Gly Phe Ser Asp Phe Pro Arg Ile Ile Lys Val Leu Phe Thr Ile Phe
 20 25 30
 Leu Val Ile Tyr Ile Thr Ser Leu Ala Trp Asn Leu Ser Leu Ile Val
 35 40 45
 Leu Ile Arg Met Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Ile Asp Val Cys Tyr Ile Ser Ser Thr Val Pro
 65 70 75 80

Lys Met Leu Ser Asn Leu Leu Gln Glu Gln Gln Thr Ile Thr Phe Val
 85 90 95
 Gly Cys Ile Ile Gln Tyr Phe Ile Phe Ser Thr Met Gly Leu Ser Glu
 100 105 110
 Ser Cys Leu Met Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Ser Ser Ile Met Ser Pro Thr Leu Cys Val Trp
 130 135 140
 Met Val Leu Gly Ala Tyr Met Thr Gly Leu Thr Ala Ser Leu Phe Gln
 145 150 155 160
 Ile Gly Ala Leu Leu Gln Leu His Phe Cys Gly Ser Asn Val Ile Arg
 165 170 175
 His Phe Phe Cys Asp Met Pro Gln Leu Leu Ile Leu Ser Cys Thr Asp
 180 185 190
 Thr Phe Phe Val Gln Val Met Thr Ala Ile Leu Thr Met Phe Phe Gly
 195 200 205
 Ile Ala Ser Ala Leu Val Ile Met Ile Ser Tyr Gly Tyr Ile Gly Ile
 210 215 220
 Ser Ile Met Lys Ile Thr Ser Ala Lys Gly Ser Pro Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Ala Val Ser Leu Phe Tyr Thr Ser Gly
 245 250 255
 Ile Phe Val Tyr Leu Arg Ser Ser Ser Gly Gly Ser Ser Ser Phe Asp
 260 265 270
 Arg Phe Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu Lys Arg
 290 295 300
 Leu Gln Lys Arg Lys Cys Cys
 305 310

<210> 2248

<211> 444

<212> PRT

<213> Homo sapien (8131622-13-5638-8129)

<220>

<221> VARIANT

<222> (1)...(444)

<223> Xaa = Any Amino Acid

<400> 2248

Met Thr Val Glu Arg Ser Ser Met Thr Ile Thr Lys Phe Ile Leu Leu
 1 5 10 15
 Gly Phe Ser Glu Tyr Ser Lys Thr Thr Ile Phe Leu Phe Ser Val Phe
 20 25 30
 Leu Gly Ile Tyr Leu Leu Thr Met Ser Xaa Asn Val Ser Leu Ile Ala
 35 40 45
 Leu Ile Arg Thr Asp Ser His Leu His Ala Pro Val Tyr Phe Phe Leu
 50 55 60
 Ser Asn Pro Ser Phe Leu Asp Ile Cys Cys Val Ser Thr Ile Ala Pro
 65 70 75 80
 Lys Met Pro Ser Asp Phe Phe Lys Lys His Lys Phe Ile Ser Phe Met
 85 90 95
 Gly Cys Thr Met Gln Tyr Phe Ser Ser Leu Asn Val Thr Glu Cys Cys
 100 105 110
 Leu Leu Thr Ala Met Ala Tyr Asp Xaa Tyr Ala Ala Ile Cys Asp Pro
 115 120 125
 Leu Leu Tyr Thr Ala Ile Met Ser Pro Ala Leu Cys Met Pro Met Val
 130 135 140
 Ala Gly Ser Cys Thr Thr Gly Tyr Phe Val Ser Phe Ile Gln Leu Cys

145 150 155 160
 Ala Leu Leu Leu Leu His Phe Cys Glu Ser Asn Ser Ser His Phe Phe
 165 170 175
 Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser Cys Ser His Thr Val Phe
 180 185 190
 Phe Phe Ser Ser His Asp His Tyr Ala His Ser Asn Leu Tyr Thr His
 195 200 205
 Leu Tyr Leu Gly Tyr His Asp Asn Leu Trp Leu Tyr His Cys Gln His
 210 215 220
 Ser Ser Leu Leu Trp Asp Ala Pro Cys Asn Thr Ser Ser Leu Ala Trp
 225 230 235 240
 Val Xaa Leu Ser Ala Val Phe Trp Lys Leu Trp Leu Ile Ile Asp Met
 245 250 255
 Leu Pro Phe Val Thr Leu Cys Ser Thr Trp Pro Ser Met Ser Pro Thr
 260 265 270
 Ser Val Cys Thr Xaa Trp Leu Glu Pro Val Xaa Leu Ser Leu Ala
 275 280 285
 His Leu Ser Asn Tyr Val Leu Cys Phe Ser Ser Ile Ser Val Gly Gln
 290 295 300
 Ile Val Asn His Phe Phe Cys Asp Leu Pro Gln Leu Leu Ile Leu Ser
 305 310 315 320
 Cys Tyr Asp Thr Phe Phe Cys Gln Val Met Thr Ser Met Leu Thr Val
 325 330 335
 Val Phe Gly Leu Thr Ser Val Leu Val Ile Met Ile Phe Tyr Gly Tyr
 340 345 350
 Val Ile Ala Thr Ile Leu Lys Ile Ile Ser Val Glu Gly Arg Ser Lys
 355 360 365
 Val Phe Asn Thr Gly Gly Ser His Leu Ile Ala Val Thr Leu Phe Tyr
 370 375 380
 Cys Ser Arg Ile Phe Val Tyr Met Cys Ser His Ser Asp Ala Ser Leu
 385 390 395 400
 Ser Arg Asn Lys Val Asp Ser Ile Val Tyr Thr Val Val Ile Pro Arg
 405 410 415
 Leu Asn Pro Leu Ile Tyr Ser Leu Ser Asp Lys Xaa Ile Lys Asp Ala
 420 425 430
 Leu Lys Arg Trp Thr Lys Arg Ile Phe Ser Trp Pro
 435 440

<210> 2249

<211> 312

<212> PRT

<213> Homo sapien (8131671-12-1836-3192)

<400> 2249

Met Gly Val Lys Asn His Ser Thr Val Thr Glu Phe Leu Leu Ser Gly
 1 5 10 15
 Leu Thr Glu Gln Ala Glu Leu Gln Leu Pro Leu Phe Cys Leu Phe Leu
 20 25 30
 Gly Ile Tyr Thr Val Thr Val Val Gly Asn Leu Ser Met Ile Ser Ile
 35 40 45
 Ile Arg Leu Asn Arg Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Ser Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Ser Gly Phe Leu Cys Arg Asp Arg Ser Ile Ser Tyr Ser Gly
 85 90 95
 Cys Met Ile Gln Leu Phe Phe Phe Cys Val Cys Val Ile Ser Glu Cys
 100 105 110
 Tyr Met Leu Ala Ala Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Ser
 115 120 125
 Pro Leu Leu Tyr Arg Val Ile Met Ser Pro Arg Val Cys Ser Leu Leu

130 135 140
 Val Ala Ala Val Phe Ser Val Gly Phe Thr Asp Ala Val Ile His Gly
 145 150 155 160
 Gly Cys Ile Leu Arg Leu Ser Phe Cys Gly Ser Asn Ile Ile Lys His
 165 170 175
 Tyr Phe Cys Asp Ile Val Pro Leu Ile Lys Leu Ser Cys Ser Ser Thr
 180 185 190
 Tyr Ile Asp Glu Leu Leu Ile Phe Val Ile Gly Gly Phe Asn Met Val
 195 200 205
 Ala Thr Ser Leu Thr Ile Ile Ser Tyr Ala Phe Ile Leu Thr Ser
 210 215 220
 Ile Leu Arg Ile His Ser Lys Lys Gly Arg Cys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Ala Val Leu Met Phe Tyr Gly Ser Leu Met
 245 250 255
 Ser Met Tyr Leu Lys Pro Ala Ser Ser Ser Leu Thr Gln Glu Lys
 260 265 270
 Val Ser Ser Val Phe Tyr Thr Thr Val Ile Leu Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Asn Glu Val Arg Asn Ala Leu Met Lys Leu
 290 295 300
 Leu Arg Arg Lys Ile Ser Leu Ser
 305 310

<210> 2250

<211> 305

<212> PRT

<213> Homo sapien (8131682-2-1-1878)

<400> 2250

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1 5 10 15
 Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
 20 25 30
 Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile
 35 40 45
 Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Val Val Gly Asn
 50 55 60
 Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
 65 70 75 80
 Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
 85 90 95
 Leu Cys Gln Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Tyr
 100 105 110
 Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro
 115 120 125
 Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val
 130 135 140
 Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys
 145 150 155 160
 Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe
 165 170 175
 Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly
 180 185 190
 Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys
 195 200 205
 Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val
 210 215 220
 Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr

245 250 255
 Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile
 260 265 270
 Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu
 290 295 300

Pro
305

<210> 2251

<211> 306

<212> PRT

<213> Homo sapien (8131682-3-415-2331)

<400> 2251

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1 5 10 15
 Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
 20 25 30
 Val Tyr Cys Leu Thr Val Val Gly Ser Ser Thr Leu Ile Val Leu Ile
 35 40 45
 Cys Asn Asp Ser Arg Leu His Thr Pro Met Tyr Phe Val Ile Gly Asn
 50 55 60
 Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val His Thr Pro Lys Ile
 65 70 75 80
 Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
 85 90 95
 Leu Cys Gln Phe Phe Ser Ala Arg Leu Ala Tyr Ser Glu Cys Tyr Leu
 100 105 110
 Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu
 115 120 125
 Leu Tyr Ala Gln Thr Met Pro Arg Arg Leu Cys Ile Cys Leu Val Leu
 130 135 140
 Tyr Ser Tyr Thr Gly Gly Phe Val Asn Ala Ile Ile Leu Thr Ser Asn
 145 150 155 160
 Thr Phe Thr Leu Asp Phe Cys Gly Asp Asn Val Ile Asp Asp Phe Phe
 165 170 175
 Cys Asp Val Pro Pro Leu Val Lys Leu Ala Cys Ser Val Arg Glu Ser
 180 185 190
 Tyr Gln Ala Val Leu His Phe Leu Leu Ala Ser Asn Val Ile Ser Pro
 195 200 205
 Thr Val Leu Ile Leu Ala Ser Tyr Leu Ser Ile Ile Thr Thr Ile Leu
 210 215 220
 Arg Ile His Ser Thr Gln Gly Arg Ile Lys Val Phe Ser Thr Cys Ser
 225 230 235 240
 Ser His Leu Ile Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr Asn
 245 250 255
 Tyr Ser Arg Pro Ser Ser Ser Tyr Ser Leu Lys Arg Asp Lys Met Val
 260 265 270
 Ser Thr Phe Tyr Thr Met Leu Phe Pro Met Leu Asn Pro Met Ile Tyr
 275 280 285
 Ser Leu Arg Ser Lys Asp Met Lys Asp Ala Leu Lys Lys Phe Phe Lys
 290 295 300
 Ser Ala
 305

<210> 2252

<211> 324

<212> PRT

<213> Homo sapien (8152118-1-59952-61847)

<220>
 <221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 2252

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20              25              30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35              40              45
Ile Leu Ala Val Arg Ser Glu Ser Pro Leu His Thr Thr Met Tyr Phe
      50              55              60
Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
      65              70              75              80
Val Pro Lys Met Ile Val Asp Met Gln Trp Tyr Ser Lys Val Ile Ser
      85              90              95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100             105             110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
      115             120             125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
      130             135             140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
      145             150             155             160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
      165             170             175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
      180             185             190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Gly Ser Thr Met
      195             200             205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
      210             215             220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
      225             230             235             240
Phe Ser Thr Tyr Gly Ser His Leu Ala Val Phe Cys Xaa Phe Asp Gly
      245             250             255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg
      260             265             270
Asn Gly Val Val Val Ser Val Lys Xaa Ala Val Val Thr Pro Met Pro
      275             280             285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
      290             295             300
Arg Arg Leu Pro Asn Lys Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
      305             310             315             320
Phe Phe Trp Cys

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<210> 2253
 <211> 212
 <212> PRT
 <213> Homo sapien (8247820-10-10207-11695)

<220>
 <221> VARIANT
 <222> (1)...(212)
 <223> Xaa = Any Amino Acid

<400> 2253

```

Thr Met Phe Tyr Lys Ile Ser Ala Leu Phe Xaa Cys Xaa Cys Ile Thr
 1          5          10          15
Leu Phe Xaa Xaa Lys Leu Ser Lys Gln Lys Ile Tyr Trp Val Leu Thr
      20          25          30
Ile Phe Gly Phe Leu Glu Ala Phe Ile Ala Met Asn Lys Leu Xaa Lys
      35          40          45
Leu Tyr Ser Ser Leu Ile Cys Leu Tyr Phe Ile Ile Xaa Ile Phe Lys
      50          55          60
Phe Ser Asn Met Phe Ile Phe Tyr Asn Met Asn Ile Ser Val His Tyr
65          70          75          80
Phe Leu Lys Cys Ile Phe Phe Phe Cys Ile Cys Cys Leu Xaa Leu Leu
      85          90          95
Ile Phe Asp Ser Phe Ser Thr His Pro Pro Leu Pro Leu Leu Xaa Glu
      100          105          110
Ala Asp Ile Cys Ala Asn Ser Xaa Pro Cys Tyr Thr Asn Thr Thr Ala
      115          120          125
Ser Xaa Xaa His Phe Tyr Ile Ile Leu Asn Phe Cys Leu Ser Tyr Xaa
      130          135          140
Pro Ser Val Ser Ser Met Leu Tyr Gly Arg Leu Phe Leu Met Tyr Leu
145          150          155          160
Met Pro Glu Asn Ser Leu Asp Thr Asp Arg Met Ala Ser Val Phe Tyr
      165          170          175
Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Trp Ser Pro Arg Asn
      180          185          190
Lys Asp Val Thr Ser Ala Leu Arg Lys Val Met Val Asn Arg Lys Gln
      195          200          205
Ala Leu Phe Cys
      210

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<210> 2254

<211> 314

<212> PRT

<213> Homo sapien (8247820-11-34143-40656)

<220>

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 2254

```

Ile Xaa Met Ala Asp Arg Asn Val Thr Val Ile Thr Glu Phe Ile Leu
 1          5          10          15
Leu Gly Leu Thr Asp Asn Pro Glu Met Asn Val Val Leu Ser Val Leu
      20          25          30
Phe Leu Leu Ile Tyr Leu Ile Thr Val Leu Gly Asn Phe Trp Ile Ile
      35          40          45
Ile Ile Ile Leu Ala Ser Ala Gln Leu His Ser Pro Met Tyr Phe Phe
      50          55          60
Leu Ser Gln Leu Ala Phe Leu Asp Phe Cys Tyr Ser Ser Val Leu Ile
65          70          75          80
Pro Lys Met Leu Val Asn Tyr Ile Ala Gly Gln Lys Val Ile Ser Tyr
      85          90          95
His Gly Cys Leu Leu Gln Tyr Ser Phe Val Ser Leu Phe Leu Thr Thr
      100          105          110
Glu Cys Phe Leu Leu Ala Ala Met Ala Cys Asp Arg Tyr Leu Ala Val
      115          120          125
Cys His Pro Leu His Tyr Lys Gly Leu Met Thr Pro Thr Phe Xaa Ile
      130          135          140
Tyr Leu Val Thr Val Ser Tyr Leu Leu Gly Ser Val Asn Ser Leu Thr
145          150          155          160
His Leu Ser Ser Leu Leu Ser Leu Ser Phe Cys Gly Ser Asn Val Ile

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      165      170      175
Asn Arg Tyr Phe Cys Asp Ile Pro Leu Leu Phe Gln Leu Ser Cys Ser
      180      185      190
Asn Thr Gln His Ser Lys Ile Leu Phe Thr Val Leu Ser Gly Ala Thr
      195      200      205
Ser Val Thr Thr Phe Leu Ile Val Val Ser Ser Tyr Leu Val Ile Leu
      210      215      220
Leu Ile Val Leu Lys Ile His Ser Thr Arg Gly Arg Asn Lys Ala Ile
      225      230      235      240
Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu Phe Tyr Arg Thr
      245      250      255
Val Ile Phe Thr Tyr Leu Gly Ala Asn Pro Gly Tyr Ser Gln Asp Arg
      260      265      270
Pro Lys Ile Leu Pro Val Glu Cys Thr Leu Leu Leu Ser Ile Leu Asn
      275      280      285
Leu Leu Ile Tyr Ser Val Arg Asn Arg Glu Val Lys Glu Ala Ile Lys
      290      295      300
Ile Ile Ile Lys Arg Lys Ile Leu Pro Gln
      305      310

```

<210> 2255

<211> 245

<212> PRT

<213> Homo sapien (8247820-7-4578-5918)

<220>

<221> VARIANT

<222> (1)...(245)

<223> Xaa = Any Amino Acid

<400> 2255

```

Met Ser Xaa Xaa Ile Phe Cys Leu Pro Lys Ile Ile Ile Thr Leu Leu
  1      5      10      15
Gln Xaa Glu Trp Asp Ala Leu Asn Leu Glu Thr Arg Val Phe Leu Glu
      20      25      30
Glu Asp Phe Pro Cys Gly Phe Ser Leu Trp Ile Val Arg Gln Leu Ser
      35      40      45
Phe Phe Leu Glu Ile Asn Xaa Phe Ala His Leu Lys Lys Xaa Cys Arg
      50      55      60
Lys His Thr Ser Thr Phe Ser Leu Ser Asn Leu Ala Phe Xaa Asp Phe
      65      70      75      80
Cys Tyr Ala Ser Val Ile Thr Ser Lys Met Phe Gly Ser Phe Leu Tyr
      85      90      95
Lys Gln Lys Lys Leu Thr Phe Asn Ala Leu Gly Cys Ser Leu Thr Phe
      100      105      110
Met Thr Thr Glu Cys Leu Leu Leu Ala Phe Met Ala Cys Asp Gln Tyr
      115      120      125
Leu Val Ile Cys Asn Pro Pro Leu Tyr Met Val Thr Met Ser Pro Pro
      130      135      140
Gln Gly Val Cys Ile Gln Leu Met Pro Ala Ser Tyr Ser Tyr Ser Phe
      145      150      155      160
Leu Met Thr Leu Ser His Tyr Leu Ser Ala Phe Arg Leu Pro Tyr Cys
      165      170      175
Pro Ser Val Ser Leu Met Phe Asn Gly Ser Leu Phe Leu Tyr Cys Thr
      180      185      190
Xaa Cys Ser Glu Asn Ser Leu Asp Thr Asp Arg Met Ala Ser Val Phe
      195      200      205
Tyr Thr Val Val Ile Pro Met Leu Ser Pro Leu Ile Trp Ser Leu Arg
      210      215      220
Asn Lys Asp Val Lys Asp Ala Leu Arg Lys Val Ile Val Asn Arg Asn
      225      230      235      240

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Gln Ala Leu Phe Cys
245

<210> 2256
<211> 302
<212> PRT
<213> Homo sapien (8308370-1-1-2758)

<220>
<221> VARIANT
<222> (1)...(302)
<223> Xaa = Any Amino Acid

<400> 2256
Ile Arg Glu Thr His Ser His Val Pro Tyr Thr Ser Val Phe Leu Pro
1 5 10 15
Val Phe Tyr Thr Ala Val Phe Leu Thr Gly Val Leu Gly Asn Leu Val
20 25 30
Leu Met Gly Ala Leu His Phe Lys Pro Gly Ser Arg Arg Leu Ile Asp
35 40 45
Ile Phe Ile Ile Asn Leu Ala Ser Asp Phe Ile Val Ser Cys His
50 55 60
Ile Ala Ser Leu Gly Gly Xaa Arg Thr Ser Leu Gly Leu Trp Arg Thr
65 70 75 80
Gly Ser Phe Leu Cys Lys Gly Ser Ser Tyr Met Ile Ser Val Asn Met
85 90 95
His Cys Ser Val Leu Leu Leu Thr Cys Met Ser Val Asp Arg Tyr Leu
100 105 110
Ala Ile Val Trp Pro Val Val Ser Arg Lys Phe Arg Arg Thr Asp Cys
115 120 125
Ala Tyr Val Val Cys Ala Ser Ile Trp Phe Asn Leu Leu Pro Ala Gly
130 135 140
Val Ala Tyr Ser Ser Val Gln Gly Ala His Ala Val Asp Asp Lys Pro
145 150 155 160
Tyr Cys Ala Glu Lys Lys Ala Thr Pro Ile Lys Leu Ile Trp Ser Leu
165 170 175
Val Ala Leu Ile Phe Thr Phe Phe Val Pro Leu Leu Ser Ile Val Thr
180 185 190
Cys Tyr Cys Cys Ile Ala Arg Lys Leu Cys Ala His Tyr Gln Gln Ser
195 200 205
Gly Lys His Asn Lys Lys Leu Lys Lys Ser Ile Lys Ile Ile Phe Ile
210 215 220
Val Val Ala Ala Phe Leu Val Ser Trp Leu Pro Phe Asn Thr Phe Lys
225 230 235 240
Phe Leu Ala Ile Val Ser Gly Leu Arg Gln Glu His Tyr Leu Pro Ser
245 250 255
Ala Ile Leu Gln Leu Gly Met Glu Val Ser Gly Pro Leu Ala Phe Ala
260 265 270
Asn Ser Cys Val Asn Pro Phe Ile Tyr Tyr Ile Phe Asp Ser Tyr Ile
275 280 285
Arg Arg Ala Ile Val His Cys Leu Cys Pro Cys Leu Lys Asn
290 295 300

<210> 2257
<211> 336
<212> PRT
<213> Homo sapien (8318124-7-422-2124)

<220>
<221> VARIANT
<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 2257

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Met Val Leu Glu Asn Leu Leu Ile Ile Leu
 35 40 45
 Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly
 85 90 95
 Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu
 100 105 110
 Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115 120 125
 His Pro Leu Tyr Arg Ser Ala Thr Leu Asn Pro Cys Phe Cys Gly Phe
 130 135 140
 Leu Asp Leu Leu Ser Phe Phe Phe Ser Leu Arg Leu Leu Asp Ser
 145 150 155 160
 Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
 165 170 175
 Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala
 180 185 190
 Cys Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala
 195 200 205
 Val Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys
 210 215 220
 Met Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
 225 230 235 240
 Ala Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr
 245 250 255
 Gly Thr Gly Phe Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro
 260 265 270
 Arg Lys Gly Ala Val Ala Ser Val Met Tyr Ser Val Val Thr Pro Met
 275 280 285
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val
 290 295 300
 Leu Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile
 305 310 315 320
 Cys Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys
 325 330 335

<210> 2258

<211> 319

<212> PRT

<213> Homo sapien (8348136-100-2086-3409)

<220>

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 2258

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
 1 5 10 15
 Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu
 20 25 30

Phe Leu Ser Met Cys Leu Val Thr Met Leu Arg Glu Leu Leu Ile Ile
 35 40 45
 Leu Ala Val Thr Ser Asp Ser His Leu His Ile Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Val Leu Gly His Asp Ile Gly Phe Thr Xaa Ala Thr
 65 70 75 80
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Ala Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys
 100 105 110
 Ile Asp Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala
 115 120 125
 Ile Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys
 130 135 140
 Val Phe Leu Val Leu Met Phe Phe Leu Ser Leu Leu Asp Ser Xaa Leu
 145 150 155 160
 His Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
 180 185 190
 Val Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser
 210 215 220
 Ile Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val
 260 265 270
 Val Ala Ser Val Leu Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu
 290 295 300
 Cys Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser
 305 310 315

<210> 2259

<211> 186

<212> PRT

<213> Homo sapien (8389427-13-4913-5701)

<220>

<221> VARIANT

<222> (1)...(186)

<223> Xaa = Any Amino Acid

<400> 2259

Pro Val Pro Gln His Leu Phe Phe Phe Leu Lys Val Thr Gly His Leu
 1 5 10 15
 Leu Thr Xaa Ile Arg Asn Leu Xaa Phe Val Pro Asp Phe Ser Phe Ser
 20 25 30
 Leu Ala Leu His Ile Tyr Gln Xaa Tyr Xaa Phe Xaa Thr Asn Leu Asn
 35 40 45
 Glu Leu His Leu Cys Pro Ser Leu Ile Ser Pro Pro Ser Leu Ser Val
 50 55 60
 His Xaa Leu Arg Leu His His Val Asn Tyr Tyr His Gly Met Leu Thr
 65 70 75 80
 Glu Leu Leu Leu Pro Met Val Pro Cys His Asn Ser Ser Phe Ile Trp
 85 90 95
 Leu Pro Ile Asn Phe Xaa Lys Phe Ile Cys Ile Cys Tyr Phe Ser Gly

	100		105		110										
Xaa	Lys	Leu	Pro	Met	His	Val	Glu	Asp	Gly	Met	Gln	Thr	Ala	Leu	His
	115		120		125										
Ala	Cys	Pro	Leu	Leu	Met	Gln	Leu	Leu	Leu	Ser	Ile	Pro	His	Ser	Tyr
	130		135		140										
Pro	Leu	Leu	Leu	Asp	Asn	Ser	Phe	Leu	Phe	Leu	Arg	Leu	His	Pro	Arg
145			150		155				155						160
Ser	Lys	Leu	Ser	Tyr	Phe	Leu	His	Ile	Leu	Leu	Ser	Xaa	Pro	Phe	Thr
			165		170				170						175
Tyr	Val	Asn	His	Leu	Leu	Pro	Phe	Leu	Leu						
			180		185										

<210> 2260

<211> 304

<212> PRT

<213> Homo sapien (8389428-12-1-2464)

<400> 2260

Met	Arg	Asn	Gly	Thr	Val	Ile	Thr	Glu	Phe	Ile	Leu	Leu	Gly	Phe	Pro
1			5					10					15		
Val	Ile	Gln	Gly	Leu	Gln	Thr	Pro	Leu	Phe	Ile	Ala	Ile	Phe	Leu	Thr
		20					25					30			
Tyr	Ile	Leu	Thr	Leu	Ala	Gly	Asn	Gly	Leu	Ile	Ile	Ala	Thr	Val	Trp
	35					40					45				
Ala	Glu	Pro	Arg	Leu	Gln	Ile	Pro	Met	Tyr	Phe	Phe	Leu	Cys	Asn	Leu
	50				55					60					
Ser	Phe	Leu	Glu	Ile	Trp	Tyr	Thr	Thr	Thr	Val	Ile	Pro	Lys	Leu	Leu
65			70					75						80	
Gly	Thr	Phe	Val	Val	Ala	Arg	Thr	Val	Ile	Cys	Met	Ser	Cys	Cys	Leu
			85					90					95		
Leu	Gln	Ala	Phe	Phe	His	Phe	Phe	Val	Gly	Thr	Thr	Glu	Phe	Leu	Ile
		100						105				110			
Leu	Thr	Ile	Met	Ser	Phe	Asp	Arg	Tyr	Leu	Thr	Ile	Cys	Asn	Pro	Leu
	115					120					125				
His	His	Pro	Thr	Ile	Met	Thr	Ser	Lys	Leu	Cys	Leu	Gln	Leu	Ala	Leu
	130				135						140				
Ser	Ser	Trp	Val	Val	Gly	Phe	Thr	Ile	Val	Phe	Cys	Gln	Thr	Met	Leu
145					150					155					160
Leu	Ile	Gln	Leu	Pro	Phe	Cys	Gly	Asn	Asn	Val	Ile	Ser	His	Phe	Tyr
			165					170						175	
Cys	Asp	Val	Gly	Pro	Ser	Leu	Lys	Ala	Ala	Cys	Ile	Asp	Thr	Ser	Ile
		180					185					190			
Leu	Glu	Leu	Leu	Gly	Val	Ile	Ala	Thr	Ile	Leu	Val	Ile	Pro	Gly	Ser
	195						200					205			
Leu	Leu	Phe	Asn	Met	Ile	Ser	Tyr	Ile	Tyr	Ile	Leu	Ser	Ala	Ile	Leu
	210					215					220				
Arg	Ile	Pro	Ser	Ala	Thr	Gly	His	Gln	Lys	Thr	Phe	Ser	Thr	Cys	Ala
225				230						235					240
Ser	His	Leu	Thr	Val	Ser	Leu	Leu	Tyr	Gly	Ala	Val	Leu	Phe	Met	
			245					250					255		
Tyr	Leu	Arg	Pro	Thr	Ala	His	Ser	Ser	Phe	Lys	Ile	Asn	Lys	Val	Val
		260						265					270		
Ser	Val	Leu	Asn	Thr	Ile	Leu	Thr	Pro	Leu	Leu	Asn	Pro	Phe	Ile	Tyr
	275					280						285			
Thr	Ile	Arg	Asn	Lys	Glu	Val	Lys	Gly	Ala	Leu	Arg	Lys	Ala	Met	Thr
	290					295						300			

<210> 2261

<211> 275

<212> PRT

<213> Homo sapien (8439748-1-6412-8052)

<220>

<221> VARIANT

<222> (1)...(275)

<223> Xaa = Any Amino Acid

<400> 2261

```

Thr Ile Ile Asn Val Asn Ile Ser Pro Glu Phe Val Leu Val Gly Phe
 1           5           10           15
Ser Ser Asp Ala Glu Ile Gln Ile Met Leu Phe Val Leu Ile Leu Val
      20           25           30
Ile His Leu Leu Thr Leu Thr Gly Lys Leu Val Met Ile Leu Glu Ile
      35           40           45
Arg Ala Asp Ser His Leu Gln Arg Pro Met Tyr Phe Phe Leu Xaa His
      50           55           60
Leu Ser Phe Leu Asp Leu Ser Tyr Ser Ser Val Thr Val Pro Arg Met
      65           70           75           80
Leu Gln Asn Phe Leu Ser Gly Arg Lys Ala Ser Gln Cys Gly Ala Ala
      85           90           95
Ser Pro Ser Phe Phe Phe Thr Leu Ser Gly Gly Thr Glu Ala Cys Leu
      100          105          110
Phe Ser Ala Met Ala Tyr Asp His Tyr Ala Thr Ile Arg His Pro Val
      115          120          125
Val Tyr Thr Met Val Met Asn Arg Ser Leu Cys Met Val Ile Leu Arg
      130          135          140
Ile Ala Trp Ala Ala Gly Phe Leu Ile Ser Leu Met Asp Ser Leu Phe
      145          150          155          160
Thr His Lys Leu His Phe Cys Gly Pro Asp Ile Ile Pro Tyr Phe Arg
      165          170          175
Cys Lys Leu Pro Pro Phe Phe Pro Leu Ser Tyr Ile Asp Pro Thr Val
      180          185          190
Asn Glu Ile Leu Leu Ala Val Ser Gln Ala Phe Trp Gly Leu Leu Thr
      195          200          205
Leu Ser Leu Ile Phe Phe Ser Tyr Ser Arg Ile Thr Ser Val Ile Leu
      210          215          220
Ser Ile Cys Ser Ser Glu Gly Gln Gly Lys Ala Phe Ser Ala Cys Pro
      225          230          235          240
Ser His Leu Ala Val Val Leu Ser Phe Tyr Gly Thr Ala Phe Phe Arg
      245          250          255
Tyr Pro Gly Ser Thr Ser Gly Ser Val Leu Gly Gln Val Val Ser Val
      260          265          270
Gln Tyr Ser
      275

```

<210> 2262

<211> 317

<212> PRT

<213> Homo sapien (8439748-5-3942-6516)

<400> 2262

```

Met Leu Arg Asn Gly Ser Ile Val Thr Glu Phe Ile Leu Val Gly Phe
 1           5           10           15
Gln Gln Ser Ser Thr Ser Thr Arg Ala Leu Leu Phe Ala Leu Phe Leu
      20           25           30
Ala Leu Tyr Ser Leu Thr Met Ala Met Asn Gly Leu Ile Ile Phe Ile
      35           40           45
Thr Ser Trp Thr Asp Pro Lys Leu Asn Ser Pro Met Tyr Phe Phe Leu
      50           55           60
Gly His Leu Ser Leu Leu Asp Val Cys Phe Ile Thr Thr Thr Ile Pro
      65           70           75           80
Gln Met Leu Ile His Leu Val Val Arg Asp His Ile Val Ser Phe Val

```


85 90 95
 Cys Cys Met Thr Gln Met Tyr Phe Val Phe Cys Val Gly Val Ala Glu
 100 105 110
 Cys Ile Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Tyr Pro Leu Asn Tyr Val Pro Ile Ile Ser Gln Lys Val Cys Val Arg
 130 135 140
 Leu Val Gly Thr Ala Trp Phe Phe Gly Leu Ile Asn Gly Ile Phe Leu
 145 150 155 160
 Glu Tyr Ile Ser Phe Arg Glu Pro Phe Arg Arg Asp Asn His Ile Glu
 165 170 175
 Ser Phe Phe Cys Glu Ala Pro Ile Val Ile Gly Leu Ser Cys Gly Asp
 180 185 190
 Pro Gln Phe Ser Leu Trp Ala Ile Phe Ala Asp Ala Ile Val Val Ile
 195 200 205
 Leu Ser Pro Met Val Leu Thr Val Thr Ser Tyr Val His Ile Leu Ala
 210 215 220
 Thr Ile Leu Ser Lys Ala Ser Ser Ser Gly Arg Gly Lys Thr Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Val Val Ile Phe Leu Tyr Thr Ser Ala
 245 250 255
 Met Phe Ser Tyr Met Asn Pro His Ser Thr His Gly Pro Asp Lys Asp
 260 265 270
 Lys Pro Phe Ser Leu Leu Tyr Thr Ile Ile Thr Pro Met Cys Asn Pro
 275 280 285
 Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Glu Ala Met Val Arg
 290 295 300
 Ala Leu Gly Arg Thr Arg Leu Ala Gln Pro Gln Ser Val
 305 310 315

<210> 2263

<211> 320

<212> PRT

<213> Homo sapien (8439993-14-9565-12410)

<400> 2263

Met Leu His Thr Asn Asn Thr Gln Phe His Pro Ser Thr Phe Leu Val
 1 5 10 15
 Val Gly Val Pro Gly Leu Glu Asp Val His Val Trp Ile Gly Phe Pro
 20 25 30
 Phe Phe Ala Val Tyr Leu Thr Ala Leu Leu Gly Asn Ile Ile Leu
 35 40 45
 Phe Val Ile Gln Thr Glu Gln Ser Leu His Gln Pro Met Phe Tyr Phe
 50 55 60
 Leu Ala Met Leu Ala Gly Thr Asp Leu Gly Leu Ser Thr Ala Thr Ile
 65 70 75 80
 Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gly Glu Ile Ala Phe
 85 90 95
 Gly Ala Cys Ile Thr Gln Met Tyr Thr Ile His Ile Cys Thr Gly Leu
 100 105 110
 Glu Ser Val Val Leu Thr Val Thr Gly Ile Asp Arg Tyr Ile Ala Ile
 115 120 125
 Cys Asn Pro Leu Arg Tyr Ser Met Ile Leu Thr Asn Lys Val Ile Ala
 130 135 140
 Ile Leu Gly Ile Val Ile Ile Val Arg Thr Leu Val Phe Val Thr Pro
 145 150 155 160
 Phe Thr Phe Leu Thr Leu Arg Leu Pro Phe Cys Gly Val Arg Ile Ile
 165 170 175
 Pro His Thr Tyr Cys Glu His Met Gly Leu Ala Lys Leu Ala Cys Ala
 180 185 190
 Ser Ile Asn Val Ile Tyr Gly Leu Ile Ala Phe Ser Val Gly Tyr Ile

195	200	205
Asp Ile Ser Val Ile Gly Phe Ser Tyr Val Gln Ile Leu Arg Ala Val		
210	215	220
Phe His Leu Pro Ala Trp Asp Ala Arg Leu Lys Ala Leu Ser Thr Cys		
225	230	235
Gly Ser His Val Cys Val Met Leu Ala Phe Tyr Leu Pro Ala Leu Phe		
245	250	255
Ser Phe Met Thr His Arg Phe Gly His Asn Ile Pro His Tyr Ile His		
260	265	270
Ile Leu Leu Ala Asn Leu Tyr Val Val Phe Pro Pro Ala Leu Asn Ser		
275	280	285
Val Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gln Val Leu Arg		
290	295	300
Ile Leu Asn Pro Lys Ser Phe Trp His Phe Asp Pro Lys Arg Ile Phe		
305	310	315
		320

<210> 2264

<211> 329

<212> PRT

<213> Homo sapien (8439993-17-12459-15729)

<220>

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 2264

Met Asn Gly Ala Asn Ser Ser Ser Leu Thr Pro Arg Tyr Phe Ile Leu		
1	5	10
Ser Gly Val Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Leu Pro		
20	25	30
Phe Cys Phe Met Tyr Ile Ile Val Val Leu Gly Asn Cys Gly Leu Ile		
35	40	45
Tyr Leu Ile Ser His Glu Glu Ala Leu His Gln Pro Thr Tyr Tyr Phe		
50	55	60
Leu Asp Leu Leu Ser Leu Thr Asp Val Thr Gly Cys Thr Ser Phe Val		
65	70	75
Pro Asn Met Leu Cys Ile Phe Trp Phe Gly Leu Lys Glu Ile Asp Phe		
85	90	95
Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Met Leu Thr Gly Met		
100	105	110
Glu Ser Gly Ala Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile		
115	120	125
Cys Tyr Pro Leu His Tyr Ser Thr Ile Phe Thr Asn Thr Val Ile Thr		
130	135	140
Lys Val Gly Leu Val Thr Phe Ile Gln Ser Val Leu Leu Met Ile Pro		
145	150	155
Phe Ala Phe Leu Ile Lys Cys Leu Pro Tyr Cys Arg Gly Asn Leu Ile		
165	170	175
His His Thr Tyr Cys Xaa His Met Ser Val Ala Lys Leu Ser Cys Gly		
180	185	190
Asn Val Gln Ile Asn Ala Ile Tyr Gly Leu Ile Ala Ala Ile Leu Ile		
195	200	205
Gly Gly Phe Asp Met Phe Cys Ile Ser Met Ser Tyr Thr Met Ile Ile		
210	215	220
Arg Ala Val Val Asn Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe		
225	230	235
Ser Thr Cys Thr Ala His Ile Cys Ala Ile Phe Ile Thr Tyr Val Pro		
245	250	255
Ala Phe Phe Asn Phe Phe Thr His Arg Phe Gly Gly His Thr Ile Pro		
260	265	270

His His Val His Ile Phe Ile Ala Asn Leu Tyr Leu Met Leu Pro Pro
 275 280 285
 Thr Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu
 290 295 300
 Gly Val Ile Lys Leu Phe Phe Arg Glu Lys Val Tyr Phe Lys Tyr Asp
 305 310 315 320
 Ile Asn Leu Xaa Tyr Arg Ser Leu Asn
 325

<210> 2265

<211> 324

<212> PRT

<213> Homo sapien (8439993-2-191-1624)

<400> 2265

Met Pro Leu Phe Asn Ser Leu Cys Trp Phe Pro Thr Ile His Val Thr
 1 5 10 15
 Pro Pro Ser Phe Ile Leu Asn Gly Ile Pro Gly Leu Glu Arg Val His
 20 25 30
 Val Trp Ile Ser Leu Pro Leu Cys Thr Met Tyr Ile Ile Phe Leu Val
 35 40 45
 Gly Asn Leu Gly Leu Val Tyr Leu Ile Tyr Tyr Glu Glu Ser Leu His
 50 55 60
 His Pro Met Tyr Phe Phe Phe Gly His Ala Leu Ser Leu Ile Asp Leu
 65 70 75 80
 Leu Thr Cys Thr Thr Thr Leu Pro Asn Ala Leu Cys Ile Phe Trp Phe
 85 90 95
 Ser Leu Lys Glu Ile Asn Phe Asn Ala Cys Leu Ala Gln Met Phe Phe
 100 105 110
 Val His Gly Phe Thr Gly Val Glu Ser Gly Val Leu Met Leu Met Ala
 115 120 125
 Leu Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr Ala Thr Thr
 130 135 140
 Leu Thr Asn Pro Ile Ile Ala Lys Ala Glu Leu Ala Thr Phe Leu Arg
 145 150 155 160
 Gly Val Leu Leu Met Ile Pro Phe Pro Phe Leu Val Lys Arg Leu Pro
 165 170 175
 Phe Cys Gln Ser Asn Ile Ile Ser His Thr Tyr Cys Asp His Met Ser
 180 185 190
 Val Val Lys Leu Ser Cys Ala Ser Ile Lys Val Asn Val Ile Tyr Gly
 195 200 205
 Leu Met Val Ala Leu Leu Ile Gly Val Phe Asp Ile Cys Cys Ile Ser
 210 215 220
 Leu Ser Tyr Thr Leu Ile Leu Lys Ala Ala Ile Ser Leu Ser Ser Ser
 225 230 235 240
 Asp Ala Arg Gln Lys Ala Phe Ser Thr Cys Thr Ala His Ile Ser Ala
 245 250 255
 Ile Ile Ile Thr Tyr Val Pro Ala Phe Phe Thr Phe Phe Ala His Arg
 260 265 270
 Phe Gly Gly His Thr Ile Pro Pro Ser Leu His Ile Ile Val Ala Asn
 275 280 285
 Leu Tyr Leu Leu Leu Pro Pro Thr Leu Asn Pro Ile Val Tyr Gly Val
 290 295 300
 Lys Thr Lys Gln Ile Arg Lys Ser Val Ile Lys Phe Phe Gln Gly Asp
 305 310 315 320
 Lys Gly Ala Gly

<210> 2266

<211> 312

<212> PRT

<213> Homo sapien (8516051-13-18887-21998)

<400> 2266

```

Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly
 1          5          10          15
Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu
 20          25          30
Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val
 35          40          45
Val Cys Leu Asp Ser Arg Leu His Thr Pro-Met Tyr His Phe Val Ser
 50          55          60
Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys
 65          70          75          80
Met Leu Ala Asn Leu Leu Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly
 85          90          95
Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys
 100         105         110
Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
 115         120         125
Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile
 130         135         140
Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile
 145         150         155         160
Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
 165         170         175
Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
 180         185         190
Ser Ile Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
 195         200         205
Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
 210         215         220
Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
 225         230         235         240
Cys Ala Ser His Phe Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
 245         250         255
Ser Met Tyr Val Gln Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
 260         265         270
Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
 275         280         285
Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Glu Ala Val Arg Arg Gln
 290         295         300
Leu Lys Arg Ile Gly Ile Leu Ala
 305         310

```

<210> 2267

<211> 289

<212> PRT

<213> Homo sapien (8516051-8-7333-8874)

<220>

<221> VARIANT

<222> (1)...(289)

<223> Xaa = Any Amino Acid

<400> 2267

```

Leu Leu Phe Phe Ile Leu Leu Leu Ile Tyr Leu Phe Thr Ile Ile
 1          5          10          15
Gly Ser Leu Met Val Phe Phe Ala Ile Lys Leu Asp Phe Cys Leu His
 20          25          30
Ser Ser Leu Tyr Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Trp
 35          40          45

```

Tyr Thr Thr Ile Thr Ile Pro Lys Met Phe Phe Asn Leu Ala Ser Glu
 50 55 60
 Gln Lys Thr Thr Ser Leu Asp Gly Cys Leu Leu Gln Met Tyr Phe Phe
 65 70 75 80
 Tyr Ser Leu Gly Ile Thr Glu Val Cys Leu Leu Thr Thr Arg Ala Met
 85 90 95
 Asp Arg Tyr Leu Ala Ile Cys Asn His Leu Cys Tyr Pro Thr Val Thr
 100 105 110
 Thr Pro Xaa Leu Tyr Thr Gln Val Ile Leu Gly Cys Cys Ile Cys Gly
 115 120 125
 Phe Phe Thr Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe
 130 135 140
 Cys Gly Pro Asn Gln Ile His Asn Ile Phe Cys Asp Leu Asp Pro Ile
 145 150 155 160
 Leu Asn Leu Ala Cys Val Asp Thr Gly Pro Val Val Leu Ile Lys Val
 165 170 175
 Val Asp Ile Val His Ala Val Glu Ile Ile Thr Ala Ile Met Leu Val
 180 185 190
 Thr Leu Ala Tyr Val Gln Ile Ile Ala Val Ile Leu Arg Asn Cys Ser
 195 200 205
 Ala Asp Gly Cys Gln Lys Ala Phe Ser Thr Tyr Ala Phe His Leu Ala
 210 215 220
 Ile Phe Leu Ile Phe Phe Gly Ser Val Ala Leu Met Tyr Leu Leu Phe
 225 230 235 240
 Ser Ala Lys Tyr Ser Phe Phe Trp Asp Thr Thr Ile Ser Leu Met Phe
 245 250 255
 Ala Val Leu Ser Pro Thr Pro Ile Ile Cys Ser Leu Arg Asn Lys Glu
 260 265 270
 Ile Lys Glu Ala Ile Lys Lys His Met Cys Gln Ser Met Ile Cys Thr
 275 280 285
 His

<210> 2268

<211> 166

<212> PRT

<213> Homo sapien (8516144-1-909-1747)

<220>

<221> VARIANT

<222> (1)...(166)

<223> Xaa = Any Amino Acid

<400> 2268

Met Tyr Thr Thr Leu Leu Met Ala Arg Leu Cys Leu Cys Ala Asp Asn
 1 5 10 15
 Val Ile Pro His Ser Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala
 20 25 30
 Leu Ser Asp Thr Arg Val Asn Glu Xaa Val Ile Phe Ile Met Gly Gly
 35 40 45
 Leu Ile Leu Val Ile Pro Ser Ile Leu Ile Leu Gly Ser Tyr Ala Arg
 50 55 60
 Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Cys Ile Cys Lys
 65 70 75 80
 Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
 85 90 95
 Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr
 100 105 110
 Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met
 115 120 125
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala

130 135 140
 Leu Ser Arg Val Ile His Gln Lys Lys Thr Phe Phe Ser Leu Xaa Xaa
 145 150 155 160
 Xaa His Leu Glu Leu Leu
 165

<210> 2269
 <211> 540
 <212> PRT
 <213> Homo sapien (8516144-24-10674-13726)

<220>
 <221> VARIANT
 <222> (1)...(540)
 <223> Xaa = Any Amino Acid

<400> 2269
 Met Asp Leu Gly Asn Ser Gly Asn Asp Ser Val Val Thr Lys Phe Val
 1 5 10 15
 Leu Leu Gly Leu Thr Glu Thr Ala Ala Leu Gln Pro Ile Leu Phe Val
 20 25 30
 Ile Phe Leu Leu Ala Tyr Val Thr Thr Ile Gly Gly Thr Leu Ser Ile
 35 40 45
 Leu Ala Ala Ile Leu Met Glu Thr Lys Leu His Ser Pro Met Tyr Phe
 50 55 60
 Phe Leu Gly Asn Leu Ser Leu Pro Asp Val Gly Cys Val Ser Val Thr
 65 70 75 80
 Val Pro Ala Met Leu Ser His Phe Ile Ser Asn Asp Arg Ser Ile Pro
 85 90 95
 Tyr Lys Ala Cys Leu Ser Glu Leu Phe Phe Phe His Leu Leu Ala Gly
 100 105 110
 Ala Asp Cys Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Leu Ala
 115 120 125
 Ile Cys Gln Ser Leu Thr Tyr Ser Ser Arg Met Ser Trp Gly Ile Gln
 130 135 140
 Gln Ala Leu Val Gly Met Ser Trp Val Phe Ser Phe Thr Asn Ala Leu
 145 150 155 160
 Thr Gln Thr Val Ala Leu Ser Pro Leu Asn Phe Cys Gly Pro Asn Val
 165 170 175
 Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Pro Phe Gln Leu Ser Cys
 180 185 190
 Ser Ser Val His Leu Asn Gly Gln Leu Leu Phe Val Ala Ala Ala Phe
 195 200 205
 Met Gly Val Ala Pro Leu Val Leu Ile Thr Val Ser Tyr Ala His Val
 210 215 220
 Ala Ala Ala Val Leu Arg Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
 245 250 255
 Thr Gly Val Phe Ser Tyr Thr Arg Leu Gly Ser Val Glu Ser Ser Asp
 260 265 270
 Lys Asp Lys Gly Ile Gly Ile Leu Asn Thr Val Ile Ser Pro Met Leu
 275 280 285
 Asn Pro Leu Ile Tyr Trp Thr Ser Leu Leu Asp Val Gly Cys Ile Ser
 290 295 300
 His Cys Ser Ser Asp Ala Gly Val Ser Pro Gly Pro Pro Val Gln Ser
 305 310 315 320
 Pro Tyr Ala Ala Cys Ser Ser Gln Leu Phe Phe Pro His Leu Leu Ala
 325 330 335
 Gly Val Asp Cys His Leu Leu Ile Ala Met Ala Tyr Asp Arg Tyr Leu
 340 345 350

Ala Ile Cys Gln Leu Leu Thr Asn Ser Thr Arg Met Ser Cys Glu Val
 355 360 365
 Gln Gly Ala Leu Val Gly Ile Cys Cys Thr Val Ser Phe Ile Asn Ala
 370 375 380
 Leu Thr His Thr Val Ala Val Ser Ala Leu Asp Phe Cys Gly Pro Asn
 385 390 395 400
 Val Val Asn His Phe Tyr Cys Asp Leu Pro Pro Leu Phe Gln Leu Ser
 405 410 415
 Cys Ser Ser Ile His Leu Asn Gly Gln Leu Leu Leu Val Gly Ala Thr
 420 425 430
 Phe Ile Gly Val Ile Pro Met Ile Phe Ile Ser Val Ser Tyr Ala His
 435 440 445
 Val Thr Ala Ala Ile Leu Gln Ile Arg Ser Ala Glu Gly Arg Lys Lys
 450 455 460
 Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Xaa Ile Phe Tyr
 465 470 475 480
 Gly Thr Gly Phe Phe Ser Tyr Met Cys Leu Gly Ser Val Ser Ala Ser
 485 490 495
 Asp Lys Asp Lys Gly Ile Gly Ile Leu Asn Thr Ile Leu Ser Pro Met
 500 505 510
 Leu Asn Pro Val Ile Tyr Ser Leu Gln Asn Pro Asp Val Gln Gly Thr
 515 520 525
 Leu Lys Arg Val Leu Thr Gly Lys Arg Pro Pro Ala
 530 535 540

<210> 2270
 <211> 106
 <212> PRT
 <213> Homo sapien (8518017-12-460-1010)

<220>
 <221> VARIANT
 <222> (1)...(106)
 <223> Xaa = Any Amino Acid

<400> 2270
 Gln Leu Leu Ile Leu Ala Cys Ser Glu Ser Ser Leu Asn Ser Leu Tyr
 1 5 10 15
 Ser Phe Ile His Ser Phe Phe Cys Ser Phe Leu Pro Asn Ser Gly Tyr
 20 25 30
 Leu Val Ser Gln Thr Asp Leu Val Pro Asp Leu Arg Glu Phe Arg Ile
 35 40 45
 Xaa Ser Arg Arg His Ile Arg Asn Trp Asn Val Met Gly Ala Met Ile
 50 55 60
 Leu Asn Val Cys Glu Ala Thr Gly Asn Gly Val Ala Leu Pro Ile Ser
 65 70 75 80
 Lys Ala Ala Thr Pro Glu Ala Met Thr Gly Val Xaa Ser Glu His Asp
 85 90 95
 Ile Ala Leu Leu Phe Trp Leu Leu Arg Leu
 100 105

<210> 2271
 <211> 223
 <212> PRT
 <213> Homo sapien (8546599-5-2194-2867)

<220>
 <221> VARIANT
 <222> (1)...(223)
 <223> Xaa = Any Amino Acid

<400> 2271

```

Val Arg His Pro Leu Arg Cys Gly Lys Xaa Glu Pro Ala Pro Leu Pro
 1           5           10           15
Pro Leu Ala Leu Arg Asn Pro Ile Met Thr Ser Cys Phe Cys Gly Phe
          20           25           30
Leu Val Leu Phe Phe Phe Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln
          35           40           45
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp Ala Glu
          50           55           60
Ile Pro Ser Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
65           70           75           80
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Leu Pro Ala Ala Ile
          85           90           95
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
          100          105          110
Val Ser Ser Ile Leu Arg Val Ser Ser Arg Gly Lys Tyr Lys Ala
          115          120          125
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
          130          135          140
Thr Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
145          150          155          160
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Ser Met Leu
          165          170          175
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu
          180          185          190
Arg Gln Pro His Gly Ser Thr Val Gln Phe Gln Tyr Leu Leu Ile Cys
          195          200          205
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
          210          215          220

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<210> 2272

<211> 120

<212> PRT

<213> Homo sapien (8546616-1-110163-110999)

<220>

<221> VARIANT

<222> (1)...(120)

<223> Xaa = Any Amino Acid

<400> 2272

```

Val Cys Ile Asn Ile Ser Xaa His His Xaa His Met Tyr Phe Xaa Leu
 1           5           10           15
Ser Tyr Gly Ser Phe Xaa Glu Leu Leu Val His Ser Ala Glu Leu Pro
          20           25           30
Ser Arg Ile Trp Arg Leu Lys Ser Ser Xaa Ser Cys Lys Ile Leu Ser
          35           40           45
Gly Tyr Ser Asn Glu Val Trp Phe His Cys Ile Phe Leu Cys Leu Leu
          50           55           60
Ser Lys Arg Leu Lys Xaa Ala His Ser Asp Lys Cys Gly Gln Val Ser
65           70           75           80
Leu Pro Leu His Pro Ser Leu Cys Leu Leu Leu Ser Leu Gly Asn Trp
          85           90           95
Cys Gly Lys Ser Leu Cys Pro Gly Met Ala Thr Leu Leu Val Ser Arg
          100          105          110
Leu Ile Gln Ser Ser Leu Cys Ser
          115          120

```

<210> 2273

<211> 260

<212> PRT

<213> Homo sapien (8547576-2-9950-11981)

<220>

<221> VARIANT

<222> (1)...(260)

<223> Xaa = Any Amino Acid

<400> 2273

```

Val Leu Cys Val Ile Phe Cys Lys Xaa Asn His His Ile Ser Leu Leu
 1           5           10           15
Ser Phe Phe Glu Tyr Leu Met Thr Xaa Xaa Lys Lys Tyr Gly Ser Ile
      20           25           30
Cys Ser Thr Met Leu Val Ser Ile Arg Ile Lys Tyr Leu Glu Val Phe
      35           40           45
Ala Glu Asn Leu Phe Gly Ala Ala Glu Ile Ile Pro Leu Met Trp Met
 50           55           60
Val His Gly Cys Tyr Val Thr Val Cys Asn Tyr Met Thr Ile Val Asn
 65           70           75           80
Gln Tyr Arg Cys Ser His Leu Thr Gly Met Ala Trp Thr Glu Ser Phe
      85           90           95
Ile His Gly Thr Val Xaa Ile Leu Ser Pro Val Xaa Leu Pro Phe Tyr
      100          105          110
Asp Pro Asn Val Ile Ala His Phe Met Cys Asp Leu Asn Thr Phe Leu
      115          120          125
Lys Leu Leu Cys Met Gly Thr Thr Asn Thr Ile Gly Phe Phe Val Ala
      130          135          140
Ala Asn Gly Gly Phe Asn Tyr Leu Leu Asn Ile Ile Phe Leu Met Val
      145          150          155          160
Ser Xaa Val Ala Ile Leu Cys Thr Leu Lys Thr His Ser Leu Glu Glu
      165          170          175
Arg Cys Xaa Ser Leu Ser Thr Cys Ile Ser His Thr Thr Met Val Ile
      180          185          190
Leu Phe Phe Glu Phe Cys Ile Ser Val Tyr Leu Cys Pro Val Thr Leu
      195          200          205
Leu Pro Ile Asn Lys Ala Met Ala Val Phe His Thr Val Ile Asn Pro
      210          215          220
Met Leu Lys Pro Leu Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser
      225          230          235          240
Ala Leu Arg Lys Val Trp Val Lys Arg Xaa Pro Glu Glu Arg Asn Asn
      245          250          255
Leu Asn Ile Arg
      260

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<210> 2274

<211> 328

<212> PRT

<213> Homo sapien (8567470-5-1-1337)

<220>

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 2274

```

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu
 1           5           10           15
Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys
      20           25           30
Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala
      35           40           45
Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys

```

50	55	60
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys		
65	70	75
Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly		80
	85	90
Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu		95
	100	105
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys		110
	115	120
His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe		125
	130	135
Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln Leu		140
145	150	155
Gln Asn Leu Ile Ala Leu Gln Ile Thr Cys Ser Lys Asp Val Glu Ile		160
	165	170
Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys		175
	180	185
Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe		190
	195	200
Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val		205
	210	215
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Ser Tyr Lys Ala Phe		220
225	230	235
Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr		240
	245	250
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys		255
	260	265
Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn		270
	275	280
Pro Leu Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu Trp		285
	290	295
Gln Pro Cys Ser Arg Thr Ala Ala Gln Ser Pro Ser Gln Tyr Leu His		300
305	310	315
Leu Phe His Ser Phe Cys Arg Met		320
	325	

<210> 2275
 <211> 310
 <212> PRT
 <213> Homo sapien (8567878-9-2833-5012)

<220>
 <221> VARIANT
 <222> (1)...(310)
 <223> Xaa = Any Amino Acid

<400> 2275

Met Ala Lys Thr Asn Asn Ser Glu Val Thr Glu Phe Ile Leu Leu Gly		
1	5	10
Leu Thr Asp Asn Pro Glu Leu Gln Ala Leu Phe Trp Gly Ile Phe Leu		15
	20	25
Val Ile Asn Leu Ser Ser Val Met Gly Ser Leu Gly Leu Ile Met Leu		30
	35	40
Ile His Ile Ser Pro Gln Leu His Thr Ala Met Tyr Phe Phe Leu Ser		45
	50	55
His Val Ala Phe Val Tyr Phe Cys Tyr Thr Ser Ile Thr Pro Asn		60
65	70	75
Ser Leu Val Asn Leu Leu Gln Glu Thr Lys Arg Ile Ser Leu Pro Thr		80
	85	90
Cys Ala Ser Gln Leu His Cys Phe Ile Met Phe Val Val Cys Asp Met		95
	100	105
		110

Tyr Val Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Ile Ile Met Asn Arg Arg Val Cys Ile Gln Met
 130 135 140
 Val Val Ser Thr Tyr Leu Tyr Gly Phe Ser Val Arg Leu Leu Gln Ala
 145 150 155 160
 Ile Leu Thr Phe His Leu Ser Phe Xaa Asp Ser Asn Ile Ile Asn Asn
 165 170 175
 Ser Tyr Cys Asp Asp Val Pro Leu Ala Cys Leu Pro Tyr His Lys Asn
 180 185 190
 His Tyr Lys Asp Val Lys Glu Leu Ile Leu Phe Thr Leu Ala Gly Phe
 195 200 205
 Asn Thr Leu Phe Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile Ser Val
 210 215 220
 Leu Ser Ala Ile Leu Arg Ile Asn Ser Ala Glu Ser Arg Gln Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Asp Ser His Leu Thr Ser Ile Ile Phe Tyr Gly
 245 250 255
 Ile Ile Thr Phe Met Tyr Met Gln Xaa Lys Thr Asn Asn Ser Leu Asp
 260 265 270
 Thr Asp Lys Ile Ala Ser Val Phe Cys Ile Val Lys Ile Pro Ser Ile
 275 280 285
 Tyr Ser Leu Arg Asn His Glu Val Lys Asp Ala Leu Lys Met Ile Met
 290 295 300
 Glu Asn Leu Cys Leu Thr
 305 310

<210> 2276

<211> 358

<212> PRT

<213> Homo sapien (8567902-2-5416-6914)

<220>

<221> VARIANT

<222> (1)...(358)

<223> Xaa = Any Amino Acid

<400> 2276

Val Ser Met Ser Phe Leu Ile Arg Ser Asp Ser Thr Leu His Thr Pro
 1 5 10 15
 Met Cys Leu Phe Leu Ser His Leu Ser Phe Val Asp Leu Tyr Tyr Ala
 20 25 30
 Thr Asn Ala Thr Pro Pro Met Leu Val Asn Phe Val Phe Ser Lys Arg
 35 40 45
 Lys Thr Val Ser Phe Ile Gly Cys Phe Ile Gln Phe His Leu Phe Ile
 50 55 60
 Ala Leu Val Ile Thr Asp Tyr His Met Leu Thr Val Met Val Tyr Asp
 65 70 75 80
 His Tyr Met Ala Ile Cys Lys Pro Leu Leu Tyr Gly Ser Lys Met Ser
 85 90 95
 Arg Cys Val Cys Leu Cys Leu Thr Ala Ala Pro Tyr Ile Tyr Gly Ser
 100 105 110
 Ala Asn Gly Leu Val Gln Val Ile Leu Met Leu Cys Leu Phe Phe Cys
 115 120 125
 Glu Pro His Glu Ile Asn His Phe Phe Phe Phe Gly Glu Asn Ala Leu
 130 135 140
 Tyr Ala His Leu Ile Pro Leu Xaa Ile Phe Glu Trp Thr Val Gly Glu
 145 150 155 160
 Glu Gly Arg Asn Asn Ile Asn Gly Glu Asn Thr Thr Gln Lys Val Tyr
 165 170 175
 Thr Met Gly Glu Arg Asn Leu Leu Ile Gln Val Ser Ile Phe Leu Leu

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      180      185      190
Trp His Ile Arg Ser Xaa Leu Phe Ser Gln Tyr Glu Ala Ser Pro Arg
      195      200      205
Ala Asp Ser Asp Val Lys Leu Glu Ile Asn His Phe Tyr Tyr Ala Glu
      210      215      220
Pro Pro Leu Leu Val Leu Ala Cys Leu Asp Thr Tyr Val Lys Glu Thr
      225      230      235      240
Ala Met Phe Met Val Ala Gly Ser Asn Leu Ile Cys Pro Leu Thr Ile
      245      250      255
Ile Phe Ile Ser Tyr Thr Phe Ile Phe Thr Asp Ile Leu His Ile Cys
      260      265      270
Thr Ala Glu Gly Arg Tyr Asn Ala Phe Ser Thr Cys Gly Ser Leu Val
      275      280      285
Thr Ala Val Thr Val Phe Gln Gly Thr Leu Phe His Met Cys Leu Arg
      290      295      300
Pro Pro Ser Glu Ala Ser Val Glu Gln Gly Lys Ile Val Ala Ala Phe
      305      310      315      320
Tyr Ile Phe Val Ser Pro Thr Leu Asn Pro Leu Ile Tyr Arg Leu Arg
      325      330      335
Asn Lys Asn Val Lys Arg Thr Ile Arg Glu Val Ile Gln Lys Lys Leu
      340      345      350
Phe Ala Lys Xaa Gly Arg
      355

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<210> 2277

<211> 305

<212> PRT

<213> Homo sapien (8567902-4-4497-6890)

<400> 2277

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Met Ser Asn Thr Asn Gly Ser Ala Ile Thr Glu Phe Ile Leu Leu Gly
  1      5      10      15
Leu Thr Asp Cys Pro Glu Leu Gln Ser Leu Leu Phe Val Leu Phe Leu
      20      25      30
Val Val Tyr Leu Val Thr Leu Leu Gly Asn Leu Gly Met Ile Met Leu
      35      40      45
Met Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50      55      60
Asn Leu Ala Phe Val Asp Leu Cys Tyr Thr Ser Asn Ala Thr Pro Gln
      65      70      75      80
Met Ser Thr Asn Ile Val Ser Glu Lys Thr Ile Ser Phe Ala Gly Cys
      85      90      95
Phe Thr Gln Cys Tyr Ile Phe Ile Ala Leu Leu Leu Thr Glu Phe Tyr
      100      105      110
Met Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr Asp Pro
      115      120      125
Leu Arg Tyr Ser Val Lys Thr Ser Arg Arg Val Cys Ile Cys Leu Ala
      130      135      140
Thr Phe Pro Tyr Val Tyr Gly Phe Ser Asp Gly Leu Phe Gln Ala Ile
      145      150      155      160
Leu Thr Phe Arg Leu Thr Phe Cys Arg Ser Ser Val Ile Asn His Phe
      165      170      175
Tyr Cys Ala Asp Pro Pro Leu Ile Lys Leu Ser Cys Ser Asp Thr Tyr
      180      185      190
Val Lys Glu His Ala Met Phe Ile Ser Ala Gly Phe Asn Leu Ser Ser
      195      200      205
Ser Leu Thr Ile Val Leu Val Ser Tyr Ala Phe Ile Leu Ala Ala Ile
      210      215      220
Leu Arg Ile Lys Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr Cys
      225      230      235      240
Gly Ser His Met Met Ala Val Thr Leu Phe Tyr Gly Thr Leu Phe Cys

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245 250 255
 Met Tyr Ile Arg Pro Pro Thr Asp Lys Thr Val Glu Glu Ser Lys Ile
 260 265 270
 Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Val Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Leu Lys Asn Val Leu
 290 295 300
 Arg
 305

<210> 2278

<211> 319

<212> PRT

<213> Homo sapien (8567954-21-10804-13693)

<220>

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 2278

Met Gly Val His Asn Leu Phe Thr Val Thr Gln Phe Ile Leu Ile Gly
 1 5 10 15
 Leu Ser Tyr Phe Ser Asn Glu His Tyr Leu Leu Phe Val Ala Leu Ala
 20 25 30
 Ile Ile Cys Gln Val Phe Leu Val Arg Ser Gly Asp Ile Leu Leu Ala
 35 40 45
 Ile Gly Thr Val Ile Lys Leu His Thr Thr Met Tyr Tyr Phe Leu Ala
 50 55 60
 Asn Val Ser Ile Leu Asp Ile Leu Cys Ser Ser Ala Thr Ile Pro Lys
 65 70 75 80
 Met Pro Lys Ile Leu Xaa Thr Glu Asp His Ser Ile Ser Phe Val Arg
 85 90 95
 Xaa Ala Leu Gln Pro Tyr Phe Leu Val Ala Trp Ala Gly Lys Lys Cys
 100 105 110
 Phe Leu Thr Val Thr Ala Tyr Asp Trp Cys Val Val Thr Cys Phe Ser
 115 120 125
 Leu Cys Tyr Ile Leu Ile Met Asn Lys Leu Val Ser Val Gln Leu Val
 130 135 140
 Tyr Gly Thr Xaa Ala Ala Gly Phe Leu Asn Phe Leu Leu Leu His Val
 145 150 155 160
 Val Ser Thr Leu Cys Leu Ser Phe Cys Lys Pro Asp Arg Val Asn Gln
 165 170 175
 Tyr Tyr Cys Asp Ile Ser Pro Met Gly Ala Leu Leu Cys Gln Ser Met
 180 185 190
 His Leu Ala Asn Met Leu Val Leu Val Glu Ser Val Ile Leu Gly Ile
 195 200 205
 Ser Ala Phe Leu Ala Ala Phe Asn Phe Tyr Ile Tyr Ile Ile Ser Thr
 210 215 220
 Ile Leu Lys Ile Gln Cys Val Glu Trp Ser Ala Lys Cys Phe Ser Thr
 225 230 235 240
 Cys Thr Ser His Leu Leu Thr Val Cys Leu Phe Tyr Gly Ile Leu Thr
 245 250 255
 Phe Thr Tyr Ile Tyr Ser Phe Ser Ser His Thr His Met Ser Lys Ala
 260 265 270
 Ser Pro Asp Leu Ala Thr Asp Arg Leu Ile Ser Met Leu Tyr Arg Val
 275 280 285
 Ile Thr Leu Met Phe Asn Phe Ile Thr Asp Asn Leu Arg Asn Thr Glu
 290 295 300
 Val Lys Gly Ala Ser Glu Arg Phe Tyr Val Ile Glu His Val Tyr
 305 310 315

<210> 2279
 <211> 307
 <212> PRT
 <213> Homo sapien (8567954-21-4824-8043)

<400> 2279
 Met Asn His Ser Val Val Thr Glu Phe Ile Ile Leu Gly Leu Thr Lys
 1 5 10 15
 Lys Pro Glu Leu Gln Gly Ile Ile Phe Leu Phe Phe Leu Ile Val Tyr
 20 25 30
 Leu Val Ala Phe Leu Gly Asn Met Leu Ile Ile Ile Ala Lys Ile Tyr
 35 40 45
 Asn Asn Thr Leu His Thr Pro Met Tyr Val Phe Leu Leu Thr Leu Ala
 50 55 60
 Val Val Asp Ile Ile Cys Thr Thr Ser Ile Ile Pro Lys Met Leu Gly
 65 70 75 80
 Thr Met Leu Thr Ser Glu Asn Thr Ile Ser Tyr Ala Gly Cys Met Ser
 85 90 95
 Gln Leu Phe Leu Phe Thr Trp Ser Leu Gly Ala Glu Met Val Leu Phe
 100 105 110
 Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 115 120 125
 Tyr Ser Thr Val Met Asn His His Met Cys Val Ala Leu Leu Ser Met
 130 135 140
 Val Met Ala Ile Ala Val Thr Asn Ser Trp Val His Thr Ala Leu Ile
 145 150 155 160
 Met Arg Leu Thr Phe Cys Gly Pro Asn Thr Ile Asp His Phe Phe Cys
 165 170 175
 Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Pro Val Arg Ile Asn
 180 185 190
 Glu Val Met Val Tyr Val Ala Asp Ile Thr Leu Ala Ile Gly Asp Phe
 195 200 205
 Ile Leu Thr Cys Ile Ser Tyr Gly Phe Ile Ile Val Ala Ile Leu Arg
 210 215 220
 Ile Arg Thr Val Glu Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser
 225 230 235 240
 His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val Ile Tyr Thr Tyr
 245 250 255
 Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp Lys Val Val Ala
 260 265 270
 Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro Met Val Tyr Ser
 275 280 285
 Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys Val Phe Ala Phe
 290 295 300
 Leu Lys His
 305

<210> 2280
 <211> 104
 <212> PRT
 <213> Homo sapien (8568141-22-12851-13662)

<220>
 <221> VARIANT
 <222> (1)...(104)
 <223> Xaa = Any Amino Acid

<400> 2280
 Leu Pro Pro Asn Ile Leu Cys Val Ile Ile Ser Tyr Ser Arg His Phe
 1 5 10 15

Ser Lys Leu Leu Lys Ile Pro Asn Ile Arg Thr Gln Ile Gln Lys Phe
 20 25 30
 Ser His Ile Ser Xaa Asn Leu Lys Lys Val Ser Val Leu Arg Leu Thr
 35 40 45
 Trp Thr Arg Tyr Pro Ser Xaa Met Leu Pro Xaa Tyr Pro Ala Pro Thr
 50 55 60
 Leu Thr Lys His Ile Pro Cys Gly Leu Val Thr Cys Leu Leu Gln Pro
 65 70 75 80
 Arg Met Ser Cys Trp Arg Ala Arg Asn Ala Pro Ser Thr Cys Leu Ala
 85 90 95
 Leu Thr Ala Lys His Ile Ser Ala
 100

<210> 2281

<211> 333

<212> PRT

<213> Homo sapien (8568143-10-1394-2684)

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 2281

Met Gly Pro Lys Asn Leu Thr Arg Val Leu Glu Phe Phe Leu Leu His
 1 5 10 15
 Phe Leu Asp Asp Leu Glu Leu Gln Pro Phe Leu Ser Gly Cys Pro Xaa
 20 25 30
 Thr Met His Leu Val Thr Val Leu Ala Asn Leu Leu Thr Ser Phe Xaa
 35 40 45
 Leu Ser Ala Leu Pro His Leu His Asn Pro Met Asn Phe Asn Leu Ser
 50 55 60
 Leu Ala Asp Ile Gly Phe Thr Pro Ala Thr Ile Ser Lys Ile Thr Val
 65 70 75 80
 Asp Leu Gln Thr His Ser Arg Ile Ile Leu Tyr Met Ser Cys Leu Lys
 85 90 95
 Xaa Met Ser Phe Lys Ile Ile Phe Gly Cys Leu His Asn Leu Leu Ile
 100 105 110
 Thr Val Met Ala Tyr Asp Pro Phe Val Ala Thr Cys His Leu Leu Tyr
 115 120 125
 Tyr Thr Val Ile Arg Asn Pro His Leu Cys Gly Leu Leu Leu Val
 130 135 140
 Ser Leu Phe Ser Leu Ser Phe Phe Phe Leu Ile Ser Leu Leu Glu Thr
 145 150 155 160
 Gln Leu Tyr Ser Leu Met Val Ser Gln Val Leu Cys Met Gln Asp Val
 165 170 175
 Asp Ile Pro His Phe Phe Cys Asp Pro Ser Gln Phe Leu His Leu Ser
 180 185 190
 Cys Ser Asp Thr Ala Thr Asn Asn Thr Leu Met His Phe Ile Gly Ala
 195 200 205
 Ile Phe Cys Gly Pro Phe Ser Gly Ile Leu Tyr Cys Tyr Thr Gln Ile
 210 215 220
 Met Phe Ser Ile Leu Ile Thr Leu Xaa Asn Val Gly Ser Ile Lys Gln
 225 230 235 240
 Thr Phe Ser Thr His Arg Ser His Leu Ser Val Val Cys Leu Phe Tyr
 245 250 255
 Gly Thr Gly Leu Gly Val Tyr Leu Ser Leu Ala Gly Ser Pro Ser Pro
 260 265 270
 Arg Thr Gly Val Val Ala Ser Met Val Tyr Thr Thr Val Thr Leu Met
 275 280 285
 Leu Asn Pro Val Ile His Ser Leu Arg Asn Arg Asp Ile Lys Asn Thr

290 295 300
 Trp Trp Trp Leu Leu Ser Ile Thr Ala Trp Tyr Gln Tyr Leu Cys Tyr
 305 310 315 320
 Pro Leu Trp Ser Val Val Arg Lys Asn Ser Lys Leu Lys
 325 330

<210> 2282
 <211> 157
 <212> PRT
 <213> Homo sapien (8568247-23-1134-2556)

<220>
 <221> VARIANT
 <222> (1)...(157)
 <223> Xaa = Any Amino Acid

<400> 2282
 Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
 1 5 10 15
 Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
 20 25 30
 Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
 35 40 45
 Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
 50 55 60
 Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu
 65 70 75 80
 Cys Thr Cys Leu Asp Thr Phe Thr Lys Ser Tyr Ile Thr Xaa Ile Arg
 85 90 95
 Gly Leu Lys Gly Phe Asn His Leu Cys Phe Leu Leu His Tyr Cys His
 100 105 110
 Cys Ala Arg Ala Gln Val Ser Xaa Asn Ala Pro Trp Ser Leu Ala Gln
 115 120 125
 Arg Cys Gln Pro Asn Met Leu Ile Arg Xaa Leu Phe Cys Leu Lys Leu
 130 135 140
 Val Val His Asp Arg Leu Xaa His Val Leu Ser Leu Leu
 145 150 155

<210> 2283
 <211> 91
 <212> PRT
 <213> Homo sapien (8568259-4-1499-2114)

<220>
 <221> VARIANT
 <222> (1)...(91)
 <223> Xaa = Any Amino Acid

<400> 2283
 Gln Glu Ile Ser Ala Ala Arg Glu Arg Lys Ala Thr Lys Ile Leu Gly
 1 5 10 15
 Ile Ile Leu Gly Ala Phe Ile Ile Cys Trp Leu Pro Phe Phe Val Val
 20 25 30
 Ser Leu Val Leu Pro Ile Cys Arg Asp Ser Cys Trp Ile His Pro Ala
 35 40 45
 Leu Phe Asp Phe Phe Thr Trp Leu Gly Tyr Leu Asn Ser Leu Ile Asn
 50 55 60
 Pro Ile Ile Tyr Thr Val Phe Asn Glu Glu Phe Arg Gln Ala Phe Gln
 65 70 75 80
 Lys Ile Val Pro Phe Arg Lys Ala Ser Xaa Ser
 85 90

<210> 2284
 <211> 320
 <212> PRT
 <213> Homo sapien (8569904-8-5520-7957)

<400> 2284

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Met Asp Ser Pro Ser Asn Ala Thr Val Pro Cys Gly Phe Leu Leu Gln
 1              5              10              15
Gly Phe Ser Glu Phe Pro His Leu Arg Pro Val Leu Phe Leu Leu
 20              25              30
Leu Gly Val His Leu Ala Thr Leu Gly Gly Asn Leu Leu Ile Leu Val
 35              40              45
Ala Val Ala Ser Met Pro Ser Arg Gln Pro Met Leu Leu Phe Leu Cys
 50              55              60
Gln Leu Ser Ala Ile Glu Leu Cys Tyr Thr Leu Val Val Val Pro Arg
 65              70              75              80
Ser Leu Val Asp Leu Ser Ser Arg Gly His Arg Arg Gly Ser Pro Ile
 85              90              95
Ser Phe Leu Ser Cys Ala Phe Gln Met Gln Met Phe Val Ala Leu Gly
 100             105             110
Gly Ala Glu Cys Phe Leu Leu Ala Ala Met Ala Asn Asp Arg Tyr Val
 115             120             125
Ala Ile Cys His Pro Leu Arg Tyr Arg Ala Val Val Thr Pro Gly Leu
 130             135             140
Cys Ala Arg Leu Val Ser Gly Cys Cys Leu Arg Gly Leu Ala Val Ser
 145             150             155             160
Leu Gly Leu Thr Val Leu Ile Phe His Leu Pro Phe Cys Gly Ser Arg
 165             170             175
Leu Leu Leu His Phe Phe Cys Asp Ile Thr Ala Leu Leu His Leu Ala
 180             185             190
Cys Thr Arg Thr Thr Pro His Glu Leu Pro Leu Leu Gly Ala Cys Leu
 195             200             205
Val Leu Leu Leu Leu Pro Ser Val Leu Ile Leu Ala Ser Tyr Gly Ala
 210             215             220
Ile Ala Ala Ala Leu Val Arg Leu Arg Cys Pro Lys Gly Arg Gly Lys
 225             230             235             240
Ala Ala Ser Thr Cys Ala Leu His Leu Ala Val Thr Phe Leu His Tyr
 245             250             255
Gly Cys Ala Thr Phe Met Tyr Val Arg Pro Arg Ala Ser Tyr Ser Pro
 260             265             270
Arg Leu Asp Arg Thr Leu Ala Leu Val Tyr Thr Asn Val Thr Pro Leu
 275             280             285
Leu Cys Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Ile Thr Ala Ala
 290             295             300
Leu Ser Arg Val Leu Gly Arg Arg Arg Pro Gly Gln Ala Pro Gly Gly
 305             310             315             320

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<210> 2285
 <211> 130
 <212> PRT
 <213> Homo sapien (8569934-12-21632-22280)

<220>
 <221> VARIANT
 <222> (1)...(130)
 <223> Xaa = Any Amino Acid

<400> 2285

```

Lys Val Cys Leu Phe Gln Ala Leu Met Cys Trp Leu Ser Leu Xaa Gln
 1              5              10              15

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Gln Pro Phe Thr Gln Ser Ala Ser Thr Leu Leu Leu Pro Leu Cys Ile
 20 25 30
 Pro Arg Gln Ala Pro Gln Cys Pro Gly Asp Leu Arg Thr Ala Leu Arg
 35 40 45
 Ala Val Met Cys Thr Arg Gly Cys Val Phe Xaa Ala Trp Glu Trp Val
 50 55 60
 Ala Ser Tyr Ile His Leu Ile Pro Leu Cys Ile Pro Val Arg Ser Ala
 65 70 75 80
 Tyr Asn Leu Gly Arg Val Leu Asn Gly Val Lys Trp Cys Ser Xaa Gly
 85 90 95
 Gln Gln Val Glu Phe Cys Ser Cys Lys Ala Lys Leu Met Leu Leu Ala
 100 105 110
 Ser Val Asp Val Val Leu Val Ser Thr Gln Pro Xaa Asn Pro Arg Pro
 115 120 125
 His Glu
 130

<210> 2286

<211> 318

<212> PRT

<213> Homo sapien (8569993-13-6018-8083)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2286

Ile Ser Thr Met Ser Val Phe Lys Ser Ser Ala Xaa Asn Pro Arg Phe
 1 5 10 15
 Leu Gln Thr Gly Leu Ser Gly Leu Glu Ser Arg Tyr Asp Leu Ile Ser
 20 25 30
 Leu Pro Ile Phe Leu Val Tyr Ala Thr Ser Ile Ala Gly Asn Ile Ser
 35 40 45
 Ile Leu Phe Ile Ile Arg Thr Glu Ser Ser Leu His Gln Pro Met Tyr
 50 55 60
 Tyr Phe Leu Ser Met Leu Ala Phe Thr Asp Leu Gly Leu Ser Asn Thr
 65 70 75 80
 Thr Leu Pro Thr Met Phe Ser Val Phe Trp Phe His Ala Arg Glu Ile
 85 90 95
 Ser Phe Asn Ala Cys Leu Val Gln Met Tyr Phe Ile His Val Phe Ser
 100 105 110
 Ile Ile Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Cys Phe Ile
 115 120 125
 Ala Ile Xaa Glu Pro Leu Arg Tyr Ala Ala Ile Leu Thr Asn Asp Val
 130 135 140
 Ile Ile Gly Ile Gly Leu Ala Ile Ala Gly Arg Ala Leu Ala Leu Val
 145 150 155 160
 Phe Pro Ala Ser Phe Leu Leu Lys Arg Leu Gln Tyr His Asp Val Asn
 165 170 175
 Ile Leu Ser Tyr Leu Phe Cys Leu His Gln Asp Leu Ile Lys Thr Thr
 180 185 190
 Val Ser Asn Cys Arg Val Ser Ser Ile Tyr Gly Leu Met Val Val Ile
 195 200 205
 Cys Ser Met Gly Leu Asp Ser Val Leu Leu Leu Leu Ser Tyr Val Leu
 210 215 220
 Ile Leu Gly Thr Ala Leu Ser Ile Ala Ser Lys Ala Glu Arg Val Arg
 225 230 235 240
 Ala Leu Asn Thr Cys Ile Ser His Ile Cys Ala Val Leu Thr Phe Tyr
 245 250 255
 Thr Pro Met Ile Gly Leu Ser Met Ile His Arg Tyr Gly Gln Asn Ala

260	265	270
Pro His Ile Val His Val Leu Met Ala Asn Val Tyr Leu Met Gly Pro		
275	280	285
Pro Leu Met Asn Pro Val Phe Tyr Ser Val Lys Thr Arg Gln Ile Arg		
290	295	300
Asp Arg Ile Phe Gln Ile Lys Phe Arg Asn Met Lys Cys Arg		
305	310	315

<210> 2287
 <211> 235
 <212> PRT
 <213> Homo sapien (8570235-22-3034-4808)

<220>
 <221> VARIANT
 <222> (1)...(235)
 <223> Xaa = Any Amino Acid

<400> 2287

Met Leu Phe Ile Ser Gln Trp Gly Glu Arg Xaa Arg Val Arg Arg Asn		
1	5	10
Val Gln Leu Met Thr Ala Phe Ile Leu Met Asp Leu Pro His Val Pro		
20	25	30
Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val Tyr Val Leu		
35	40	45
Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg Val Tyr Ser		
50	55	60
His Leu His Thr Pro Lys Tyr Tyr Phe Leu Thr Asn Leu Ser Phe Ile		
65	70	75
Asp Leu Trp Phe Phe Thr Val Met Val Pro Lys Met Pro Arg Thr Leu		
85	90	95
Leu Ser Leu Cys Gly Lys Ala Val Ser Phe His Ser Cys Met Thr Gln		
100	105	110
Leu Tyr Phe Phe Tyr Phe Leu Gly Ser Thr Glu Cys Leu Leu Tyr Thr		
115	120	125
Val Met Ser Tyr Asp Arg Tyr Arg Gly Asn Thr Gln His Phe Pro Gly		
130	135	140
Ser Glu Asn Leu Pro Thr Lys Xaa Ala Lys Cys Xaa Trp Pro Gly Gly		
145	150	155
His Thr Gly Xaa Pro Leu Ile Ile Leu Ala Asp Leu Ser Gly Xaa Leu		
165	170	175
Arg Val Asp Ser Ser Xaa Trp Ala Ile Gln Asn Xaa Xaa Tyr Asn Leu		
180	185	190
Val Ile Gln Val Lys Phe Ile Thr Cys Ile Gly Leu Ser Ile Lys His		
195	200	205
Tyr Ser Lys Gln Leu Ala Gln Leu Xaa Phe Phe His Arg Leu Ser Lys		
210	215	220
Thr Phe Leu Asn Ser Gln Leu Asp Phe Tyr Leu		
225	230	235

<210> 2288
 <211> 325
 <212> PRT
 <213> Homo sapien (8570522-1-103735-108559)

<220>
 <221> VARIANT
 <222> (1)...(325)
 <223> Xaa = Any Amino Acid

<400> 2288

```

Met Lys Ile Asn Gln Thr Ile Leu Lys Glu Phe Ile Leu Val Gly Phe
 1          5          10          15
Ser Val Tyr Pro His Val Gln Thr Phe Leu Phe Val Val Phe Phe Cys
          20          25          30
Leu Tyr Leu Leu Thr Leu Ala Gly Asn Leu Thr Ile Met Gly Leu Thr
          35          40          45
Xaa Val Asp Arg Ser Leu His Thr Pro Met Tyr Leu Phe Leu Ser Ala
          50          55          60
Leu Ser Phe Ser Glu Thr Cys Tyr Thr Leu Thr Ile Val Pro Lys Met
65          70          75          80
Leu Glu Asp Leu Leu Ala Lys Asp Arg Ser Ile Ser Val Thr Gly Cys
          85          90          95
Ser Leu Gln Met Cys Phe Phe Leu Gly Leu Gly Gly Thr Asn Cys Ile
          100          105          110
Ile Leu Thr Leu Met Gly Tyr Asp Arg Phe Leu Ala Ile Cys Asn Pro
          115          120          125
Leu Arg Tyr Pro Leu Leu Met Thr Asn Ile Val Cys Gly Gln Leu Val
          130          135          140
Ala Ser Ala Cys Thr Ala Gly Phe Phe Ile Ser Leu Thr Glu Thr Ala
145          150          155          160
Leu Ile Phe Arg Asp Ser Phe Cys Arg Pro Asn Leu Val Lys His Phe
          165          170          175
Phe Cys His Met Leu Ala Val Ile Arg Leu Ser Cys Ile Asp Ser Asn
          180          185          190
His Thr Glu Phe Ile Ile Thr Leu Ile Ser Val Ser Gly Leu Leu Gly
          195          200          205
Thr Leu Leu Leu Ile Ile Leu Thr Asp Val Phe Ile Ile Ser Thr Val
          210          215          220
Leu Arg Ile Pro Ser Ala Glu Gly Lys Gln Lys Ala Phe Thr Thr Cys
225          230          235          240
Ala Ser His Leu Thr Val Val Ile Ile His Phe Gly Phe Ala Ser Ile
          245          250          255
Val Tyr Leu Lys Pro Glu Ala Ser Gly Asp Asp Thr Leu Ile Ala Val
          260          265          270
Pro Tyr Thr Val Ile Thr Pro Phe Leu Ser Pro Ile Ile Phe Ser Leu
          275          280          285
Arg Asn Lys Asp Met Lys Asn Ala Phe Arg Arg Met Met Gly Asn Thr
          290          295          300
Val Ala Leu Lys Lys Xaa Ile Leu Gly Cys Cys Cys Leu Phe Glu Glu
305          310          315          320
Gly Leu Asn Val Pro
          325

```

<210> 2289

<211> 151

<212> PRT

<213> Homo sapien (8570523-1-20584-21124)

<220>

<221> VARIANT

<222> (1)...(151)

<223> Xaa = Any Amino Acid

<400> 2289

```

Cys Val Ser Xaa Gln Arg Ser Pro His Phe Leu Cys Ser Gly Asp Ser
 1          5          10          15
Val Phe Cys Leu Val His Ser Val Gly Cys Cys Thr Leu Leu Ser
          20          25          30
Gln Ser Leu Arg Leu Leu Ser Val Phe Leu Leu Ser Ser Cys Ala Ala
          35          40          45
Ser Trp Lys Lys Val His Ser Met Asn Leu Tyr Thr Pro Phe Cys Leu

```

```

      50              55              60
Ser Lys Trp Xaa Asn His Val Asn Asn Ala Phe Asn Leu Pro Ser Trp
65              70              75              80
Lys Lys Ser Lys Ser Val Val Thr Met Phe Xaa Gly Pro Ala Met Ile
      85              90              95
Thr Tyr Leu Arg Ser Asp Ser Xaa Tyr Asn Pro Thr Val Gly Lys Gln
      100            105            110
Leu Val Leu Phe Tyr Ser Ile Val Ser Ala Phe Ile Lys Pro Ile Ile
      115            120            125
Ser Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Ser Trp Lys Val Leu
      130            135            140
Arg Val Lys Gly Thr Ala Gln
145              150

```

<210> 2290
 <211> 96
 <212> PRT
 <213> Homo sapien (8570526-1-82280-82723)

<220>
 <221> VARIANT
 <222> (1)...(96)
 <223> Xaa = Any Amino Acid

```

<400> 2290
Ile Val Val Asp Tyr Leu Ile Ile Lys Ser Ser Ile Phe Pro Pro Ala
1              5              10              15
Asn Ser Asn Leu Phe Lys Leu Ile Arg Lys Ser Ile Pro Ile Leu Ala
      20            25            30
Cys Xaa Arg Val Met Met Asp Leu Gly Xaa Thr Gln Asn Val Ser Thr
      35            40            45
Ser Lys Xaa Gly Cys Val Asp Lys Glu Tyr Asn Cys Phe Ile Pro Phe
      50            55            60
Leu Ile Ala Trp His Leu Xaa His Arg Glu Xaa Arg Ile Ile Xaa Asp
65              70              75              80
Arg Ile Ser Ile Leu Val Xaa Lys Ala Leu Trp Met Lys Asn Lys Gly
      85              90              95

```

<210> 2291
 <211> 162
 <212> PRT
 <213> Homo sapien (8575931-7-5387-5879)

<220>
 <221> VARIANT
 <222> (1)...(162)
 <223> Xaa = Any Amino Acid

```

<400> 2291
Leu Leu Ile Ile Pro Ala Ile Ala Thr Asp Thr Arg Leu Ser Val Leu
1              5              10              15
Val Arg Phe Phe Leu Ala Asn Leu Ala Phe Val Val Thr Cys Phe Thr
      20            25            30
Ser Thr Thr Ile Pro Lys Met Leu Ala Cys Lys Glu Ile Pro Cys Val
      35            40            45
Met Ser Gly Cys Lys Gly Ile Pro Tyr Ala Gly Cys Leu Thr Gln Met
      50            55            60
Leu Phe Phe Ile Trp Leu Gly Ile His Ser Phe Leu Leu Thr Ala Met
65              70              75              80
Ala Asn Glu His Cys Val Ala Ile Cys His Ser Leu Asn Ser Ile Arg
      85              90              95

```

Ser Val Thr Pro Xaa Leu Cys Gly Leu Leu Val Val Ala Ser Trp Thr
 100 105 110
 Phe Ala Phe Arg Asn Ala Leu Thr His Pro Val Leu Leu Thr Arg Leu
 115 120 125
 Ser Leu Cys Thr Tyr Glu Trp Val Ser His Val Phe Cys Asn Leu Ser
 130 135 140
 Gln Leu Leu Lys Leu Ala Cys Ser Asp Ala Thr Leu Asn Asn Val Thr
 145 150 155 160
 Val Gln

<210> 2292

<211> 264

<212> PRT

<213> Homo sapien (8648586-17-1126-4850)

<220>

<221> VARIANT

<222> (1)...(264)

<223> Xaa = Any Amino Acid

<400> 2292

Ala Cys Val Thr Phe Leu Val Glu Val Thr Val Met Pro Phe Ser Thr
 1 5 10 15
 Val Arg Phe Val Lys Ser Cys Trp Tyr Phe Gly Asp Ser Ser Cys Lys
 20 25 30
 Phe Asn Thr Trp Phe Asp Thr Ser Phe Cys Phe Ala Ser Leu Phe His
 35 40 45
 Xaa Gly Cys Ile Ser Val Asp Arg Tyr Met Leu Val Ser Asp Leu Leu
 50 55 60
 Thr Tyr Pro Thr Lys Phe Thr Val Ser Val Leu Gly Ile Cys Met Val
 65 70 75 80
 Leu Cys Trp Phe Leu Phe Cys Pro Tyr Ser Phe Ser Ile Phe Asn Thr
 85 90 95
 Gly Ala Asn Glu Glu Gly Ile Glu Glu Leu Val Val Ala Leu Thr Cys
 100 105 110
 Val Gly Gly Cys Gln Ala Pro Leu Asn Gln Asn Trp Val Leu Leu Cys
 115 120 125
 Phe Leu Leu Phe Phe Ile Pro Asn Val Ala Met Val Phe Ile Tyr Ser
 130 135 140
 Lys Ile Phe Leu Val Ala Lys His Gln Ala Arg Lys Ile Glu Ser Thr
 145 150 155 160
 Ala Ser Gln Ala Gln Ser Ser Ser Glu Ser Tyr Lys Glu Arg Val Ala
 165 170 175
 Lys Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile Ala Met Ala Ala
 180 185 190
 Phe Leu Val Ser Trp Leu Pro Tyr Leu Val Asp Ala Val Ile Asp Ala
 195 200 205
 Tyr Met Asn Phe Ile Thr Pro Tyr Val Tyr Glu Ile Leu Val Trp
 210 215 220
 Cys Val Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Phe Phe
 225 230 235 240
 Tyr Gln Trp Phe Gly Lys Ala Ile Lys Leu Ile Val Ser Gly Lys Val
 245 250 255
 Leu Arg Thr Asp Ser Ser Thr Thr
 260

<210> 2293

<211> 126

<212> PRT

<213> Homo sapien (8648858-36-1-1206)

<220>

<221> VARIANT

<222> (1)...(126)

<223> Xaa = Any Amino Acid

<400> 2293

Leu	Cys	Met	Leu	Cys	Trp	Gln	Trp	Pro	Ala	Val	Met	Thr	Asp	Arg	Thr
1				5					10					15	
Ile	Ala	Thr	Cys	Lys	Ser	Arg	His	Phe	Leu	Phe	Leu	Ile	Leu	Val	Leu
		20						25					30		
Thr	Cys	Ser	Leu	Ile	Pro	Ala	Xaa	Ala	Trp	Phe	Thr	Tyr	Phe	Phe	Phe
		35					40					45			
Asn	Ser	Lys	Ser	Cys	Val	Val	Leu	Phe	Gln	His	Ile	His	Phe	Cys	Leu
	50				55						60				
Leu	Xaa	Ile	Pro	Ser	Asn	Phe	Tyr	Cys	Leu	Xaa	Thr	Thr	Ala	Tyr	Leu
65					70					75					80
Lys	Xaa	Leu	Leu	Asn	Met	Xaa	Leu	Lys	His	Xaa	Ile	Lys	Xaa	Thr	Tyr
				85					90					95	
Ile	Val	Phe	Leu	Ala	Val	Arg	Ile	Leu	Xaa	Ala	Phe	Leu	Ile	Leu	Ile
		100						105					110		
Cys	Ile	Met	Asn	Leu	Gln	Leu	Arg	Gln	Cys	Ala	Thr	His	Phe		
		115					120					125			

<210> 2294

<211> 183

<212> PRT

<213> Homo sapien (8649180-1-4193-6564)

<220>

<221> VARIANT

<222> (1)...(183)

<223> Xaa = Any Amino Acid

<400> 2294

Val	Ile	Met	His	Lys	Lys	Glu	Cys	Xaa	Lys	Lys	Thr	His	Asn	Ile	Val
1				5					10					15	
Phe	Leu	Leu	Met	Val	Trp	Glu	Phe	Phe	Tyr	Lys	Phe	Leu	Val	Phe	Phe
		20						25					30		
Phe	Phe	Ser	Leu	His	Xaa	Cys	Val	Ser	Ser	Ile	Ile	Met	Ser	Val	Tyr
		35				40						45			
Tyr	Xaa	Lys	Ile	Asn	Ile	Phe	Ile	Xaa	Ile	Glu	Thr	Lys	Leu	Leu	Phe
	50				55						60				
His	Ile	Ser	Arg	Xaa	Asp	Arg	Met	Ile	Arg	Cys	Ser	Phe	Gln	Lys	Asn
65				70						75					80
Tyr	Leu	Leu	Asn	His	Asn	Gly	Leu	Met	Cys	Arg	Ser	Lys	Cys	Gln	Leu
			85						90					95	
Val	Tyr	Gln	Thr	Val	Ser	Asn	Ser	Leu	Asn	Tyr	Phe	Tyr	Ile	Thr	Pro
		100						105					110		
Ile	Xaa	Leu	Phe	Gln	Ile	Val	Val	Tyr	Lys	Lys	Tyr	Lys	Phe	Leu	His
	115					120						125			
Cys	Ile	Val	Leu	Asp	Val	Pro	Ala	Tyr	Ile	Asn	Ile	Leu	Gly	Cys	Ile
	130					135					140				
Val	Ser	Phe	Leu	His	Val	Ile	Cys	Asn	Val	Xaa	Leu	Tyr	Val	Ile	Asn
145				150						155					160
Lys	Thr	Xaa	Asn	Xaa	Tyr	Lys	Ser	Arg	Phe	Ser	Thr	Cys	Leu	Ser	His
			165						170					175	
Ser	Asp	Ile	Thr	Asp	Leu	Phe									
			180												

<210> 2295

<211> 157

<212> PRT

<213> Homo sapien (902315-1-1-472)

<400> 2295

```

Ile Cys His Pro Leu Gln Tyr Thr Ile Leu Met Asn Pro Glu Leu Cys
 1           5           10           15
Val Phe Met Thr Val Ala Ser Trp Thr Leu Gly Ser Leu Asp Gly Ile
      20           25           30
Ile Val Leu Ala Ala Val Leu Ser Phe Ser Tyr Cys Ser Ser Leu Glu
      35           40           45
Ile His His Phe Phe Cys Asp Val Ala Ala Leu Leu Pro Leu Ser Cys
      50           55           60
Thr Glu Thr Ser Ala Phe Glu Arg Leu Leu Val Ile Cys Cys Val Val
      65           70           75           80
Met Leu Ile Phe Pro Val Ser Val Ile Ile Leu Ser Tyr Ser His Val
      85           90           95
Leu Arg Ala Val Ile His Met Gly Ser Gly Glu Ser Arg Arg Lys Ala
      100          105          110
Phe Thr Thr Cys Ser Ser His Pro Ser Val Val Gly Leu Tyr Tyr Gly
      115          120          125
Ala Ala Met Phe Met Tyr Met Arg Pro Ala Ser Lys His Thr Pro Asp
      130          135          140
Gln Asp Lys Met Val Ser Ala Phe Tyr Thr Asn Pro Ala
      145          150          155

```

<210> 2296

<211> 325

<212> PRT

<213> Mus musculus (M1 4726083-1-12568-18197 3361-4335)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2296

```

Thr Met Trp Ser Asn Ile Ser Ala Ala Pro Phe Leu Leu Thr Gly Phe
 1           5           10           15
Pro Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala
      20           25           30
Ile Tyr Ile Ser Val Leu Leu Gly Asn Gly Thr Leu Leu Tyr Leu Ile
      35           40           45
Lys Asp Asp His Asn Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met
      50           55           60
Leu Ala Gly Thr Asp Leu Thr Val Thr Leu Thr Thr Met Pro Thr Val
      65           70           75           80
Met Ala Val Leu Trp Val Asn His Arg Glu Ile Arg His Gly Ala Cys
      85           90           95
Phe Leu Gln Ala Tyr Ile Ile His Ser Leu Ser Ile Val Glu Ser Gly
      100          105          110
Val Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro
      115          120          125
Leu His Tyr Asn Ser Ile Leu Thr Asn Ser Arg Val Ile Ala Ile Gly
      130          135          140
Leu Gly Val Val Leu Arg Gly Phe Leu Ser Leu Val Pro Pro Ile Leu
      145          150          155          160
Pro Leu Phe Trp Phe Ser Tyr Cys Arg Ser His Val Leu Ser His Ala
      165          170          175
Phe Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr
      180          185          190

```


Phe Asn Arg Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu
 195 200 205
 Asp Ala Leu Ile Ile Val Phe Ser Tyr Val Leu Ile Leu Lys Thr Val
 210 215 220
 Met Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys
 225 230 235 240
 Val Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly
 245 250 255
 Leu Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His
 260 265 270
 Ile Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro
 275 280 285
 Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Val Leu His
 290 295 300
 Leu Leu Ser Val Xaa Asp Asp Val Asn His Tyr Ile Ile Ile Gln Arg
 305 310 315 320
 Ser Leu Gly Met Phe
 325

<210> 2297

<211> 318

<212> PRT

<213> Mus musculus (M2 4726083-1-175-4296 2476-1523)

<400> 2297

Leu Ser Ala Met Pro Ser Met Trp Leu Asn Ile Ser Ser Ser Pro Phe
 1 5 10 15
 Leu Leu Thr Gly Phe Pro Gly Leu Glu Lys Ala His His Leu Ile Ser
 20 25 30
 Leu Pro Leu Leu Met Ala Tyr Ile Ser Ile Leu Leu Gly Asn Gly Thr
 35 40 45
 Leu Leu Phe Leu Ile Lys Asp Asp His Asn Leu His Glu Pro Met Tyr
 50 55 60
 Tyr Phe Leu Gly Met Leu Ala Ala Thr Asp Leu Gly Val Thr Leu Thr
 65 70 75 80
 Thr Met Pro Thr Val Leu Ser Val Leu Trp Leu Asn His Arg Glu Ile
 85 90 95
 Gly His Gly Ala Cys Phe Ser Gln Ala Tyr Phe Ile His Thr Leu Ser
 100 105 110
 Ile Val Glu Ser Gly Val Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile
 115 120 125
 Ala Ile Arg Asn Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asp Thr Lys
 130 135 140
 Val Ile Lys Ile Gly Ile Gly Leu Val Met Arg Ala Gly Leu Ser Ile
 145 150 155 160
 Met Pro Ile Ile Ile Arg Leu His Trp Phe Pro Tyr Cys Arg Ser His
 165 170 175
 Val Leu Ser His Ala Phe Cys Leu His Gln Asp Val Ile Lys Leu Ala
 180 185 190
 Cys Ala Asp Ile Thr Phe Asn Arg Leu Tyr Pro Val Val Val Phe
 195 200 205
 Ala Met Val Leu Leu Asp Phe Leu Ile Ile Phe Phe Ser Tyr Val Leu
 210 215 220
 Ile Leu Lys Thr Val Met Gly Ile Ala Ser Thr Asp Glu Arg Ala Lys
 225 230 235 240
 Ala Leu Asn Thr Cys Val Ser His Ile Cys Cys Ile Leu Val Phe Tyr
 245 250 255
 Val Thr Val Val Gly Leu Thr Phe Ile His Arg Phe Gly Lys Asn Val
 260 265 270
 Pro His Val Val His Ile Thr Met Ser Tyr Ile Tyr Phe Leu Phe Pro
 275 280 285

Pro Phe Met Asn Pro Val Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln
 290 295 300
 Ser Gly Leu Leu Arg Leu Phe Ser Leu Pro Cys Ser Lys Thr
 305 310 315

<210> 2298

<211> 351

<212> PRT

<213> Mus musculus (M3 4726083-1-26023-28273 267-1318)

<220>

<221> VARIANT

<222> (1)...(351)

<223> Xaa = Any Amino Acid

<400> 2298

Leu Ser Pro Ser Leu Lys Pro Ser Cys Asn Cys Asp Pro Thr Met Trp
 1 5 10 15
 Pro Asn Ser Ser Asp Ala Pro Phe Leu Leu Thr Gly Phe Leu Gly Leu
 20 25 30
 Glu Met Ile His His Trp Ile Ser Ile Pro Phe Phe Val Ile Tyr Phe
 35 40 45
 Ser Ile Ile Val Gly Asn Gly Thr Leu Leu Phe Ile Ile Trp Ser Asp
 50 55 60
 His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Val Leu Ala Ser
 65 70 75 80
 Met Asp Leu Gly Met Thr Leu Thr Thr Met Pro Thr Val Leu Gly Val
 85 90 95
 Leu Val Leu Asn Gln Arg Glu Ile Val His Gly Ala Cys Phe Ile Gln
 100 105 110
 Ser Tyr Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Val Leu Leu
 115 120 125
 Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu His Tyr
 130 135 140
 Asn Ser Ile Leu Thr Asn Ser Arg Val Met Lys Met Ala Leu Gly Ala
 145 150 155 160
 Leu Leu Arg Gly Phe Val Ser Ile Val Pro Pro Ile Met Pro Leu Phe
 165 170 175
 Trp Phe Pro Tyr Cys His Ser His Val Leu Ser His Ala Phe Cys Leu
 180 185 190
 His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn Leu
 195 200 205
 Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp Ala Leu
 210 215 220
 Ile Ile Ile Phe Ser Tyr Val Leu Ile Leu Lys Lys Val Met Gly Ile
 225 230 235 240
 Ala Ser Gly Glu Glu Arg Lys Lys Ser Leu Asn Thr Cys Val Ser His
 245 250 255
 Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu Thr Phe
 260 265 270
 Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile Thr Met
 275 280 285
 Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile Ile Tyr
 290 295 300
 Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Leu Arg Leu Leu Ser
 305 310 315 320
 Lys His Ser Arg Thr Xaa Ile Leu Ile Ile Asp Ser Gln Val Leu Tyr
 325 330 335
 Tyr Phe Trp Pro Phe Ile Arg Asn Lys Ser Cys Leu Lys Xaa Tyr
 340 345 350

<210> 2299
 <211> 339
 <212> PRT
 <213> Mus musculus (M4 4761596-1-24347-28106 1259-2275)

<220>
 <221> VARIANT
 <222> (1)...(339)
 <223> Xaa = Any Amino Acid

<400> 2299
 Ala Ser Ser Phe His Asn Asp Thr Asn Pro Gln Asp Val Trp Tyr Val
 1 5 10 15
 Leu Ile Gly Ile Pro Gly Leu Glu Asp Leu His Ser Trp Ile Ala Ile
 20 25 30
 Pro Ile Cys Ser Met Tyr Ile Val Ala Val Ile Gly Asn Val Leu Leu
 35 40 45
 Ile Phe Leu Ile Val Thr Glu Arg Ser Leu His Glu Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Met Leu Ala Leu Ala Asp Leu Leu Leu Ser Thr Ala Thr
 65 70 75 80
 Ala Pro Lys Met Leu Ala Ile Phe Trp Phe His Ser Arg Gly Ile Ser
 85 90 95
 Phe Gly Ser Cys Val Ser Gln Met Phe Phe Ile His Phe Ile Phe Val
 100 105 110
 Ala Glu Ser Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Ser Ser Val Ile
 130 135 140
 Gly Lys Ile Gly Thr Ala Val Val Arg Ser Phe Leu Ile Cys Phe
 145 150 155 160
 Pro Phe Ile Phe Leu Val Tyr Arg Leu Leu Tyr Cys Gly Lys His Ile
 165 170 175
 Ile Pro His Ser Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys
 180 185 190
 Asp Asn Ile Thr Val Asn Ile Ile Tyr Gly Leu Thr Met Ala Leu Leu
 195 200 205
 Ser Thr Gly Leu Asp Ile Leu Leu Ile Ile Ile Ser Tyr Thr Met Ile
 210 215 220
 Leu Arg Thr Val Phe Gln Ile Pro Ser Trp Ala Ala Arg Tyr Lys Ala
 225 230 235 240
 Leu Asn Thr Cys Gly Ser His Ile Cys Val Ile Leu Leu Phe Tyr Thr
 245 250 255
 Pro Ala Phe Phe Ser Phe Phe Ala His Arg Phe Gly Gly Lys Thr Val
 260 265 270
 Pro Arg His Ile His Ile Leu Val Ala Asn Leu Tyr Val Val Val Pro
 275 280 285
 Pro Met Leu Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Gln
 290 295 300
 Asp Arg Val Val Phe Leu Phe Ser Ser Val Ser Thr Cys Gln His Asp
 305 310 315 320
 Ser Arg Cys Xaa Arg Xaa His Ile Pro Lys Glu Asn Ser Phe Lys Cys
 325 330 335
 His Pro Cys

<210> 2300
 <211> 344
 <212> PRT
 <213> Mus musculus (M5 4761596-1-36028-37764 563-1594)

<220>

<221> VARIANT

<222> (1)...(344)

<223> Xaa = Any Amino Acid

<400> 2300

```

Ile Ser Glu Leu Thr Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro
 1           5           10          15
Ser Val Leu Thr Leu Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys
          20          25          30
Trp Ile Gly Ile Pro Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly
          35          40          45
Asn Ser Leu Ile Leu Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile
          50          55          60
Pro Met Tyr Ile Phe Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu
65          70          75          80
Ser Thr Cys Ile Leu Pro Lys Met Leu Gly Ile Phe Trp Phe His Met
          85          90          95
Pro Gln Ile Ser Phe Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His
          100         105         110
Ser Phe Gln Ala Thr Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp
          115         120         125
Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser
130          135         140
Pro Gln Leu Thr Thr Cys Leu Gly Ala Gly Ala Leu Leu Arg Ala Phe
145          150         155         160
Ile Leu Val Ser Pro Ser Ile Leu Leu Ile Lys Cys Arg Leu Lys Tyr
          165         170         175
Phe Arg Thr Thr Ile Ile Ser His Ser Tyr Cys Glu His Met Ala Ile
          180         185         190
Val Lys Leu Ala Ala Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu
          195         200         205
Leu Val Ala Phe Ala Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe
210          215         220
Ser Tyr Val Arg Ile Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu
225          230         235         240
Ala Arg Phe Lys Ala Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe
          245         250         255
Leu Gln Phe Tyr Leu Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe
          260         265         270
Gly Ala His Ile Pro Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr
          275         280         285
Leu Leu Val Pro Pro Phe Leu Asn Pro Ile Val Tyr Gly Val Lys Thr
          290         295         300
Lys Gln Ile Arg Asp Gln Val Leu Lys Met Leu Phe Ser Lys Lys Pro
305          310         315         320
Leu Val Ser Leu Ser Val Glu Lys Leu Cys Gly Phe Xaa Xaa Gln Leu
          325         330         335
Xaa Xaa Val Lys Leu Phe Ile Phe
          340

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<210> 2301

<211> 347

<212> PRT

<213> Mus musculus (M6 4761596-1-45918-48570 619-1659)

<220>

<221> VARIANT

<222> (1)...(347)

<223> Xaa = Any Amino Acid

<400> 2301

```

Thr Gly Arg Phe Ser Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro
 1          5          10          15
Ser Val Leu Thr Leu Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys
          20          25          30
Trp Ile Gly Ile Pro Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly
          35          40          45
Asn Ser Leu Ile Leu Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile
          50          55          60
Pro Met Tyr Ile Phe Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu
65          70          75          80
Ser Thr Cys Ile Leu Pro Lys Met Leu Gly Ile Phe Trp Phe His Met
          85          90          95
Pro Gln Ile Ser Phe Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His
          100          105          110
Ser Phe Gln Ala Thr Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp
          115          120          125
Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser
          130          135          140
Pro Gln Leu Thr Thr Cys Leu Gly Ala Gly Ala Leu Leu Arg Ser Leu
145          150          155          160
Ile Thr Thr Phe Pro Leu Ile Leu Leu Ile Lys Phe Cys Leu Lys Tyr
          165          170          175
Phe Arg Thr Thr Ile Ile Ser His Ser Tyr Cys Glu His Met Ala Ile
          180          185          190
Val Lys Leu Ala Ala Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu
          195          200          205
Leu Val Ala Phe Ala Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe
          210          215          220
Ser Tyr Val Arg Ile Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu
225          230          235          240
Ala Arg Phe Lys Ala Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe
          245          250          255
Leu Gln Phe Tyr Leu Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe
          260          265          270
Gly Ala His Ile Pro Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr
          275          280          285
Leu Leu Val Pro Pro Phe Leu Asn Pro Ile Val Tyr Gly Ile Lys Thr
          290          295          300
Lys Gln Ile Arg Asp Gln Val Leu Lys Met Phe Phe Ser Lys Lys Pro
305          310          315          320
Leu Xaa Thr Ser Val Thr Arg Ser Val Glu Lys Leu Cys Gly Phe Xaa
          325          330          335
Leu Glu Leu Glu Xaa Val Lys Pro Xaa Ile Phe
          340          345

```

<210> 2302

<211> 351

<212> PRT

<213> Mus musculus (M7 5051393-1-104482-107691 2444-1393)

<220>

<221> VARIANT

<222> (1)... (351)

<223> Xaa = Any Amino Acid

<400> 2302

```

Val Leu Cys Thr Thr Leu Ser Xaa Gln Ser His Ser Ser Asn Xaa Ile
 1          5          10          15
Gln Met Thr Met Val Asn Gln Ser Thr Pro Val Gly Phe Leu Leu Leu
          20          25          30

```

Gly Phe Ser Glu His Pro Gln Leu Glu Lys Val Leu Phe Val Val Val
 35 40 45
 Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu Ile Leu Leu
 50 55 60
 Leu Ser Thr Leu Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu
 65 70 75 80
 Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr Cys Val Pro
 85 90 95
 Gln Met Leu Phe Asn Leu Trp Gly Pro Thr Lys Thr Ile Ser Phe Leu
 100 105 110
 Gly Cys Ser Val Gln Leu Phe Ile Phe Met Leu Leu Gly Thr Thr Glu
 115 120 125
 Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys
 130 135 140
 Gln Pro Leu His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Arg Gln
 145 150 155 160
 Leu Ala Gly Val Ala Trp Ala Ile Gly Leu Val Gln Ser Ile Val Gln
 165 170 175
 Ile Pro Pro Thr Leu Thr Leu Pro Phe Cys Ser His Arg Gln Ile Asp
 180 185 190
 Asp Phe Leu Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp
 195 200 205
 Thr Thr Phe Asn Glu Ile Gln Leu Ser Val Ala Gly Val Ile Phe Leu
 210 215 220
 Leu Val Pro Leu Ser Leu Ile Ile Val Ser Tyr Gly Val Ile Ala Arg
 225 230 235 240
 Ala Val Leu Lys Thr Asn Ser Ser Lys Gly Arg Arg Lys Ala Phe Gly
 245 250 255
 Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr Ser Ser Val
 260 265 270
 Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Glu Arg Ser
 275 280 285
 Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Thr Leu Asn Pro
 290 295 300
 Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala Phe Trp Arg
 305 310 315 320
 Leu Leu Gly Lys Asp Ala Ala Ser Gly Arg Asn Xaa Gly Gln Ile Leu
 325 330 335
 Val Xaa Phe Leu Asn Tyr Lys Val Ser Ser Xaa Tyr Val Tyr Cys
 340 345 350

<210> 2303

<211> 320

<212> PRT

<213> Mus musculus (M8 5051393-1-124150-125858 1430-472)

<220>

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 2303

Arg Leu Asp Thr Glu Ile Met Val Asn Gln Ser Ser Pro Val Val Phe
 1 5 10 15
 Phe Leu Leu Gly Phe Ser Glu His Pro Gln Leu Glu Lys Val Leu Phe
 20 25 30
 Val Val Val Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu
 35 40 45
 Ile Leu Leu Leu Ser Thr Leu Asp Pro Arg Leu His Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr

```

65          70          75          80
Cys Val Pro Gln Met Leu Phe Asn Leu Trp Gly Pro Glu Lys Thr Ile
      85          90          95
Ser Phe Leu Gly Cys Phe Val Xaa Leu Phe Ile Phe Met Ser Leu Gly
      100        105        110
Thr Thr Glu Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val
      115        120        125
Ala Val Cys Gln Pro Leu His Tyr Ala Thr Val Ile Asn Pro Arg Leu
      130        135        140
Cys Gln Gln Leu Ala Gly Ile Ala Trp Ala Ile Gly Leu Val Gln Ser
145      150      155      160
Ile Val Gln Thr Pro Pro Thr Leu Lys Leu Pro Phe Cys Ser His Arg
      165        170        175
Gln Ile Asp Asn Phe Val Cys Glu Val Pro Ser Leu Ile Gln Leu Ser
      180        185        190
Cys Gly Asp Ile Thr Tyr Asn Glu Ile Gln Met Ala Val Ala Ser Ile
      195        200        205
Phe Ile Val Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala
      210        215        220
Ile Ala Arg Ala Val Leu Lys Ile Ser Ser Ala Lys Gly Arg Arg Lys
225      230      235      240
Ala Phe Gly Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr
      245        250        255
Ser Ser Val Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Arg
      260        265        270
Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Ile
      275        280        285
Leu Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala
290      295      300
Phe Trp Lys Leu Leu Arg Lys Asp Glu Asp Ser Glu Glu Ser Trp Arg
305      310      315      320

```

<210> 2304

<211> 317

<212> PRT

<213> Mus musculus (M9 5051393-1-149569-151395 1755-805)

<220>

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 2304

```

Pro Gln Ala Asn His Ser Ser Ala Glu Arg Phe Leu Leu Leu Gly Phe
1          5          10          15
Ser Asp Trp Pro Ser Leu Gln Pro Val Leu Phe Ala Leu Val Leu Leu
      20        25        30
Cys Tyr Leu Leu Thr Leu Thr Gly Asn Ala Ala Leu Val Leu Leu Ala
      35        40        45
Ile Arg Asp Pro Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Cys His
50      55      60
Leu Ala Leu Val Asp Val Gly Phe Thr Thr Ser Val Val Pro Pro Leu
65      70      75      80
Leu Ala Ser Leu Arg Gly Ser Met Leu Gln Leu Pro Arg Ala Gly Cys
      85      90      95
Met Ala Gln Leu Cys Ser Ser Leu Ala Leu Gly Ser Ala Glu Cys Val
      100      105      110
Leu Leu Ala Val Met Ala Leu Asp Arg Ala Ala Ala Val Cys Asn Pro
      115      120      125
Leu Arg Tyr Thr Ser Leu Ala Ser Pro Leu Leu Cys Arg Thr Leu Ala
130      135      140

```

Gly Val Ser Trp Leu Gly Gly Leu Ala Asn Ser Ala Ala Gln Thr Ala
 145 150 155 160
 Leu Leu Ala Ala Arg Pro Leu Cys Ala Pro Arg Cys Leu Asp His Phe
 165 170 175
 Ile Cys Glu Leu Pro Ala Leu Leu Gln Leu Ala Cys Arg Gly Gly Arg
 180 185 190
 Ser Ala Thr Glu Arg Gln Met Phe Ala Ala Arg Val Val Ile Leu Leu
 195 200 205
 Val Pro Ser Ala Val Ile Leu Ala Ser Tyr Ile Ala Val Gly Arg Ala
 210 215 220
 Val Trp Gly Met His Ser Ser Ser Gly Trp Arg Lys Ala Ala Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Ala Val Cys Leu Phe Tyr Gly Ser Ala Thr
 245 250 255
 Tyr Thr Tyr Leu Gln Pro Thr His Ser Tyr Asn Gln Gly Arg Gly Lys
 260 265 270
 Phe Val Ser Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Ala Leu Arg Leu
 290 295 300
 Leu Arg Ser Leu Gly Arg Pro Xaa Val Gly Gln Xaa Lys
 305 310 315

<210> 2305

<211> 348

<212> PRT

<213> Mus musculus (M10 5051393-1-39874-41685 1277-235)

<220>

<221> VARIANT

<222> (1)...(348)

<223> Xaa = Any Amino Acid

<400> 2305

Val Leu Cys Thr Thr Leu Ser Xaa Gln Ser His Pro Ser Asn Xaa Ile
 1 5 10 15
 Gln Met Thr Met Val Asn Gln Ser Ser Pro Val Gly Phe Leu Leu Leu
 20 25 30
 Gly Phe Ser Glu His Pro Gln Leu Glu Lys Val Leu Ile Val Val Val
 35 40 45
 Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu Ile Leu Leu
 50 55 60
 Leu Ser Thr Leu Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu
 65 70 75 80
 Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr Cys Val Pro
 85 90 95
 Gln Met Leu Phe Asn Leu Trp Gly Pro Ala Lys Thr Ile Ser Phe Leu
 100 105 110
 Gly Cys Phe Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu
 115 120 125
 Cys Ile Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys
 130 135 140
 Gln Pro Leu His Tyr Ala Thr Val Ile His Pro Arg Leu Cys Cys Gln
 145 150 155 160
 Leu Ala Ala Val Ala Cys Thr Ile Gly Leu Val Glu Ser Val Val Gln
 165 170 175
 Thr Pro Ser Thr Leu Arg Leu Pro Phe Cys Pro His His Gln Val Asp
 180 185 190
 Asp Phe Val Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Gly Asp
 195 200 205
 Thr Thr Tyr Asn Glu Ile Gln Met Ala Val Ala Ser Val Phe Ile Leu

210	215	220
Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Ala Arg		
225	230	235
Ala Val Leu Arg Ile Ser Ser Ala Lys Gly Arg Arg Lys Ala Phe Gly		
	245	250
Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr Ser Ser Val		
	260	265
Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Arg Glu Arg Gly		
	275	280
Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro		
	290	295
Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala Phe Arg Arg		
305	310	315
Leu Leu Trp Lys Glu Val Lys Pro Ser Xaa His Thr Leu Ser Lys Leu		
	325	330
Asn Gly Lys Ser Ala Cys Leu Val Gly Leu Ser Phe		
	340	345

<210> 2306

<211> 347

<212> PRT

<213> Mus musculus (M11 5051393-1-46409-49345 2458-1419)

<220>

<221> VARIANT

<222> (1)...(347)

<223> Xaa = Any Amino Acid

<400> 2306

Cys Pro Lys Ser Thr Thr Ser Gly His Ile Glu Ser Cys Met Gly Gln	
1	5
Tyr Phe Gln Leu Asp Ser Xaa Gln Lys Gln Thr Met Val Asn Gln Ser	
	20
Ser Pro Val Gly Phe Leu Leu Leu Gly Phe Ser Glu His Pro Gln Leu	
	35
Glu Lys Val Leu Phe Val Ile Val Leu Cys Ser Tyr Leu Leu Thr Leu	
	50
Leu Gly Asn Thr Leu Ile Leu Leu Leu Ser Thr Leu Asp Pro Arg Leu	
65	70
His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu	
	85
Cys Phe Thr Thr Thr Cys Val Pro Gln Met Leu Phe Asn Leu Trp Gly	
	100
Pro Ala Lys Thr Ile Ser Phe Leu Gly Cys Ser Val Gln Leu Phe Ile	
	115
Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr Val Met Ser	
	130
Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu His Tyr Ala Thr Val	
145	150
Ile His Pro Arg Leu Cys Trp Lys Leu Ala Ala Val Ala Trp Met Met	
	165
Gly Leu Leu Gln Ser Ile Val Gln Thr Pro Pro Thr Leu Lys Leu Pro	
	180
Phe Cys Pro His Arg Gln Ile Asp Asp Phe Leu Cys Glu Val Pro Ser	
	195
Leu Ile Arg Leu Ser Cys Gly Asp Thr Thr Phe Asn Glu Ile Gln Leu	
	210
Ala Val Ser Ser Val Ile Leu Val Val Val Pro Leu Ser Leu Ile Leu	
225	230
Val Ser Tyr Gly Ala Ile Ala Arg Ala Val Met Arg Ile Asn Ser Thr	
	245
	250
	255

Glu Ala Trp Lys Lys Ala Leu Arg Thr Cys Ser Ser His Leu Ile Val
 260 265 270
 Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro Lys
 275 280 285
 Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr Ala
 290 295 300
 Val Gly Thr Pro Thr Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys
 305 310 315 320
 Glu Val Lys Arg Ala Phe Trp Arg Leu Leu Gly Lys Asp Gly Asp Ser
 325 330 335
 Lys Asn Thr Xaa Glu Ile Asn Ser Arg Arg Thr
 340 345

<210> 2307

<211> 326

<212> PRT

<213> Mus musculus (M12 5051393-1-65471-67664 1437-460)

<220>

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 2307

Leu Asp Thr Glu Ile Met Val Asn Gln Ser Ser Pro Val Val Phe Phe
 1 5 10 15
 Leu Leu Gly Phe Ser Glu His Pro Gln Leu Lys Lys Val Leu Phe Val
 20 25 30
 Val Val Leu Cys Ser Tyr Leu Leu Thr Leu Leu Gly Asn Thr Leu Ile
 35 40 45
 Leu Leu Leu Ser Thr Leu Asp Pro Arg Leu His Ser Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Thr Cys
 65 70 75 80
 Val Pro Gln Met Leu Phe Asn Leu Trp Gly Pro Ala Lys Thr Ile Ser
 85 90 95
 Phe Leu Gly Cys Phe Val Gln Leu Phe Ile Phe Met Ser Leu Gly Thr
 100 105 110
 Thr Glu Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125
 Val Cys Gln Pro Leu His Tyr Ala Thr Lys Ile Asn Pro His Leu Cys
 130 135 140
 Arg Gln Leu Ala Gly Ile Ala Trp Ala Ile Gly Leu Val Gln Ser Ile
 145 150 155 160
 Val Gln Thr Pro Pro Thr Leu Lys Leu Pro Phe Cys Ser His Arg Gln
 165 170 175
 Ile Asp Asn Phe Leu Cys Glu Val Pro Ser Leu Ile Gln Leu Ser Cys
 180 185 190
 Gly Asp Thr Thr Tyr Asn Glu Ile Gln Met Ala Val Ala Ser Ile Phe
 195 200 205
 Ile Val Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile
 210 215 220
 Ala Arg Ala Val Leu Lys Ile Ser Ser Ala Lys Gly Arg Arg Lys Ala
 225 230 235 240
 Phe Gly Thr Cys Ser Ser His Leu Ile Val Val Thr Leu Phe Tyr Ser
 245 250 255
 Ser Val Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Arg Glu
 260 265 270
 Arg Gly Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Thr Leu
 275 280 285
 Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Val Lys Arg Ala Phe

290 295 300
 Trp Lys Leu Leu Arg Lys Asp Glu Asp Ser Glu Glu Ser Xaa Arg Arg
 305 310 315 320
 Asn Thr Xaa His Thr Phe
 325

<210> 2308

<211> 282

<212> PRT

<213> Mus musculus (M13 6143913-1-1-2867 848-3)

<400> 2308

Leu Ile Ile Tyr Cys Leu Phe Leu Ser Phe Pro Gly Ile Met Asp His
 1 5 10 15
 Val Asn Tyr Thr Trp Thr Arg Thr Phe Ile Leu Ala Gly Phe Thr Thr
 20 25 30
 Ser Gly Thr Leu Gln His Leu Ala Val Phe Gly Thr Leu Cys Ile Tyr
 35 40 45
 Leu Leu Thr Leu Ala Gly Asn Leu Phe Ile Ile Val Leu Val Gln Ala
 50 55 60
 Asp Ser Gly Leu Ser Thr Pro Met Tyr Phe Phe Ile Ser Val Leu Ser
 65 70 75 80
 Phe Leu Glu Leu Trp Tyr Val Ser Thr Thr Val Pro Thr Leu Leu His
 85 90 95
 Thr Leu Leu His Gly Pro Ser Pro Ile Pro Ser Ser Ala Cys Phe Val
 100 105 110
 Gln Leu Tyr Val Phe His Ser Leu Gly Met Thr Glu Cys Tyr Leu Leu
 115 120 125
 Gly Val Met Ala Leu Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His
 130 135 140
 Tyr His Ala Leu Met Ser Arg Gln Val Gln Lys Gln Leu Val Gly Val
 145 150 155 160
 Thr Trp Leu Ala Gly Phe Ser Ala Ala Leu Val Pro Ala Gly Leu Thr
 165 170 175
 Ala Ser Leu Pro Tyr Cys Leu Lys Glu Val Ala His Tyr Phe Cys Asp
 180 185 190
 Leu Ala Pro Val Met Gln Leu Ala Cys Val Asp Thr Ser Trp His Ala
 195 200 205
 Arg Leu Tyr Ile Ala Val Ile Gly Met Ile Asn Thr Cys Asn Leu Thr
 210 215 220
 Phe Ile Leu Gly Leu Tyr Gly Gly Ile Val Arg Ala Val Leu Lys Leu
 225 230 235 240
 Pro Ser Ala Ala Ser Arg Ala Lys Ala Phe Ser Thr Cys Ser Ser His
 245 250 255
 Ile Thr Val Val Thr Leu Phe Phe Gly Ser Ala Phe Ile Val Tyr Val
 260 265 270
 Gly Pro Pro Glu Ile Arg Ala Glu Gly Arg
 275 280

<210> 2309

<211> 333

<212> PRT

<213> Mus musculus (M14 6143913-1-6180-10825 2950-1952)

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 2310

Leu Leu Leu Gly Thr Met Asp His Val Asn Tyr Thr Trp Thr Arg Thr

```

1           5           10           15
Phe Ile Leu Ala Gly Phe Thr Thr Ser Gly Ala Leu Arg Pro Leu Ala
20           25           30
Phe Leu Gly Thr Leu Cys Ile Tyr Leu Leu Thr Leu Ala Gly Asn Leu
35           40           45
Phe Ile Ile Val Leu Val Gln Ala Asp Ser Gly Leu Ser Thr Pro Met
50           55           60
Tyr Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Leu Trp Tyr Val Ser
65           70           75           80
Thr Thr Val Pro Thr Leu Leu His Thr Leu Leu His Gly His Ser Pro
85           90           95
Ile Pro Ser Ser Ala Cys Phe Val Gln Leu Tyr Val Phe His Ser Leu
100          105          110
Gly Met Thr Glu Cys Tyr Leu Leu Gly Val Met Ala Leu Asp Arg Tyr
115          120          125
Leu Ala Ile Cys Arg Pro Leu His Tyr His Ala Leu Met Ser Lys Gln
130          135          140
Val Gln Leu Trp Leu Ala Gly Ala Thr Trp Val Ala Gly Phe Ser Ala
145          150          155          160
Ala Leu Val Pro Ala Cys Leu Thr Ala Ser Leu Pro Tyr Cys Leu Lys
165          170          175
Glu Ile Ala His Tyr Phe Cys Asp Leu Ala Pro Leu Met Arg Leu Ala
180          185          190
Cys Val Ser Thr Arg Trp His Ala Arg Val His Gly Ala Val Ile Gly
195          200          205
Val Ala Thr Gly Cys Asn Phe Val Leu Ile Leu Gly Leu Tyr Gly Gly
210          215          220
Ile Leu Thr Ala Val Leu Lys Leu Pro Ser Ala Ala Ser Arg Ala Lys
225          230          235          240
Ala Phe Ser Thr Cys Ser Ser His Met Thr Val Val Ala Leu Phe Tyr
245          250          255
Ala Ser Ala Phe Thr Val Tyr Val Gly Ser Pro Gln Ser Arg Pro Glu
260          265          270
Gly Thr Asp Lys Leu Ile Ala Leu Val Tyr Ala Leu Leu Thr Pro Phe
275          280          285
Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala
290          295          300
Val Lys Arg Val Ser Glu Lys Ile Arg Thr Leu Leu Arg Asp Thr Xaa
305          310          315          320
Leu Ser Leu Leu Thr Leu Pro Thr Phe Arg Val Asn Ala
325          330

```

<210> 2311

<211> 120

<212> PRT

<213> Mus musculus (M15 6143913-1-66312-67763 687-330)

<220>

<221> VARIANT

<222> (1)...(120)

<223> Xaa = Any Amino Acid

<400> 2311

```

Val Thr Val Gly His Cys Leu Gly Gln Met Ser Leu Ser Val Asp Thr
1           5           10           15
Asp Phe Leu Ile Glu Phe Phe Cys Leu Lys Arg Lys Glu Lys Lys Arg
20           25           30
Lys Lys Lys Asp Cys Ser Pro Leu Tyr Leu Asp Ser Xaa Phe Gln Ser
35           40           45
His Glu Ile Thr Gly Ser Phe Ser Phe Ser Val Phe His Arg Ser Leu
50           55           60

```

Leu Ser Asn Ile Ser Leu Gln Met Met Ala Tyr Phe Gln Ile Thr Leu
 65 70 75 80
 Pro Ser Thr Phe Cys Ile Pro Xaa Gln Arg Ser Gln Thr Ser Ala Cys
 85 90 95
 Ile Tyr Val Leu Asn Asn Leu Leu Ser Leu Phe His Ser Leu Ile Ser
 100 105 110
 Ser Leu Xaa Pro Thr Ala Ser Thr
 115 120

<210> 2312

<211> 323

<212> PRT

<213> Mus musculus (M16 6456795-1-106495-108409 847-1815)

<400> 2312

Leu Ser Ser Tyr Gln Phe Leu Leu Glu Lys Lys Arg Pro Ile Met Asn
 1 5 10 15
 Cys Ser Lys Thr Pro Gly Phe Ile Leu Leu Gly Leu Ser Ser Asp Pro
 20 25 30
 Glu Lys Trp Gln Pro Leu Phe Asn Ile Phe Leu Cys Leu Tyr Leu Leu
 35 40 45
 Gly Leu Leu Gly Asn Leu Leu Leu Leu Ala Ile Gly Thr Asp Val
 50 55 60
 His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Gln Leu Ser Leu Val
 65 70 75 80
 Asp Leu Cys Phe Ile Thr Thr Thr Ala Pro Lys Met Leu Glu Ala Leu
 85 90 95
 Trp Thr Gly Asp Gly Ser Ile Ser Phe Ser Gly Cys Leu Thr Gln Phe
 100 105 110
 Tyr Phe Phe Ala Val Phe Ala Asp Met Asp Asn Leu Leu Ala Val
 115 120 125
 Met Ala Ile Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Phe Tyr Pro
 130 135 140
 Phe Leu Met Thr Pro Cys Arg Cys Glu Val Leu Ala Ser Gly Ser Trp
 145 150 155 160
 Gly Ile Ala His Cys Val Ser Leu Phe Tyr Thr Leu Leu Leu Ser Gln
 165 170 175
 Phe Tyr Tyr His Thr Asn Gln Gly Ile Pro His Phe Phe Cys Asp Ser
 180 185 190
 Arg Pro Leu Leu Leu Leu Ser Cys Ser Asp Thr His Leu Ser Glu Gly
 195 200 205
 Leu Met Met Ala Leu Ser Gly Val Leu Gly Met Ser Ser Val Leu Cys
 210 215 220
 Leu Val Ser Ser Tyr Gly Cys Ile Phe Tyr Ala Val Ala Arg Val Pro
 225 230 235 240
 Ser Ala Gln Gly Lys Arg Lys Ser Leu Ala Thr Cys Ser Ser His Leu
 245 250 255
 Ser Val Val Leu Leu Phe Tyr Ser Thr Val Phe Ala Thr Tyr Leu Lys
 260 265 270
 Pro Pro Ser Thr Ser His Ser Ser Ala Glu Val Val Ala Ala Val Met
 275 280 285
 Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro Phe Ile Tyr Ser Leu Arg
 290 295 300
 Asn Lys Asp Val Lys Ser Ser Leu Arg Lys Ile Leu Asn Met Asp Lys
 305 310 315 320
 Phe Gln Gly

<210> 2313

<211> 284

<212> PRT

<213> Mus musculus (M17 6456795-1-108765-110526 1744-894)

<220>

<221> VARIANT

<222> (1)...(284)

<223> Xaa = Any Amino Acid

<400> 2313

```

Cys Ile Tyr Ile Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val
1      5      10      15
Cys Ile Ser Ile Cys Thr Tyr Leu His Ile Xaa Ile His Met Cys Val
20      25      30
Gln Val Val Ile Lys Leu Lys Val Lys Xaa Val Thr Trp Lys Glu Val
35      40      45
Xaa Lys Met Ser Val Glu Lys Arg Thr Gln Ser Arg Gln Lys Ser Gly
50      55      60
Tyr Leu Ala Asn Cys Phe Leu Gln Ser Phe Ile Leu Gly Ser Val Asp
65      70      75      80
Arg Asn Ile Cys Leu Leu Ile Val Met Val Tyr Asp His Tyr Leu Thr
85      90      95
Ile Cys His His Leu Xaa Tyr Pro Phe Leu Met Gly Pro Leu Trp Gly
100     105     110
Leu Gly Phe Gly Leu Thr Thr Ser Phe Val Val Asp Glu Leu Ile Val
115     120     125
Ala Leu Met Ala Gln Leu Arg Phe Cys Val Pro Lys Gln Ile Asp His
130     135     140
Phe Tyr Tyr Asp Phe Ser Pro Leu Val Val Leu Ala Tyr Thr Asp Thr
145     150     155     160
Gly Leu Val Gln Val Thr Thr Phe Val Leu Phe Val Val Phe Leu Thr
165     170     175
Val Pro Phe Gly Leu Val Leu Ile Ser Cys Ala Gln Ile Ala Val Thr
180     185     190
Val Leu Arg Val Pro Ser Arg Thr Arg Arg Asn Lys Ala Phe Ser Thr
195     200     205
Cys Ser Ser His Leu Asp Glu Val Ser Thr Phe Tyr Gly Ser Leu Met
210     215     220
Val Trp Tyr Thr Glu Pro Ser Ala Val His Ser Gln Ile Leu Ser Lys
225     230     235     240
Val Ile Ala Leu Leu Tyr Thr Val Val Thr Thr Ile Phe Asp Pro Gly
245     250     255
Ile Tyr Thr Leu Arg Asn Gln Glu Val Gln Gln Ser Leu Arg Arg His
260     265     270
Leu Tyr Cys Lys Pro Thr Glu Met Xaa Pro Lys Arg
275     280

```

<210> 2314

<211> 312

<212> PRT

<213> Mus musculus (M18 6456795-1-142088-143512 370-1305)

<400> 2314

```

Ile Ser Pro Arg Met Asn Cys Ser Gln Ala Pro Gly Phe Ile Leu Leu
1      5      10      15
Gly Leu Pro Arg Glu Pro Glu Lys Trp Gln His Phe Phe Ile Ile Phe
20      25      30
Leu Gly Leu Tyr Leu Leu Gly Leu Leu Gly Asn Leu Leu Leu Leu
35      40      45
Ala Ile Gly Ser Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
50      55      60
Ser Gln Leu Ser Leu Val Asp Leu Cys Phe Ile Thr Thr Thr Ala Pro
65      70      75      80

```

Lys Thr Leu Glu Thr Trp Trp Thr Gly Asp Gly Ser Ile Ser Phe Ser
 85 90 95
 Gly Cys Leu Thr Gln Leu Tyr Phe Phe Gly Val Phe Ala Asp Met Asp
 100 105 110
 Asn Leu Leu Leu Ala Val Met Ala Ile Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 His Pro Leu Leu Tyr Pro Leu Leu Met Thr Pro Cys Arg Cys Glu Val
 130 135 140
 Leu Val Ser Gly Ser Trp Gly Ile Ala His Cys Val Ser Leu Met Tyr
 145 150 155 160
 Thr Leu Leu Leu Ser Gln Leu Tyr Phe His Thr Asn Gln Glu Ile Pro
 165 170 175
 Arg Phe Phe Cys Asp Cys Arg Pro Leu Leu Leu Leu Ser Cys Ser Asp
 180 185 190
 Thr His Leu Asn Glu Val Leu Met Met Ala Leu Ala Gly Val Leu Gly
 195 200 205
 Val Ser Ala Val Leu Cys Ile Val Ser Ser Tyr Gly Cys Ile Phe Tyr
 210 215 220
 Ala Val Ala Arg Val Pro Ser Ala Gln Gly Lys Arg Lys Ala Leu Thr
 225 230 235 240
 Thr Cys Ser Ser His Leu Ser Val Val Leu Phe Tyr Ser Thr Val
 245 250 255
 Phe Ala Thr Tyr Leu Lys Pro Pro Ser Thr Ser His Ser Ser Gly Glu
 260 265 270
 Val Val Ala Ala Val Met Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ser Ser Leu Arg Arg
 290 295 300
 Val Leu Asn Ile Glu Lys Ser Gln
 305 310

<210> 2315

<211> 325

<212> PRT

<213> Mus musculus (M19 6456795-1-14626-16881 1501-527)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2315

Cys Pro Phe Leu Xaa Val Met Ser Asn Gln Thr Ser Val Thr Glu Phe
 1 5 10 15
 Leu Leu Leu Gly Val Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe
 20 25 30
 Val Ile Phe Phe Thr Ile Tyr Phe Val Asn Ile Thr Gly Asn Gly Ala
 35 40 45
 Ile Leu Met Ile Val Ile Leu Asp Pro Arg Leu His Ser Pro Met Tyr
 50 55 60
 Phe Phe Leu Gly Asn Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val
 65 70 75 80
 Thr Leu Pro Lys Met Leu Gln Asn Leu Leu Ser Thr Asn Lys Ala Ile
 85 90 95
 Ser Phe Leu Gly Cys Ile Thr Gln Leu His Phe Phe His Phe Leu Gly
 100 105 110
 Ser Thr Glu Ala Met Leu Leu Pro Val Met Ala Phe Asp Arg Phe Val
 115 120 125
 Ala Ile Cys Arg Pro Leu His Tyr Ser Val Ile Met Asn His Gln Leu
 130 135 140
 Cys Ile His Met Thr Val Thr Ile Trp Thr Leu Gly Phe Phe His Ala

```
<210> 2316
<211> 237
<212> PRT
<213> Mus musculus (M20 6456795-1-147325-149242 1694-983)
```

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<220>
<221> VARIANT
<222> (1)...(237)
<223> Xaa = Any Amino Acid
```

<400>	2316														
Leu	Xaa	Thr	Tyr	Ile	Pro	Thr	His	Thr	His	Thr	His	Thr	His	Thr	His
1				5					10					15	
Thr	His	Thr	His	Ile	Tyr	Ile	Cys	Asn	Tyr	Asn	Val	Gln	Arg	Asn	Asn
			20					25					30		
Gly	Tyr	Gln	Val	Asp	His	Tyr	Leu	Xaa	Ile	Cys	His	Pro	Leu	His	Tyr
		35					40					45			
Pro	Leu	Leu	Met	Gly	His	Gln	Trp	Cys	Leu	Gly	Phe	Val	Leu	Thr	Leu
	50					55					60				
Gln	Leu	Phe	Gly	Ile	Thr	Val	Asp	Gly	Leu	Val	Val	Ile	Leu	Val	Ala
65					70					75					80
Gln	Met	Trp	Phe	Cys	Gly	Pro	Asn	Leu	Ile	Asp	Tyr	Phe	Xaa	Tyr	Asn
				85					90					95	
Phe	Ser	Pro	Ile	Met	Asp	Leu	Ala	Xaa	Ser	Asp	Thr	Gln	Val	Phe	Gln
			100					105					110		
Val	Ile	Thr	Phe	Val	Leu	Ser	Val	Val	Phe	Leu	Thr	Val	Pro	Phe	Gly
		115					120					125			
Leu	Val	Leu	Ile	Ser	Tyr	Ile	Gln	Ile	Val	Val	Thr	Val	Leu	Arg	Val
	130					135					140				
Leu	Ser	Gly	Asp	Arg	Arg	Thr	Lys	Asp	Phe	Ser	Thr	Cys	Ser	Ser	His
145					150					155					160
Leu	Ala	Val	Val	Ser	Thr	Phe	Tyr	Arg	Ser	Leu	Met	Val	Leu	Tyr	Thr
				165					170					175	
Val	Pro	Leu	Leu	Leu	Ser	Lys	Val	Ile	Ala	Leu	Leu	Tyr	Lys	Val	Val
		180						185					190		
Ile	Pro	Ile	Phe	Asn	His	Val	Ile	Tyr	Thr	Leu	Arg	Asn	Gln	Glu	Val
		195					200					205			

Pro Xaa Ala Leu Arg Arg His Leu Tyr Cys Lys Pro Thr Glu Met Xaa
 210 215 220
 Pro Lys Met Glu Gly Ser Lys Asp Phe Leu Phe Asn Cys
 225 230 235

<210> 2317

<211> 237

<212> PRT

<213> Mus musculus (M21 6456795-1-153518-155435 1694-983)

<220>

<221> VARIANT

<222> (1)...(237)

<223> Xaa = Any Amino Acid

<400> 2317

Leu Xaa Thr Tyr Ile Pro Thr His Thr His Thr His Thr His
 1 5 10 15
 Thr His Thr His Ile Tyr Ile Cys Asn Tyr Asn Val Gln Arg Asn Asn
 20 25 30
 Gly Tyr Gln Val Asp His Tyr Leu Xaa Ile Cys His Pro Leu His Tyr
 35 40 45
 Pro Leu Leu Met Gly His Gln Trp Cys Leu Gly Phe Val Leu Thr Leu
 50 55 60
 Gln Leu Phe Gly Ile Thr Val Asp Gly Leu Val Val Ile Leu Val Ala
 65 70 75 80
 Gln Met Trp Phe Cys Gly Pro Asn Leu Ile Asp Tyr Phe Xaa Tyr Asn
 85 90 95
 Phe Ser Pro Ile Met Asp Leu Ala Xaa Ser Asp Thr Gln Val Phe Gln
 100 105 110
 Val Ile Thr Phe Val Leu Ser Val Val Phe Leu Thr Val Pro Phe Gly
 115 120 125
 Leu Val Leu Ile Ser Tyr Ile Gln Ile Val Val Thr Val Leu Arg Val
 130 135 140
 Leu Ser Gly Asp Arg Arg Thr Lys Asp Phe Ser Thr Cys Ser Ser His
 145 150 155 160
 Leu Ala Val Val Ser Thr Phe Tyr Arg Ser Leu Met Val Leu Tyr Thr
 165 170 175
 Val Pro Leu Leu Leu Ser Lys Val Ile Ala Leu Leu Tyr Lys Val Val
 180 185 190
 Ile Pro Ile Phe Asn His Val Ile Tyr Thr Leu Arg Asn Gln Glu Val
 195 200 205
 Pro Xaa Ala Leu Arg Arg His Leu Tyr Cys Lys Pro Thr Glu Met Xaa
 210 215 220
 Pro Lys Met Glu Gly Ser Lys Asp Phe Leu Phe Asn Cys
 225 230 235

<210> 2318

<211> 318

<212> PRT

<213> Mus musculus (M22 6456795-1-37464-41929 1501-549)

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 2318

Cys Val Ile Phe Xaa Val Met Leu Asn Gln Thr Ser Val Thr Glu Phe
 1 5 10 15
 Ile Leu Leu Gly Val Arg Asp Ile Gln Glu Pro Gln Pro Phe Leu Phe

```

      20      25      30
Ala Ile Phe Phe Thr Ile Tyr Phe Val Asn Ile Thr Gly Asn Gly Ala
      35      40      45
Ile Leu Met Ile Val Ile Leu Asp Pro Arg Leu His Ser Pro Met Tyr
      50      55      60
Phe Phe Leu Gly Asn Leu Ala Cys Leu Asp Ile Ser Tyr Ser Thr Val
65      70      75      80
Thr Val Pro Lys Met Leu Glu Asn Leu Leu Ser Thr Asn Lys Ala Ile
      85      90      95
Ser Leu Leu Gly Cys Ile Thr Gln Leu His Phe Phe His Phe Leu Gly
      100      105      110
Thr Thr Glu Ser Leu Leu Leu Ala Val Met Ala Phe Asp Arg Phe Val
      115      120      125
Ala Ile Cys Arg Pro Leu His Tyr Ser Val Ile Met Asn Trp Gln Val
      130      135      140
Cys Ile Leu Met Ala Val Thr Ile Trp Thr Ile Ala Phe Leu His Ala
145      150      155      160
Leu Leu His Ser Val Met Thr Ser Arg Leu Ser Phe Cys Gly Leu Asn
      165      170      175
His Ile His His Phe Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala
      180      185      190
Cys Gly Asn Thr Glu Leu Asn Leu Trp Leu Leu Asn Thr Val Thr Gly
      195      200      205
Thr Ile Ala Ser Val Pro Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr
      210      215      220
Ile Ile Thr Tyr Leu Phe Leu Lys Thr Arg Ser Cys Ser Met Leu His
225      230      235      240
Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met Val Val Val Leu Phe
      245      250      255
Tyr Ala Pro Val Leu Phe Thr Tyr Ile Arg Pro Thr Ser Gly Ser Ser
      260      265      270
Leu Asp Gln Asp Arg Ile Ile Ala Ile Met Tyr Ser Val Val Thr Pro
      275      280      285
Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Ser
      290      295      300
Ala Leu Asn Arg Lys Val Arg Arg Trp Leu Leu Leu Glu Glu
305      310      315

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<210> 2319

<211> 308

<212> PRT

<213> Mus musculus (M23 6456795-1-63066-65167 771-1694)

<400> 2319

```

Val Leu Leu Asn His Thr Leu Val Thr Glu Phe Leu Leu Leu Gly Val
1      5      10      15
Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe Val Thr Val Leu Ala
      20      25      30
Met Tyr Phe Val Asn Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val
      35      40      45
Ile Ser Asp Pro Arg Leu His Leu Pro Met Tyr Phe Phe Leu Gly Asn
      50      55      60
Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val Thr Val Pro Lys Met
65      70      75      80
Leu Glu Asn Phe Phe Ser Thr Ser Lys Ala Ile Ser Phe Leu Gly Cys
      85      90      95
Ile Thr Gln Leu His Phe Phe Asn Phe Leu Gly Ser Thr Glu Ala Leu
      100      105      110
Leu Leu Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Arg Pro
      115      120      125
Leu His Tyr Pro Ala Ile Met Asn Ser Gln Val Cys Ile Gln Val Ala

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```

      130              135              140
Ile Ser Ile Trp Ala Ile Pro Phe Leu His Ala Leu Val His Ser Ile
145              150              155              160
Leu Thr Ser Gln Leu Asn Phe Cys Gly Ser Asn His Ile His His Phe
      165              170              175
Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Gly Asn Thr Glu
      180              185              190
Leu Asn Arg Trp Leu Leu Asn Thr Leu Thr Gly Thr Val Ala Ile Gly
      195              200              205
Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Ile Val Thr Tyr Leu
      210              215              220
Phe Leu Lys Thr Arg Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr
225              230              235              240
Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu
      245              250              255
Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg
      260              265              270
Ile Ile Ala Val Met Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
      275              280              285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Gly Ala Leu Asn Arg Lys
      290              295              300
Ile Arg Ile Leu
305

```

<210> 2320

<211> 325

<212> PRT

<213> Mus musculus (M24 6456795-1-750-2697 1501-527)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2320

```

Cys Pro Phe Leu Xaa Val Met Ser Asn Gln Thr Ser Val Thr Glu Phe
1      5      10      15
Leu Leu Leu Gly Val Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe
      20      25      30
Val Ile Phe Phe Thr Ile Tyr Phe Ile Asn Ile Thr Gly Asn Gly Ala
      35      40      45
Ile Leu Met Ile Val Ile Leu Asp Pro Arg Leu His Ser Pro Met Tyr
      50      55      60
Phe Phe Leu Gly Asn Leu Ala Cys Leu Asp Ile Ser Tyr Ser Thr Val
65      70      75      80
Thr Val Pro Lys Leu Leu Gln Asn Leu Leu Ser Thr Ser Lys Ala Ile
      85      90      95
Ser Phe Leu Gly Cys Ile Thr Gln Leu His Phe Phe His Phe Leu Gly
      100      105      110
Ser Thr Glu Thr Met Leu Leu Pro Val Met Ala Phe Asp Arg Phe Val
      115      120      125
Ala Ile Cys Arg Pro Leu His Tyr Ser Val Ile Met Asn His Gln Leu
      130      135      140
Cys Ile His Met Thr Val Thr Ile Trp Thr Leu Gly Phe Phe His Ala
145      150      155      160
Leu Leu His Ser Val Met Thr Ser Arg Leu Ser Phe Cys Gly Pro Asn
      165      170      175
His Val His His Phe Phe Cys Asp Ile Lys Pro Leu Leu Asp Leu Ala
      180      185      190
Cys Gly Asn Thr Glu Leu Asn Leu Trp Leu Leu Asn Thr Val Thr Gly
      195      200      205

```

```

Thr Ile Ala Leu Thr Ser Phe Phe Leu Ile Phe Leu Ser Tyr Phe Tyr
 210                215                220
Ile Ile Thr Asn Leu Leu Leu Lys Thr Arg Ser Cys Ser Met Leu His
225                230                235                240
Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met Val Val Val Leu Phe
                245                250                255
Tyr Ala Pro Val Leu Phe Thr Tyr Ile Arg Pro Ala Ser Gly Ser Ser
                260                265                270
Leu Asp Gln Asp Thr Ile Ile Ala Ile Met Tyr Ser Val Val Thr Pro
                275                280                285
Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Ser
                290                295                300
Ala Leu Asn Arg Lys Val Arg Arg Trp Leu Xaa Pro Glu Glu Ser Lys
305                310                315                320
Glu Val Phe Phe Ser
                325

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<210> 2321

<211> 177

<212> PRT

<213> Mus musculus (M25 6456795-1-78460-79066 2-526)

<220>

<221> VARIANT

<222> (1)...(177)

<223> Xaa = Any Amino Acid

<400> 2321

```

Val Ser Ala His Val Cys Met Gly Cys Xaa Leu Ser Trp Pro Val Arg
 1                5                10                15
Cys Glu Ile Ile Phe Gly Val Met His Thr Thr Val Asn Phe Ser Ile
                20                25                30
Val Leu Cys Gly Thr Ser Val Ile His Xaa Phe Cys Asp Val Leu Leu
                35                40                45
Val Leu Lys Leu Ser Cys Leu Tyr Asp His Val Ser Glu Ile Ala Ile
                50                55                60
Ser Asp Phe Ser Ile Ser Leu Ala Phe Phe Cys Phe Ile Ser Pro Asn
65                70                75                80
Phe Thr Tyr Val His Ile Phe Ser Thr Glu Leu Arg Met Pro Phe Val
                85                90                95
Glu Gly Lys Thr Ser Val Phe Ser Thr Cys Leu Cys His Met Thr Ser
                100                105                110
Ile Leu Phe Ile Pro Thr Gly Ile Phe Glu Phe Leu Arg Ser His Thr
                115                120                125
Glu Ser Ser Thr Ser Leu Asp Phe Ile Leu Asn Phe Ser Tyr Phe Ser
                130                135                140
Leu Ser Thr Leu Asn Pro Gly Ile Tyr Ser Leu Arg Asn Glu Ala Val
145                150                155                160
Asp Thr Val Gln Arg Lys Ile Phe Phe Phe Lys Glu Lys Tyr Leu Phe
                165                170                175
Leu

```

<210> 2322

<211> 308

<212> PRT

<213> Mus musculus (M26 6456795-1-84123-87238 211-1134)

<400> 2322

```

Val Leu Leu Asn His Thr Phe Ile Thr Glu Phe Leu Leu Leu Gly Val
 1                5                10                15

```

Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe Val Met Val Leu Ala
 20 25 30
 Met Tyr Phe Ile Asn Val Phe Gly Asn Gly Ala Ile Met Met Ile Val
 35 40 45
 Ile Leu Asp Ser Arg Leu Tyr Ser Pro Met Tyr Phe Phe Leu Gly Asn
 50 55 60
 Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val Thr Val Pro Lys Met
 65 70 75 80
 Leu Glu Asn Phe Phe Ser Thr Ser Lys Ala Ile Ser Phe Leu Gly Cys
 85 90 95
 Ile Thr Gln Leu His Phe Phe His Phe Leu Gly Cys Thr Asp Ala Leu
 100 105 110
 Leu Leu Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Arg Pro
 115 120 125
 Leu His Tyr Pro Ser Ile Met Asn Arg Gln Val Cys Ile Gln Val Ala
 130 135 140
 Ala Thr Ile Trp Ala Ile Pro Phe Leu His Ala Leu Val His Ser Ile
 145 150 155 160
 Leu Thr Ser Gln Leu Asn Phe Cys Gly Ser Asn Arg Ile His His Phe
 165 170 175
 Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Gly Asn Thr Glu
 180 185 190
 Leu Asn Arg Trp Leu Leu Asn Thr Leu Ala Gly Thr Ile Gly Ile Gly
 195 200 205
 Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Ile Val Thr Tyr Leu
 210 215 220
 Phe Leu Lys Thr His Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu
 245 250 255
 Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg
 260 265 270
 Ile Ile Ala Val Met Tyr Thr Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ala Leu Arg Asn Lys Glu Val Arg Cys Ala Leu Asn Arg Lys
 290 295 300
 Leu Arg Ile Leu
 305

<210> 2323

<211> 314

<212> PRT

<213> Mus musculus (M27 6456795-1-89089-90071 35-969)

<220>

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 2323

Ser Leu Phe Tyr Ser Gln Arg Ser Arg Met Asn Val Ala Asn Phe Thr
 1 5 10 15
 Ala Met Thr Ile Phe Leu Leu Leu Met Gly Phe Ser Arg Asn Ser Gln
 20 25 30
 Val Glu Ile Ile Phe Ser Thr Leu Ala Leu Val Val Leu Ile Gly Thr
 35 40 45
 Ile Ser Ile Val Ala Val Thr Ser Leu Ser Ile Arg Leu Cys Ser Leu
 50 55 60
 Met Pro Phe Leu Leu Ile His Leu Phe Cys Phe Asp Val Cys Tyr Ile
 65 70 75 80
 Ser Val Met Met Pro Lys Ser Val Cys Ser Ser Phe Met Tyr Ser Ala

```

      85      90      95
Tyr Ile Ser Leu Ile Glu Cys Thr Leu Gln Val Phe Tyr Ser Gln Ser
      100      105      110
Ser Tyr Thr Ala Met Ala Ile Leu Thr Val Met Ser Tyr Asp Cys Tyr
      115      120      125
Met Ala Val Trp His Lys Val Ile Thr Asn Val Ser Thr Cys Ile His
      130      135      140
Gly Val Leu Ala Val Leu Val Asn Gly Cys Glu Ile Ile Phe Gly Val
      145      150      155      160
Met His Thr Thr Leu Thr Phe Ser Ile Tyr Ile Cys Gly Thr Ser Thr
      165      170      175
Ile Arg Xaa Phe Cys Asp Val Leu Leu Val Leu Lys Leu Ser Phe Thr
      180      185      190
Asn Asp His Val Asn Glu Leu Glu Ser Leu Ala Phe Ser Ser Val Glu
      195      200      205
Gly Arg Thr Lys Ser Phe Ser Thr Cys Leu Gly His Val Ser Val Gly
      210      215      220
Ser Leu Phe Asn Pro Pro Gly Val Phe Glu Phe Leu Asn Pro Tyr Ser
      225      230      235      240
Glu Ser Pro Thr Ser Leu Asp Ile Ile Val Thr Val Phe Ile Leu Pro
      245      250      255
Gln Thr Leu Ser Val Glu Ile Tyr Ser Leu Ser Asn Glu Ala Ile Asp
      260      265      270
Thr Ala Xaa Arg Lys Phe Phe Phe Gln Arg Lys Thr Ser Leu Ser Ile
      275      280      285
Leu His Tyr Phe Leu Leu Gly Ser His Ile Xaa Xaa Val Leu Arg Lys
      290      295      300
Thr Thr Val Ser Met Asn Gln Leu Lys Leu
      305      310

```

<210> 2324

<211> 309

<212> PRT

<213> Mus musculus (M28 6456795-1-95949-101645 434-1360)

<400> 2324

```

Val Leu Leu Asn Gln Thr Leu Val Thr Glu Phe Leu Leu Leu Gly Val
      1      5      10      15
Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe Val Thr Val Leu Ala
      20      25      30
Met Tyr Phe Val Asn Val Ala Gly Asn Gly Ala Ile Leu Leu Ile Val
      35      40      45
Ile Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn
      50      55      60
Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val Thr Val Pro Lys Ile
      65      70      75      80
Leu Asp Asn Phe Phe Ser Thr Ser Lys Ala Ile Ser Phe Leu Gly Cys
      85      90      95
Ile Thr Gln Leu Tyr Phe Phe His Leu Leu Gly Ser Thr Glu Ala Leu
      100      105      110
Leu Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Arg Pro
      115      120      125
Leu His Tyr Pro Ser Ile Met Asn Gly Gln Val Cys Ile Gln Val Ala
      130      135      140
Ile Ser Ile Trp Ala Ile Pro Phe Val His Ala Leu Val His Ser Ile
      145      150      155      160
Leu Thr Ser Gln Leu Asn Phe Cys Gly Ser Asn Gln Ile His His Phe
      165      170      175
Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Gly Asn Thr Glu
      180      185      190
Leu Asn Arg Trp Leu Leu Asn Thr Phe Thr Gly Thr Phe Ala Ile Gly

```

```

      195              200              205
Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Ile Ile Thr Tyr Leu
  210              215              220
Phe Leu Lys Thr Arg Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr
  225              230              235              240
Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu
      245              250              255
Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg
      260              265              270
Ile Ile Ala Val Met Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
      275              280              285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Arg Gly Ala Leu Asn Arg Lys
      290              295              300
Leu Arg Ile Leu Leu
  305

```

<210> 2325

<211> 296

<212> PRT

<213> Mus musculus (M29 6691272-106-1-1090 908-19)

<220>

<221> VARIANT

<222> (1)...(296)

<223> Xaa = Any Amino Acid

<400> 2325

```

Cys Ile Phe Ile Gly Val Phe Leu Ile Ser Ser Ala Ser Gly Ala Met
  1              5              10              15
Pro Gly Gln Asn Tyr Ser Thr Ile Ser Glu Phe Ile Leu Phe Gly Phe
      20              25              30
Ser Ala Phe Pro His Gln Met Leu Pro Ala Leu Phe Leu Leu Tyr Leu
      35              40              45
Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Val Ile Met Ala Ala
      50              55              60
Ile Trp Thr Glu His Arg Leu His Thr Pro Met Tyr Leu Phe Leu Cys
      65              70              75              80
Ala Leu Ser Ile Ser Glu Ile Leu Phe Thr Val Val Ile Thr Pro Arg
      85              90              95
Met Leu Ser Asp Met Leu Ser Thr His Arg Ser Ile Thr Phe Ile Ala
      100              105              110
Cys Ala Asn Gln Leu Phe Phe Ser Phe Thr Phe Gly Tyr Thr His Ser
      115              120              125
Phe Leu Leu Val Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg
      130              135              140
Pro Leu His Tyr His Ala Leu Met Ser Leu Gln Gly Cys Ala Arg Leu
      145              150              155              160
Val Ala Trp Ser Trp Ala Gly Gly Ser Leu Ile Gly Met Ala Leu Thr
      165              170              175
Ile Ile Ile Phe His Leu Thr Phe Cys Glu Ser Asn Val Ile His His
      180              185              190
Ile Leu Cys His Val Phe Ser Leu Leu Lys Leu Ala Cys Gly Glu Arg
      195              200              205
Thr Ala Phe Val Thr Ile Ala Val Ile Leu Val Cys Val Thr Pro Leu
      210              215              220
Ile Gly Cys Leu Val Phe Ile Ile Leu Ser Tyr Ile Phe Ile Val Ala
      225              230              235              240
Ala Ile Leu Arg Ile Pro Ser Thr Glu Gly Arg His Lys Thr Phe Ser
      245              250              255
Thr Cys Ala Ser His Leu Thr Val Val Ile Val His Tyr Gly Phe Ala
      260              265              270

```

Ser Leu Ile Tyr Leu Gln Gly Tyr Pro Leu Glu Ser Asp Xaa Thr Gly
 275 280 285
 Met Ser Ser Trp His Ala Ser Phe
 290 295

<210> 2326

<211> 334

<212> PRT

<213> Mus musculus (M30 6691273-103-1206-2961 586-1585)

<220>

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 2326

Trp Ala Asn Gln Ser Arg Ala Arg Glu Leu Glu Phe Val Leu Leu Gly
 1 5 10 15
 Phe Ala His Val Pro Ser Leu Arg Pro Met Leu Ala Ala Leu Phe Leu
 20 25 30
 Ala Ala Phe Leu Leu Thr Met Ser Gly Asn Ser Leu Ile Val Leu Leu
 35 40 45
 Thr Ser Leu Asp Phe Gly Leu Arg Thr Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 Gln Leu Ala Leu Val Glu Ile Cys Phe Ser Leu Asp Val Ala Pro Arg
 65 70 75 80
 Leu Leu Val Thr Leu Leu Gln Pro Gly Arg Gly Val Ser Pro Thr Ser
 85 90 95
 Cys Ala Leu Gln Leu Leu Leu Val Leu Ser Cys Val Thr Ser Glu Cys
 100 105 110
 Phe Leu Leu Met Val Met Ala Trp Asp Arg Phe Leu Ala Ile Cys Arg
 115 120 125
 Pro Leu Arg Tyr Gly Ala Ile Met Ser Pro Gln Leu Cys Tyr Leu Leu
 130 135 140
 Ala Thr Thr Cys Trp Leu Ala Gly Ile Pro Val Ala Leu Val Phe Thr
 145 150 155 160
 Ile Trp Leu Phe Asn Phe Pro Phe Cys Gly Pro Arg Gly Ile Arg His
 165 170 175
 Phe Phe Cys Asp Ile Ala Pro Leu Leu Ser Leu Val Cys Ala Asp Thr
 180 185 190
 Arg Val Phe Glu Ala Asn Val Phe Val Ala Thr Val Leu Val Ile Met
 195 200 205
 Val Pro Phe Cys Leu Ile Ala Thr Ser Tyr Val Met Ile Leu Val Ala
 210 215 220
 Val Leu Arg Met Pro Ser Ala Ser Gly Arg His Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ile Val Val Ile Leu Phe Tyr Gly Thr Thr Gly
 245 250 255
 Val Ile His Leu Arg Pro Lys Ala Ser Tyr Ser Pro Glu Ser Lys Gln
 260 265 270
 Val Val Ser Leu Ser Tyr Thr Met Val Thr Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Phe Gly Arg Val
 290 295 300
 Cys Cys Gly Arg Xaa Glu Ser Arg Leu His Glu Xaa Thr His Leu Leu
 305 310 315 320
 Cys Gln Pro Phe Ser Val Arg Xaa Leu Leu Arg Pro Thr Phe
 325 330

<210> 2327

<211> 330

<212> PRT

<213> Mus musculus (M31 6691273-105-4369-6206 1597-608)

<220>

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 2327

```

Val Leu Leu Xaa Cys Tyr Xaa Arg Thr Asp Asp Asn Asn Trp Leu Val
 1          5          10          15
Ser Leu Gln Met Ala Arg Ser Leu Glu Leu Ala Asn Met Thr Arg Val
          20          25          30
Gln Lys Phe Leu Leu Leu Gly Leu Ser Thr Arg Leu Asp Ile Arg Asp
          35          40          45
Ala Leu Phe Ala Val Phe Leu Thr Leu Tyr Leu Leu Thr Leu Val Glu
          50          55          60
Asn Thr Leu Ile Ile Tyr Leu Ile Phe Ser His Lys Glu Leu His Lys
65          70          75          80
Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser Cys Leu Glu Met Cys Tyr
          85          90          95
Val Ser Val Thr Met Pro Thr Leu Leu Val Gly Leu Trp Thr Gly Pro
          100          105          110
Tyr His Ile Pro Phe Thr Leu Cys Met Thr Gln Leu Phe Phe Phe Ile
          115          120          125
Val Leu Ile Cys Thr Glu Cys Thr Leu Leu Ala Ser Met Ala Tyr Asp
          130          135          140
Arg Tyr Val Ala Ile Cys Arg Pro Leu His Tyr Pro Leu Leu Met Arg
145          150          155          160
Pro Gln Val Cys Leu Gly Leu Ala Leu Ser Ser Trp Leu Gly Gly Leu
          165          170          175
Ile Val Ser Val Ala Lys Thr Thr Cys Ile Ala Ser Leu Ser Tyr Cys
          180          185          190
Gly Pro Asn Val Leu Asn Gln Phe Phe Cys Asp Val Ser Pro Leu Leu
          195          200          205
Asn Leu Ser Cys Thr His Val Ala Leu Thr Glu Leu Val Asp Phe Ile
          210          215          220
Ser Ala Ile Val Ile Phe Cys Gly Thr Leu Leu Val Ser Leu Ala Ser
225          230          235          240
Tyr Ser Ala Ile Gly Met Ala Val Leu Arg Met Pro Ser Ala Ala Ala
          245          250          255
Arg Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Val Val Val Gly
          260          265          270
Ile Phe Tyr Ser Ala Ala Leu Phe Ile Tyr Cys Arg Pro Ser Arg Ile
          275          280          285
Lys Ser Met Asp Leu Asn Lys Val Leu Ser Val Ile Tyr Thr Val Val
          290          295          300
Thr Pro Leu Cys Asn Pro Ile Ile Tyr Cys Leu Arg Asn Lys Glu Val
305          310          315          320
His Thr Val Leu Lys Lys Thr Leu His Trp
          325          330

```

<210> 2328

<211> 319

<212> PRT

<213> Mus musculus (M32 6691273-108-10257-11726 1388-432)

<220>

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 2328

```

Leu Val Pro Ser Phe Gln Arg His Thr Met Ala Asn Leu Ser Thr Val
 1          5          10          15
Ser Val Phe Ile Leu Gln Gly Phe Ser Ala Val Pro Ala Leu Gln Leu
          20          25          30
Leu Ser Met Ala Ile Phe Leu Leu Ile Tyr Leu Ala Ala Val Leu Gly
          35          40          45
Asn Val Ser Ile Met Ile Ala Val Thr Leu Asp Ser His Leu His Thr
          50          55          60
Pro Met Tyr Phe Phe Ile Lys His Leu Ser Leu Val Asp Leu Cys Ser
65          70          75          80
Thr Ser Thr Thr Leu Pro Arg Ala Leu Val Ala Thr Met Ala Asp Thr
          85          90          95
Lys Glu Ile Ser Leu Pro Ala Cys Ala Ser Gln Leu Phe Ala Phe Val
          100          105          110
Cys Phe Gly Ser Leu Glu Cys Phe Leu Ile Thr Ala Met Ala Phe Asp
          115          120          125
Arg Cys Leu Ala Ile Tyr Arg Pro Leu Thr Tyr Gly Val Thr Met Ser
          130          135          140
Ser Gln Thr Cys Val Ser Leu Val Val Val Ala Trp Val Ser Gly Leu
145          150          155          160
Leu Phe Ser Thr Phe His Met Val Asn Thr Phe Ser Leu Pro Phe Cys
          165          170          175
Gly Pro Asn Met Ile Asp His Phe Phe Cys Asp Ile Pro Pro Leu Met
          180          185          190
His Leu Ala Cys Gly Asp Thr Gln Gly His Glu Ala Ala Gly Phe Ile
          195          200          205
Val Ser Gly Cys Val Ile Met Thr Cys Phe Ala Leu Thr Cys Leu Ser
          210          215          220
Tyr Val Leu Ile Val Tyr Thr Val Val His Ile Arg Ser Ala Ala Gly
225          230          235          240
Arg Trp Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ala Thr Val Leu
          245          250          255
Leu Phe Tyr Gly Thr Gly Ser Ser Ala Tyr Met Gln Pro Thr Ala His
          260          265          270
Tyr Ser Pro Leu Gln Gly Arg Met Ala Ala Ile Phe Tyr Ser Ile Leu
          275          280          285
Met Pro Thr Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Met
          290          295          300
Lys Ala Ala Leu Arg Lys Leu Tyr Pro Gln Val Pro Ser Xaa Ile
305          310          315

```

<210> 2329

<211> 133

<212> PRT

<213> Mus musculus (M33 6850399-12-3847-5066 800-1195)

<220>

<221> VARIANT

<222> (1)...(133)

<223> Xaa = Any Amino Acid

<400> 2329

```

Thr Glu Leu Asn Ser Cys Leu Gln Trp Leu Pro Ile Leu His Arg Ser
 1          5          10          15
Thr Thr Glu Ala Ser Ser Ala Val Leu Xaa Glu Leu Leu Leu Gln Arg
          20          25          30
Pro Ala Ser Ala Leu Xaa Pro Pro Ile Gly Ser Ser Asp Leu Ala Gly
          35          40          45
Cys Phe Ser Val Tyr Ile Leu Thr Leu Thr Asp Asn Thr Thr Val Arg

```

```

      50              55              60
Ile Asn Ser Phe Leu Asn His Lys Leu His Thr Pro Met Ser Ser Phe
65              70              75              80
Cys Phe Gly Leu Ser Ile Leu Asp Leu Cys Phe Thr Pro Ser Thr Val
      85              90              95
Pro Pro Asp His Gln Ile Leu Gly Asn Pro Xaa Gly Pro Glu Lys Leu
      100              105              110
Ala Ile Leu Val Xaa Ala Ile Gln Leu Ser Val Ala Leu Gly Phe Gly
      115              120              125
Ser Thr Val Cys Val
      130

```

<210> 2330
 <211> 191
 <212> PRT
 <213> Mus musculus (M35 6850399-2-1-641 21-587)

<220>
 <221> VARIANT
 <222> (1)...(191)
 <223> Xaa = Any Amino Acid

```

<400> 2330
Asp Ala Ile Ser Gln Pro Leu His Tyr Gly Ala Ile Thr His Ser Glu
1              5              10              15
Ile Leu Trp Gln Leu Ala Thr Val Ala Gln Ile Ser Gly Phe Val Glu
      20              25              30
Phe Arg Ser Pro Ser Ile Phe Gln Leu Pro Arg Cys Gly Gly Gly Gly
      35              40              45
Val Val Cys Lys Ala Xaa Asn Tyr Leu Cys Arg His Asn Phe Pro Gly
      50              55              60
Lys Xaa Leu Ser Thr Val Thr Ala Leu Cys Val Val Thr Leu Met Gly
65              70              75              80
Leu Val Leu Val Ser Tyr Val Ser Ile Val Lys Gly Val Leu Arg Gly
      85              90              95
Gly Pro Ile Glu Asp Met Gly Lys Ala Phe Gly Thr Cys Gly Tyr His
      100              105              110
Leu Ile Ala Gly Leu Leu Phe Phe Lys Ala Ile Ile Ser Val Tyr Thr
      115              120              125
His Pro Arg Asn Glu Phe Thr Gly Ser His Gly Lys Pro Phe Leu Leu
      130              135              140
Leu Tyr Pro Val Val Met Pro Ser Leu Gly Pro Leu Ile Asp Thr Leu
145              150              155              160
Arg Ser Gln Glu Ser Ser Arg Val Ile Lys Arg Leu Val Ala Lys Asp
      165              170              175
Xaa Lys Leu Ser Arg Lys Asn Thr Xaa Cys Thr Ser Arg Ser Trp
      180              185              190

```

<210> 2331
 <211> 320
 <212> PRT
 <213> Mus musculus (M36 7263202-1-54100-55962 166-1125)

```

<400> 2331
Ser Ser Gln Ala Pro Glu Lys Gln Gln Asp Asn Gly Thr Trp Leu Val
1              5              10              15
Thr Glu Phe Leu Leu Val Gly Phe Ser Asn Leu Pro Glu Leu Arg Pro
      20              25              30
Thr Leu Phe Ile Leu Phe Leu Leu Thr Tyr Leu Val Thr Leu Ser Gly
      35              40              45
Asn Ala Thr Ile Ile Thr Ile Ile Gln Val Asp Arg Thr Leu His Thr

```

50	55	60
Pro Met Tyr Arg Phe Leu Ala Val Leu Ser Leu Ser Glu Thr Cys Tyr		
65	70	75
Thr Leu Val Thr Ile Pro Asn Met Leu Ala His Leu Leu Met Glu Ser		80
	85	90
Gln Ala Ile Ser Ile Ala Gly Cys Arg Ala Gln Met Phe Phe Phe Leu		95
	100	105
Gly Leu Gly Cys Ser His Cys Phe Leu Leu Thr Leu Met Gly Tyr Asp		110
	115	120
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Ser Val Ile Met Arg		125
	130	135
Pro Thr Val Cys Leu Cys Leu Gly Ala Leu Val Phe Cys Ser Gly Phe		140
145	150	155
Ser Val Ala Leu Ile Glu Thr Cys Met Ile Phe Ser Ser Pro Phe Cys		160
	165	170
Gly Ala Gly His Val Glu His Phe Phe Cys Asp Ile Ala Pro Val Leu		175
	180	185
Lys Leu Ser Cys Asp Glu Ser Ser Leu Lys Gly Leu Gly Ile Phe Phe		190
	195	200
Leu Ser Ile Leu Val Val Leu Val Ser Phe Leu Phe Ile Leu Leu Ser		205
	210	215
Tyr Ala Phe Ile Val Ala Ala Ile Val Arg Ile Pro Ser Ala Ser Gly		220
225	230	235
Arg Arg Lys Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ile		240
	245	250
Val His Phe Gly Cys Ala Ser Ile Ile Tyr Leu Arg Pro Asp Ser Gly		255
	260	265
Ala Asn Pro Ser Gln Asp Arg Leu Val Ala Val Phe Tyr Thr Val Val		270
	275	280
Thr Pro Leu Leu Asn Pro Val Val Tyr Thr Leu Arg Asn Lys Glu Val		285
	290	295
Arg Val Ala Leu Arg Lys Asn Leu Ala Arg Gly Cys Gly Ala Phe Lys		300
305	310	315
		320

<210> 2332

<211> 122

<212> PRT

<213> Mus musculus (M38 7340303-58-1-1344 4-367)

<220>

<221> VARIANT

<222> (1)...(122)

<223> Xaa = Any Amino Acid

<400> 2332

His Leu Ser Glu Glu Val Gly Phe Ala Val Ser Ser Cys Ile Val Met	
1	5
Ser Ser Phe Ala Leu Thr Val Val Ser Tyr Ile Gly Ile Val Ala Thr	10
	15
	20
Val Leu Arg Ile Pro Ser Val Glu Gly Arg Trp Lys Ala Phe Ser Thr	25
	30
	35
Cys Ser Ser His Leu Thr Thr Val Ile Leu Phe Tyr Gly Thr Gly Ser	40
	45
	50
Phe Val Tyr Leu Arg Pro Ala Ser Gln Tyr Ser Pro Thr Leu Gly Pro	55
65	60
	70
Leu Ala Ser Ile Phe Tyr Ser Val Val Thr Pro Ser Leu Asn Pro Val	75
	80
	85
Val Tyr Cys Leu Arg Asn Lys Asp Met Lys Phe Ala Leu Gln Lys Leu	90
	95
	100
Tyr Cys Gly Arg Lys Tyr Xaa Asp Leu Glu	105
	110
	115
	120

<210> 2333

<211> 356

<212> PRT

<213> Mus musculus (M41 7363372-318-7546-10891 3278-2211)

<220>

<221> VARIANT

<222> (1)...(356)

<223> Xaa = Any Amino Acid

<400> 2333

```

Tyr Val Phe Phe Cys Phe Gln Tyr Ser Xaa Glu Trp Lys Thr Glu Leu
 1           5           10           15
Glu Met Asp Val Ser Asn Gln Thr Thr Val Thr Glu Phe Val Leu Leu
          20           25           30
Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu Ile
          35           40           45
Leu Ser Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu
          50           55           60
Val Ser Ile Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
          65           70           75           80
Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Val Pro
          85           90           95
Leu Val Leu Asp Gly Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser
          100          105          110
Gly Cys Ala Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu
          115          120          125
Cys Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
          130          135          140
Asn Pro Leu Arg Tyr Pro Val Val Met Asn Lys Ala Ala Tyr Val Pro
          145          150          155          160
Met Ala Val Ser Ser Trp Val Ala Gly Gly Ala Asn Ser Leu Val Gln
          165          170          175
Ile Ser Leu Ala Val Gln Leu Pro Phe Cys Gly Asp Asn Val Ile Asn
          180          185          190
His Phe Ile Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp
          195          200          205
Ile Ser Ile Asn Val Ile Ser Met Gly Val Ala Asn Val Ile Phe Leu
          210          215          220
Gly Val Pro Val Leu Phe Ile Phe Val Ser Tyr Ile Phe Ile Leu Ser
          225          230          235          240
Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser
          245          250          255
Thr Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile
          260          265          270
Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp
          275          280          285
Lys Gln Asp Leu Ala Asp Lys Leu Ile Ser Leu Phe Tyr Gly Leu Leu
          290          295          300
Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val
          305          310          315          320
Lys Ala Ala Val Arg Asn Leu Ala Ser His Arg Cys Leu Thr Phe Xaa
          325          330          335
Trp Arg Asp Arg Ala His Asp Pro His Val Leu Met Ala Leu Thr Xaa
          340          345          350
Glu Ser Tyr Cys
          355

```

<210> 2334

<211> 331

<212> PRT

<213> Mus musculus (M42 7363372-319-4901-8603 988-1980)

<400> 2334

Cys Pro Leu Leu Ser Gln Asp Gly Lys Arg Thr Cys Glu Met Glu Gly
 1 5 10 15
 Ala Asn Gln Ser Thr Val Ala Glu Phe Val Leu Leu Gly Leu Ser Asp
 20 25 30
 His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu Ile Leu Leu Met Tyr
 35 40 45
 Leu Val Ile Leu Leu Gly Asn Gly Val Leu Ile Leu Val Ser Ile Leu
 50 55 60
 Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Leu Ser
 65 70 75 80
 Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Ile Pro Leu Val Leu Asp
 85 90 95
 Gly Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe Ser Gly Cys Ala Val
 100 105 110
 Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu Cys Val Leu Leu
 115 120 125
 Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
 130 135 140
 Tyr Pro Val Val Met Asn Lys Ser Ala Tyr Val Pro Met Ala Val Ser
 145 150 155 160
 Ser Trp Val Ala Gly Gly Ala Asn Ser Leu Val Gln Ile Ser Leu Ala
 165 170 175
 Val Gln Leu Pro Phe Cys Gly Asp Asn Val Ile Asn His Phe Thr Cys
 180 185 190
 Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile Ser Ile Asn
 195 200 205
 Val Ile Ser Met Gly Val Ala Asn Val Ile Phe Leu Gly Val Pro Val
 210 215 220
 Leu Phe Ile Phe Val Ser Tyr Ile Phe Ile Leu Ser Thr Ile Leu Arg
 225 230 235 240
 Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ala
 245 250 255
 His Leu Thr Val Val Leu Val Phe Tyr Gly Thr Ile Leu Phe Met Tyr
 260 265 270
 Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp Lys Gln Asp Val
 275 280 285
 Ser Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Leu Thr Pro Met Leu
 290 295 300
 Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Val
 305 310 315 320
 Arg Asn Leu Val Gly Gln Lys Cys Leu Ile Gln
 325 330

<210> 2335

<211> 324

<212> PRT

<213> Mus musculus (M43 7363372-320-18353-20567 840-1811)

<220>

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 2335

Asn Met Glu Arg Ser Asn Lys Thr Thr Pro Val Ser Ser Phe Ile Leu
 1 5 10 15
 Leu Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe Val Leu

```

      20      25      30
Ile Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Val Val Leu Ile
      35      40      45
Leu Val Ser Ile Leu Asp Ser His Leu His Thr Pro Met Tyr Phe Phe
      50      55      60
Leu Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Val
65      70      75      80
Pro Leu Ile Leu Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile Ser Phe
      85      90      95
Ser Gly Cys Ala Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr
      100      105      110
Glu Cys Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile
      115      120      125
Cys Asn Pro Leu Arg Tyr Pro Val Val Met Ser Lys Ala Ala Tyr Val
      130      135      140
Pro Met Ala Ala Gly Ser Trp Val Ser Gly Ser Ile Thr Ala Thr Val
145      150      155      160
Gln Ile Ser Leu Ala Met Thr Leu Pro Phe Cys Gly Asp Asn Val Ile
      165      170      175
Asn His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala
      180      185      190
Asp Ile Ser Ile Asn Val Ile Ser Met Ala Val Ala Asn Ala Met Phe
      195      200      205
Leu Gly Val Pro Val Leu Phe Ile Phe Val Ser Tyr Ile Phe Ile Leu
      210      215      220
Ser Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe
225      230      235      240
Ser Thr Cys Ser Ala His Leu Thr Val Val Leu Val Phe Tyr Gly Thr
      245      250      255
Ile Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala
      260      265      270
Asp Lys Gln Asp Leu Ala Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val
      275      280      285
Val Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp
      290      295      300
Val Lys Ala Ala Val Thr Asn Leu Val Gly Gln Lys His Phe Lys Trp
305      310      315      320
Xaa Trp Cys Met

```

<210> 2336

<211> 257

<212> PRT

<213> Mus musculus (M44 7363372-320-22007-23346 51-820)

<220>

<221> VARIANT

<222> (1)...(257)

<223> Xaa = Any Amino Acid

<400> 2336

```

Leu Leu Phe Val Val Lys Met Lys Arg Leu Gln Thr Cys Xaa Phe Xaa
1      5      10      15
Gln Pro Ala Leu Leu Arg Gly Leu Ser Ser Leu Lys Gly Gln Arg Asp
      20      25      30
Pro Arg Leu Asn Glu Cys Cys Met Pro Leu Leu Xaa Gln Asp Pro Arg
      35      40      45
Gly Lys Ala Ser Phe Leu Val Cys Leu Val Leu Val Thr Leu Ser Cys
      50      55      60
Met Trp Gln Glu Gln Cys Pro Pro Met His Val Thr Phe Val His Ser
65      70      75      80

```

Leu Ala Val Arg Gln Leu Lys Val Ile Asn Ser Arg Ala Ala Cys Val
 85 90 95
 Leu Arg Ser Ala Glu Leu Xaa Ala Thr Gly Ala Thr Tyr Pro Leu Ser
 100 105 110
 Thr Asn Tyr Cys Ile Cys Lys Thr Arg Thr Ser Ala Arg Ala Asp Ile
 115 120 125
 Ser Ile Asn Val Ile Ser Ile Gly Val Glu Leu Gly Val Pro Val Leu
 130 135 140
 Phe Ile Phe Ile Ser Tyr Ile Phe Ile Leu Ser Thr Ile Leu Gly Ile
 145 150 155 160
 Pro Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ala His
 165 170 175
 Leu Thr Met Val Ile Ile Phe Tyr Gly Thr Ile Leu Phe Met Tyr Gly
 180 185 190
 Lys Pro Lys Ser Lys Asp Pro Leu Gly Ala Asp Lys Gln Asp Leu Ala
 195 200 205
 Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val Thr Pro Met Leu Asn
 210 215 220
 Leu Arg Thr Thr Val Arg Ala Phe Ile Phe Arg Lys Tyr Phe Ser Gln
 225 230 235 240
 Xaa Trp Trp Gln Gly Met Leu Trp Thr Val Thr His Arg Thr Glu Lys
 245 250 255
 Ile

<210> 2337

<211> 321

<212> PRT

<213> Mus musculus (M45 7363372-320-7359-9353 512-1474)

<220>

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 2337

Asp Ser Met Glu Ile Asn Asn Gln Thr Ser Phe Pro Val Ser Ser Phe
 1 5 10 15
 Ile Leu Leu Gly Leu Ser Ala His Pro Lys Leu Glu Lys Thr Phe Phe
 20 25 30
 Met Leu Ile Leu Leu Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Ile
 35 40 45
 Leu Ile Leu Val Ser Ile Leu Asp Ser His Leu His Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser
 65 70 75 80
 Ser Val Pro Leu Ile Leu Asp Ser Phe Leu Thr Pro Arg Lys Thr Ile
 85 90 95
 Ser Phe Ser Gly Cys Ala Val Gln Met Phe Leu Ser Phe Ala Met Gly
 100 105 110
 Ala Thr Glu Cys Val Leu Leu Ser Met Met Ala Phe Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Asn Pro Leu Arg Tyr Pro Val Val Met Asn Lys Ala Ala
 130 135 140
 Tyr Val Pro Met Ala Val Ser Ser Trp Ser Gly Gly Ile Ala Val Ser
 145 150 155 160
 Val Val Gln Thr Ser Leu Ala Met Lys Leu Thr Phe Cys Gly Asp Asn
 165 170 175
 Val Ile Asn His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala
 180 185 190
 Cys Ala Asp Ile Ser Ile Asn Val Ile Ser Met Gly Val Thr Asn Ile


```

      195              200              205
Ile Phe Leu Gly Val Pro Val Leu Phe Ile Ser Phe Ser Tyr Val Phe
 210              215              220
Ile Leu Val Thr Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg Lys Lys
 225              230              235              240
Ala Phe Ser Thr Cys Ser Ala His Leu Thr Val Val Leu Val Phe Tyr
      245              250              255
Gly Thr Ile Leu Phe Met Tyr Gly Lys Pro Lys Ser Lys Asp Pro Leu
      260              265              270
Gly Ala Asp Lys Gln Asp Leu Ala Asp Xaa Leu Ile Ser Leu Phe Tyr
      275              280              285
Gly Val Leu Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn
      290              295              300
Lys Asp Val Arg Ala Ala Val Thr Asn Leu Val Val Leu Lys Lys Ser
 305              310              315              320
Phe

```

<210> 2338

<211> 300

<212> PRT

<213> Mus musculus (M50 8075174-14-7636-10544 2097-1198)

<220>

<221> VARIANT

<222> (1)...(300)

<223> Xaa = Any Amino Acid

<400> 2338

```

Gln Asp Leu Val Ala Thr Gly Val Ile Gly Ala Val Leu Ser Thr Met
 1              5              10              15
Gly Val Val Gly Val Val Gly Asn Val Tyr Thr Leu Val Val Met Cys
      20              25              30
Arg Phe Leu Arg Ala Ser Ala Ser Met Tyr Val Tyr Val Val Asn Leu
      35              40              45
Ala Leu Ala Asp Leu Leu Tyr Leu Leu Ser Ile Pro Phe Ile Val Ala
      50              55              60
Thr Tyr Val Thr Lys Asp Trp His Phe Gly Asp Val Gly Cys Arg Val
      65              70              75              80
Leu Phe Ser Leu Asp Phe Leu Thr Met His Ala Ser Ile Phe Thr Leu
      85              90              95
Thr Ile Met Ser Ser Glu Arg Tyr Ala Ala Val Leu Arg Pro Leu Asp
      100              105              110
Thr Val Gln Arg Ser Lys Gly Tyr Arg Lys Leu Leu Ala Leu Gly Thr
      115              120              125
Cys Cys Trp His Cys Cys Xaa Pro Tyr Pro Xaa Cys Tyr Ala Ile Arg
      130              135              140
Leu Val Arg Arg Gly Ser Lys Ser Leu Cys Leu Pro Ala Trp Gly Pro
      145              150              155              160
Arg Ala His Arg Thr Tyr Leu Thr Leu Leu Phe Gly Thr Ser Ile Val
      165              170              175
Gly Pro Gly Leu Val Ile Gly Leu Leu Tyr Ile Arg Leu Ala Arg Ala
      180              185              190
Tyr Trp Leu Ser Gln Gln Ala Ser Phe Lys Gln Thr Arg Arg Leu Pro
      195              200              205
Asn Pro Arg Val Leu Tyr Leu Ile Leu Gly Ile Val Leu Leu Phe Trp
      210              215              220
Ala Cys Phe Leu Pro Phe Val Ala Met Ala Ala Ala Gly Pro Val Pro
      225              230              235              240
Pro Gly His Ala Thr Asp Thr Arg Ala Ala Arg Ile Ile Asn Tyr Leu
      245              250              255

```

Thr Ala Cys Leu Thr Tyr Gly Asn Ser Cys Ile Asn Pro Phe Leu Tyr
 260 265 270
 Thr Leu Leu Thr Lys Asn Tyr Arg Glu Tyr Leu Arg Gly Arg Gln Arg
 275 280 285
 Ser Leu Gly Ser Ser Cys Arg Gly Pro Gly Ser Ala
 290 295 300

<210> 2339

<211> 340

<212> PRT

<213> Mus musculus (M51 8076974-22-383-3835 1573-554)

<220>

<221> VARIANT

<222> (1)...(340)

<223> Xaa = Any Amino Acid

<400> 2339

Cys Leu Phe Phe Pro Gln Arg Asn Leu Asp Ala Met Asn Arg Ser Ala
 1 5 10 15
 Ala His Val Thr Glu Phe Val Leu Leu Gly Phe Pro Gly Ser Trp Lys
 20 25 30
 Ile Gln Ile Phe Leu Phe Val Leu Phe Leu Val Phe Tyr Val Leu Thr
 35 40 45
 Leu Leu Gly Asn Gly Ala Ile Ile Cys Ala Val Arg Cys Asp Ser Arg
 50 55 60
 Leu His Thr Pro Met Tyr Phe Leu Leu Gly Asn Phe Ala Phe Leu Glu
 65 70 75 80
 Ile Trp Tyr Val Ser Ser Thr Ile Pro Asn Ile Leu Ala Asn Ile Leu
 85 90 95
 Ser Lys Thr Lys Ala Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr
 100 105 110
 Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Leu Phe Leu Ala Val Met
 115 120 125
 Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Thr
 130 135 140
 Ile Met Thr Arg Arg Leu Cys Cys Ile Leu Val Ser Ser Cys Trp Leu
 145 150 155 160
 Ile Gly Phe Leu Gly Tyr Pro Ile Pro Ile Phe Ser Ile Ser Gln Leu
 165 170 175
 Pro Phe Cys Gly Ser Asn Ile Ile Asp His Phe Leu Cys Asp Met Asp
 180 185 190
 Pro Leu Met Ala Leu Ser Cys Ala Pro Ala Pro Ile Thr Glu Phe Ile
 195 200 205
 Phe Tyr Ala Gln Ser Ser Phe Val Leu Phe Phe Thr Ile Ala Tyr Ile
 210 215 220
 Leu Arg Ser Tyr Ile Leu Leu Arg Ala Val Phe Gln Val Pro Ser
 225 230 235 240
 Ala Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val
 245 250 255
 Val Val Ser Leu Phe Tyr Gly Thr Val Met Val Met Tyr Val Ser Pro
 260 265 270
 Thr Tyr Gly Ile Pro Ile Leu Met Gln Lys Ile Leu Thr Leu Val Tyr
 275 280 285
 Ser Val Met Thr Pro Leu Phe Asn Pro Leu Ile Tyr Ser Leu Arg Asn
 290 295 300
 Lys Asp Met Lys Leu Ala Leu Arg Asn Val Leu Leu Gly Met Arg Ile
 305 310 315 320
 Val Lys Asn Met Xaa Val Lys Ala Val Ser Tyr Ser His Val Leu Ile
 325 330 335
 Lys Asn Lys Leu

340

<210> 2340

<211> 325

<212> PRT

<213> Mus musculus (M57 8218295-1-14626-16881 1501-527)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 2340

Cys	Pro	Phe	Leu	Xaa	Val	Met	Ser	Asn	Gln	Thr	Ser	Val	Thr	Glu	Phe
1				5					10					15	
Leu	Leu	Leu	Gly	Val	Thr	Asp	Ile	Gln	Glu	Leu	Asn	Pro	Ile	Leu	Phe
			20					25					30		
Val	Ile	Phe	Phe	Thr	Ile	Tyr	Phe	Val	Asn	Ile	Thr	Gly	Asn	Gly	Ala
			35				40					45			
Ile	Leu	Met	Ile	Val	Ile	Leu	Asp	Pro	Arg	Leu	His	Ser	Pro	Met	Tyr
			50			55					60				
Phe	Phe	Leu	Gly	Asn	Leu	Ala	Cys	Leu	Asp	Ile	Cys	Phe	Ser	Thr	Val
65				70					75					80	
Thr	Leu	Pro	Lys	Met	Leu	Gln	Asn	Leu	Leu	Ser	Thr	Asn	Lys	Ala	Ile
			85					90					95		
Ser	Phe	Leu	Gly	Cys	Ile	Thr	Gln	Leu	His	Phe	Phe	His	Phe	Leu	Gly
			100				105						110		
Ser	Thr	Glu	Ala	Met	Leu	Leu	Pro	Val	Met	Ala	Phe	Asp	Arg	Phe	Val
			115				120					125			
Ala	Ile	Cys	Arg	Pro	Leu	His	Tyr	Ser	Val	Ile	Met	Asn	His	Gln	Leu
			130			135					140				
Cys	Ile	His	Met	Thr	Val	Thr	Ile	Trp	Thr	Leu	Gly	Phe	Phe	His	Ala
145				150					155					160	
Leu	Leu	His	Ser	Val	Met	Thr	Ser	Arg	Leu	Ser	Phe	Cys	Gly	Pro	Asn
			165					170					175		
His	Val	His	His	Phe	Phe	Cys	Asp	Ile	Lys	Pro	Leu	Leu	Asp	Leu	Ala
			180				185						190		
Cys	Gly	Asn	Thr	Glu	Leu	Asn	Leu	Trp	Leu	Leu	Asn	Thr	Val	Thr	Gly
		195				200					205				
Thr	Ile	Ala	Leu	Thr	Pro	Phe	Phe	Leu	Thr	Phe	Leu	Ser	Tyr	Phe	Tyr
		210				215					220				
Ile	Ile	Thr	Tyr	Leu	Phe	Leu	Lys	Thr	Arg	Ser	Cys	Ser	Met	Leu	His
225				230					235					240	
Lys	Ala	Leu	Ser	Thr	Cys	Ala	Ser	His	Phe	Met	Val	Val	Ile	Leu	Leu
			245					250					255		
Tyr	Val	Pro	Val	Leu	Phe	Thr	Tyr	Ile	Arg	Pro	Ala	Ser	Gly	Ser	Ser
		260					265						270		
Leu	Asp	Gln	Asp	Arg	Ile	Ile	Ala	Ile	Met	Tyr	Ser	Val	Val	Thr	Pro
		275					280				285				
Ala	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Arg	Ser
		290				295					300				
Ala	Leu	Asn	Arg	Lys	Val	Arg	Arg	Trp	Leu	Xaa	Phe	Glu	Glu	Ile	Xaa
305				310					315					320	
Ile	Thr	Leu	Leu	Trp											
				325											

<210> 2341

<211> 177

<212> PRT

<213> Mus musculus (M63 8218295-1-78460-79066 2-526)

<220>

<221> VARIANT

<222> (1)...(177)

<223> Xaa = Any Amino Acid

<400> 2341

Val Ser Ala His Val Cys Met Gly Cys Xaa Leu Ser Trp Pro Val Arg
 1 5 10 15
 Cys Glu Ile Ile Phe Gly Val Met His Thr Thr Val Asn Phe Ser Ile
 20 25 30
 Val Leu Cys Gly Thr Ser Val Ile His Xaa Phe Cys Asp Val Leu Leu
 35 40 45
 Val Leu Lys Leu Ser Cys Leu Tyr Asp His Val Ser Glu Ile Ala Ile
 50 55 60
 Ser Asp Phe Ser Ile Ser Leu Ala Phe Phe Cys Phe Ile Ser Pro Asn
 65 70 75 80
 Phe Thr Tyr Val His Ile Phe Ser Thr Glu Leu Arg Met Pro Phe Val
 85 90 95
 Glu Gly Lys Thr Ser Val Phe Ser Thr Cys Leu Cys His Met Thr Ser
 100 105 110
 Ile Leu Phe Ile Pro Thr Gly Ile Phe Glu Phe Leu Arg Ser His Thr
 115 120 125
 Glu Ser Ser Thr Ser Leu Asp Phe Ile Leu Asn Phe Ser Tyr Phe Ser
 130 135 140
 Leu Ser Thr Leu Asn Pro Gly Ile Tyr Ser Leu Arg Asn Glu Ala Val
 145 150 155 160
 Asp Thr Val Gln Arg Lys Ile Phe Phe Phe Lys Glu Lys Tyr Leu Phe
 165 170 175
 Leu

<210> 2342

<211> 314

<212> PRT

<213> Mus musculus (M65 8218295-1-89089-90071 35-969)

<220>

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 2342

Ser Leu Phe Tyr Ser Gln Arg Ser Arg Met Asn Val Ala Asn Phe Thr
 1 5 10 15
 Ala Met Thr Ile Phe Leu Leu Leu Met Gly Phe Ser Arg Asn Ser Gln
 20 25 30
 Val Glu Ile Ile Phe Ser Thr Leu Ala Leu Val Val Leu Ile Gly Thr
 35 40 45
 Ile Ser Ile Val Ala Val Thr Ser Leu Ser Ile Arg Leu Cys Ser Leu
 50 55 60
 Met Pro Phe Leu Leu Ile His Leu Phe Cys Phe Asp Val Cys Tyr Ile
 65 70 75 80
 Ser Val Met Met Pro Lys Ser Val Cys Ser Ser Phe Met Tyr Ser Ala
 85 90 95
 Tyr Ile Ser Leu Ile Glu Cys Thr Leu Gln Val Phe Tyr Ser Gln Ser
 100 105 110
 Ser Tyr Thr Ala Met Ala Ile Leu Thr Val Met Ser Tyr Asp Cys Tyr
 115 120 125
 Met Ala Val Trp His Lys Val Ile Thr Asn Val Ser Thr Cys Ile His
 130 135 140
 Gly Val Leu Ala Val Leu Val Asn Gly Cys Glu Ile Ile Phe Gly Val

```

145          150          155          160
Met His Thr Thr Leu Thr Phe Ser Ile Tyr Ile Cys Gly Thr Ser Thr
          165          170          175
Ile Arg Xaa Phe Cys Asp Val Leu Leu Val Leu Lys Leu Ser Phe Thr
          180          185          190
Asn Asp His Val Asn Glu Leu Glu Ser Leu Ala Phe Ser Ser Val Glu
          195          200          205
Gly Arg Thr Lys Ser Phe Ser Thr Cys Leu Gly His Val Ser Val Gly
          210          215          220
Ser Leu Phe Asn Pro Pro Gly Val Phe Glu Phe Leu Asn Pro Tyr Ser
225          230          235          240
Glu Ser Pro Thr Ser Leu Asp Ile Ile Val Thr Val Phe Ile Leu Pro
          245          250          255
Gln Thr Leu Ser Val Glu Ile Tyr Ser Leu Ser Asn Glu Ala Ile Asp
          260          265          270
Thr Ala Xaa Arg Lys Phe Phe Phe Gln Arg Lys Thr Ser Leu Ser Ile
          275          280          285
Leu His Tyr Phe Leu Leu Gly Ser His Ile Xaa Xaa Val Leu Arg Lys
          290          295          300
Thr Thr Val Ser Met Asn Gln Leu Lys Leu
305          310

```

<210> 2343

<211> 335

<212> PRT

<213> Mus musculus (M70 8439670-95-9581-11872 695-1697)

<220>

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 2343

```

His Asp His Pro Ser Ala Glu Val Gly Gly Ala Met Ala Asn Ser Thr
1          5          10          15
Thr Val Thr Glu Phe Ile Leu Leu Gly Leu Ser Asp Ala Cys Glu Leu
          20          25          30
Gln Val Leu Ile Phe Leu Gly Phe Leu Leu Thr Tyr Phe Leu Ile Leu
          35          40          45
Leu Gly Asn Phe Leu Ile Ile Phe Ile Thr Leu Val Asp Arg Arg Leu
          50          55          60
Tyr Thr Pro Met Tyr Tyr Phe Leu Arg Asn Phe Ala Met Leu Glu Ile
65          70          75          80
Trp Phe Thr Ser Val Ile Phe Pro Lys Met Leu Thr Asn Ile Ile Thr
          85          90          95
Gly His Lys Thr Ile Ser Leu Leu Gly Cys Phe Leu Gln Ala Phe Leu
          100          105          110
Tyr Phe Phe Leu Gly Thr Thr Glu Phe Phe Leu Leu Ala Val Met Ser
          115          120          125
Phe Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg Tyr Ala Thr Ile
          130          135          140
Met Ser Lys Arg Val Cys Val Gln Leu Val Phe Cys Ser Trp Met Ser
145          150          155          160
Gly Leu Leu Leu Ile Ile Val Pro Ser Ser Ile Val Phe Gln Gln Pro
          165          170          175
Phe Cys Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Asn Phe Pro
          180          185          190
Leu Met Glu Leu Ile Cys Ala Asp Thr Ser Leu Val Glu Phe Leu Gly
          195          200          205
Phe Val Ile Ala Asn Phe Ser Leu Leu Gly Thr Leu Ala Val Thr Ala
210          215          220

```

Thr Cys Tyr Gly His Ile Leu Tyr Thr Ile Leu His Ile Pro S r Ala
 225 230 235 240
 Lys Glu Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val
 245 250 255
 Val Ser Leu Phe Tyr Gly Ser Cys Ile Phe Met Tyr Val Arg Ser Gly
 260 265 270
 Lys Asn Gly Gln Gly Glu Asp His Asn Lys Val Val Ala Leu Leu Asn
 275 280 285
 Thr Val Val Thr Pro Thr Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn
 290 295 300
 Lys Gln Val Lys Gln Val Phe Arg Glu His Val Ser Lys Phe Gln Lys
 305 310 315 320
 Phe Ser Gln Thr Xaa Arg Lys Ala Pro Leu Gln Thr Cys Leu Thr
 325 330 335

<210> 2344

<211> 139

<212> PRT

<213> Mus musculus (M71 8439670-97-10488-11856 213-627)

<220>

<221> VARIANT

<222> (1)...(139)

<223> Xaa = Any Amino Acid

<400> 2344

Ser Ile Val Cys Ser Leu Ser Leu Ser Phe Phe Leu Ser Phe Phe Leu
 1 5 10 15
 Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Ser Leu
 20 25 30
 Ser Leu Ser Leu Ser Leu Ser Leu Ser Phe Phe Leu Ser Phe Phe Leu
 35 40 45
 Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Leu Pro Thr Phe Pro Pro
 50 55 60
 Ser Leu Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu
 65 70 75 80
 Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu
 85 90 95
 Ser Phe Phe Leu Ser Ser Leu Ser Phe Leu Ser Phe Tyr Ile Tyr Xaa
 100 105 110
 Trp Leu Val Cys Gly Pro Leu Pro Ser Xaa Gly Thr Val Gly Lys Gln
 115 120 125
 Ser Cys Val Met Met Leu Ile Cys Ser Trp Leu
 130 135

<210> 2345

<211> 331

<212> PRT

<213> Mus musculus (M72 8439916-11-1-1677 434-1425)

<220>

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 2345

Phe Leu Leu Ala Trp Val His Arg Phe Leu Xaa Arg Arg Met Gly Phe
 1 5 10 15
 Glu Asn Gly Ser Ser Val Thr Glu Phe Ile Leu Val Gly Leu Thr Lys
 20 25 30
 Glu Ser Asp Leu Gln Cys Pro Leu Phe Ile Leu Phe Leu Met Met Tyr

```
<210> 2346
<211> 333
<212> PRT
<213> Mus musculus (M73 8439916-12-562-4356 2317-1320)
```

```
<220>  
<221> VARIANT  
<222> (1)...(333)  
<223> Xaa = Any Amino Acid
```

<400> 2346															
Ile	Ser	Leu	Ile	Ser	Phe	Ile	Ser	Thr	Asp	Ser	Thr	Xaa	Arg	Arg	Met
1				5					10					15	
Val	Val	Thr	Asn	Gly	Ser	Leu	Val	Thr	Glu	Phe	Ile	Leu	Leu	Gly	Leu
			20					25					30		
Thr	Asp	Asn	Pro	Asp	Leu	Gln	Ile	Pro	Leu	Phe	Leu	Val	Phe	Leu	Val
		35				40						45			
Met	Tyr	Met	Ile	Thr	Ala	Phe	Gly	Asn	Leu	Thr	Leu	Ile	Leu	Leu	Thr
	50					55					60				
Val	Leu	Asn	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Phe	Asn
65				70						75				80	
Leu	Ser	Phe	Ile	Asp	Leu	Cys	Tyr	Ser	Ser	Val	Val	Thr	Pro	Lys	Leu
				85					90					95	

Leu Met Asn Phe Val Leu Lys Lys Asn Ile Ile Gly Phe Ala Gly Cys
 100 105 110
 Met Thr Gln Leu Tyr Phe Phe Cys Phe Ph Val Ile Ser Glu Cys Tyr
 115 120 125
 Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 130 135 140
 Leu Met Tyr Asn Val Thr Met Ser Pro Lys Val Cys Ser Tyr Leu Met
 145 150 155 160
 Leu Gly Ser Tyr Leu Met Gly Phe Ser Asp Ala Met Ile His Thr Gly
 165 170 175
 Cys Ile Leu Arg Leu Thr Phe Cys Asp Gly Asn Thr Ile Asn His Tyr
 180 185 190
 Phe Cys Asp Leu Leu Pro Leu Met Gln Leu Ser Cys Thr Ser Thr Tyr
 195 200 205
 Ile Asn Glu Val Glu Ile Phe Ile Val Gly Gly Lys Asp Ile Thr Val
 210 215 220
 Pro Ser Ile Val Ile Ile Ser Tyr Gly Phe Ile Leu Ser Asn Ile
 225 230 235 240
 Leu Gln Ile Lys Ser Thr Gly Gly Arg Ser Lys Ala Phe Asn Thr Cys
 245 250 255
 Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Cys Ala Phe
 260 265 270
 Met Tyr Leu Lys Pro Pro Ser Ala Gly Ser Leu Asn Glu Gly Lys Val
 275 280 285
 Ser Ser Val Phe Tyr Thr Ile Val Val Pro Met Met Asn Pro Leu Ile
 290 295 300
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Arg Lys Thr Leu
 305 310 315 320
 Ser Arg Arg Lys Phe Xaa Xaa Xaa Ile Tyr Tyr Leu Cys
 325 330

<210> 2347

<211> 343

<212> PRT

<213> Mus musculus (M74 8439916-15-1-3070 860-1887)

<220>

<221> VARIANT

<222> (1)...(343)

<223> Xaa = Any Amino Acid

<400> 2347

Phe Ser Phe Ile Phe Phe Val Ser Thr Asp Ser Leu Arg Glu Asp Met
 1 5 10 15
 Thr Phe Glu Asn Ala Ser Met Val Ile Glu Phe Ile Leu Leu Gly Ile
 20 25 30
 Thr Asp Gln Pro Asp Leu Lys Ile Pro Phe Phe Leu Leu Phe Phe Val
 35 40 45
 Gly Tyr Met Ile Thr Val Leu Gly Asn Leu Thr Leu Ile Ile Leu Ile
 50 55 60
 Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe Asn
 65 70 75 80
 Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys Met
 85 90 95
 Leu Met Ser Phe Ile Gln Lys Lys Asn Ile Ile Ser Tyr Thr Gly Cys
 100 105 110
 Met Ile Gln Leu Tyr Phe Phe Cys Phe Phe Val Ile Ser Glu Cys Tyr
 115 120 125
 Val Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 130 135 140
 Leu Leu Tyr Asn Val Thr Leu Ser Ser Lys Val Cys Cys Tyr Leu Met

145 150 155 160
 Leu Gly Ser Tyr Phe Met Gly Phe Ser Gly Ala Met Ile His Thr Gly
 165 170 175
 Cys Ile Leu Arg Leu Thr Phe Cys Asp Gly Asn Thr Ile Asn His Tyr
 180 185 190
 Phe Cys Asp Leu Leu Pro Leu Leu Gln Ile Ser Cys Thr Ser Thr Tyr
 195 200 205
 Ile Asn Glu Ile Glu Leu Phe Ile Val Ala Gly Lys Asp Ile Ile Val
 210 215 220
 Pro Thr Ile Ile Ile Phe Ile Ser Tyr Gly Phe Ile Leu Phe Ser Val
 225 230 235 240
 Leu Lys Ile Lys Ser Thr Glu Ser Arg Ser Lys Ala Phe Ser Thr Cys
 245 250 255
 Ser Ser His Met Leu Ala Val Ser Leu Phe Phe Gly Ser Gly Ala Phe
 260 265 270
 Met Tyr Leu Lys Pro Thr Ser Ala Leu Ser Ile Asn Lys Gly Lys Phe
 275 280 285
 Ser Ser Leu Phe Tyr Thr Ile Val Val Pro Met Met Asn Pro Leu Ile
 290 295 300
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu Arg Lys Thr Leu
 305 310 315 320
 Asn Arg Arg Ile Phe Ser Ser Xaa Thr Gly Tyr Leu Xaa Ala Tyr Thr
 325 330 335
 Xaa Thr Ile Glu Arg Leu Cys
 340

<210> 2348

<211> 321

<212> PRT

<213> Mus musculus (M75 8439916-16-717-3690 2556-1594)

<220>

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 2348

Lys Lys Met Ala Ser Ala Asn Val Ser Leu Val Thr Glu Phe Ile Leu
 1 5 10 15
 Val Gly Leu Thr Asn Gln Pro Asp Leu Gln Ile Pro Leu Phe Phe Val
 20 25 30
 Phe Leu Ile Met Tyr Ile Val Thr Ala Leu Gly Asn Leu Cys Leu Ile
 35 40 45
 Ile Leu Ile Val Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Phe Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Thr Val Phe Thr
 65 70 75 80
 Pro Lys Met Leu Met Asn Phe Ile Leu Ser Lys Asn Ala Ile Ser Tyr
 85 90 95
 Met Gly Cys Leu Thr Gln Leu Tyr Phe Phe Cys Phe Phe Val Ile Ser
 100 105 110
 Glu Cys Tyr Val Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro Lys Leu Cys Leu
 130 135 140
 Asn Leu Met Leu Gly Thr Tyr Ala Met Ala Phe Ser Gly Ala Met Ala
 145 150 155 160
 His Thr Gly Cys Met Leu Arg Leu Thr Phe Cys Asp Ala Asn Thr Ile
 165 170 175
 Asn His Tyr Phe Cys Asp Ile Leu Pro Val Met Gln Leu Ser Cys Thr
 180 185 190

```

Ser Thr Tyr Val Asn Glu Leu Val Val Phe Ile Val Val Gly Ile Asn
    195                200                205
Ile Ile Val Pro Ser Ile Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu
    210                215                220
Ser Ser Ile Phe His Ile Lys Ser Asn Glu Gly Arg Ser Lys Ala Phe
    225                230                235                240
Ser Thr Cys Ser Ser His Ile Ile Ala Val Cys Leu Phe Phe Gly Ser
    245                250                255
Gly Ala Phe Met Tyr Leu Lys Pro Ser Ser Ser Ser Met Asp Gln
    260                265                270
Gly Lys Thr Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Met Asn
    275                280                285
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ile Ala Leu Arg
    290                295                300
Lys Thr Leu Ser Arg Trp Lys Phe Xaa Lys Glu Thr Thr Cys Thr Cys
    305                310                315                320
Leu

```

<210> 2349

<211> 217

<212> PRT

<213> Mus musculus (M76 8439916-16-8665-10443 1774-1125)

<220>

<221> VARIANT

<222> (1)...(217)

<223> Xaa = Any Amino Acid

<400> 2349

```

Phe Leu Thr Phe Leu Pro Leu Leu Pro Phe Leu Ser Phe Phe Leu Ser
  1                5                10                15
Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Ser Glu Cys
    20                25                30
Cys Val Leu Thr Ser Met Ala Tyr Asp Ser Ile Cys Asn Pro Leu Leu
    35                40                45
Tyr Asn Leu Phe Met Ser Pro Lys Xaa Cys Leu Asn Leu Ile Leu Gly
    50                55                60
Ser Phe Phe Ile Ser Phe Ser Asp Ala Val Ala His Ser Thr Cys Arg
    65                70                75                80
Leu Lys Leu Thr Phe Cys Asp Cys Asp Ile Pro Pro Leu Leu Gln Leu
    85                90                95
Cys Cys Thr Ser Thr Tyr Val Asn Glu Leu Val Ile Phe Phe Val Val
    100                105                110
Gly Cys Ile Asn Ile Ile Val Pro Ser Ser Thr Ile Leu Ile Ser Tyr
    115                120                125
Asp Phe Ile Leu Ser Ser Met Phe Cys Ile Lys Ser Ser Glu Gly Arg
    130                135                140
Ser Lys Ala Phe Ser Thr Tyr Ser Ser His Val Ile Ser Leu Ser Leu
    145                150                155                160
Phe Phe Asp Ser Ser Ala Phe Val Tyr Phe Lys Ser Ser Ser Ala Gly
    165                170                175
Ser Leu Gly Glu Glu Asn Ile Ser Ser Val Phe Tyr Ser Asn Val Val
    180                185                190
Leu Ile Val Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Ser Leu
    195                200                205
Arg Lys Thr Leu Thr Arg Lys Asn Phe
    210                215

```

<210> 2350

<211> 333

<212> PRT

<213> Mus musculus (M77 8439916-17-1-2001 619-1618)

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 2350

```

Ile Ile Leu Xaa Tyr Asn Ser Phe Phe Leu Ser Leu Xaa Ile Pro Leu
1           5           10           15
Lys Arg Met Asp Ser Val Asn Val Ser Leu Val Thr Glu Phe Leu Leu
          20           25           30
Val Gly Leu Thr His Gln Pro Asp Arg Gln Ile Pro Leu Phe Leu Leu
          35           40           45
Phe Leu Ala Met Tyr Leu Val Thr Ala Leu Gly Asn Leu Gly Leu Ile
          50           55           60
Ile Leu Val Leu Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe
65           70           75           80
Leu Phe Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Ser Val Phe Thr
          85           90           95
Pro Lys Met Leu Met Asn Phe Ile Leu Arg Gln Asn Ala Ile Ser Tyr
          100          105          110
Met Gln Cys Met Thr Gln Leu Tyr Phe Phe Cys Phe Phe Val Val Ser
          115          120          125
Glu Cys Phe Val Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile
          130          135          140
Cys Asn Pro Leu Leu Tyr Asn Val Met Ile Ser Pro Gln Val Cys Leu
145          150          155          160
Asn Leu Met Ile Gly Ser Tyr Leu Met Ala Phe Ser Glu Ala Val Ala
          165          170          175
Leu Thr Val Cys Met Leu Thr Leu Thr Phe Cys Asp Gly Asn Ile Asn
          180          185          190
His Tyr Phe Cys Asp Ile Leu Ala Leu Phe Gln Leu Ser Cys Ser Ser
          195          200          205
Thr Tyr Val Asn Lys Leu Val Ala Tyr Val Ile Val Val Ile Asn Ile
          210          215          220
Leu Phe Ser Thr Pro Thr Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser
225          230          235          240
Ser Ile Phe Arg Ile Ser Ser Ser Lys Gly Arg Ser Lys Ala Phe Ser
          245          250          255
Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly
          260          265          270
Ala Phe Val Tyr Phe Lys Pro Ser Ser Pro Gly Ser Met Glu Trp Ala
          275          280          285
Lys Ile Ser Ser Val Phe Tyr Thr Asn Val Val Pro Met Met Asn Pro
          290          295          300
Leu Ile Tyr Ser Leu Lys Asn Lys Asp Val Lys Ile Ala Leu Arg Lys
305          310          315          320
Ser Leu Ala Arg Xaa Arg Phe Asp Trp Ile His Met Tyr
          325          330

```

<210> 2351

<211> 299

<212> PRT

<213> Mus musculus (M78 8439916-17-6970-9135 1261-2156)

<220>

<221> VARIANT

<222> (1)...(299)

<223> Xaa = Any Amino Acid

<400> 2351

```

Thr Asp Ser Pro Xaa Arg Arg Met Asp Xaa Val Asn Ile Ser Leu Val
 1           5           10           15
Thr Glu Phe Ile Val Val Gly Xaa Ala Glu Gln Pro Asp Leu Gln Ile
          20           25           30
Pro Met Phe Phe Gly Phe Leu Ala Met Tyr Thr Val Thr Ala Leu Glu
          35           40           45
Asn Leu Phe Leu Ile Ile Leu Thr Val Leu Asn Ser His Val His Thr
          50           55           60
Thr Met Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Val Val Leu Cys Tyr
65          70          75          80
Ser Ser Val Phe Thr Pro Gln Met Leu Met Asn Phe Ile Ile Arg Lys
          85          90          95
Asn Thr Ile Ser Tyr Met Glu Cys Ile Thr Xaa Leu Phe Phe Leu Ser
          100         105         110
Phe Phe Leu Ile Phe Leu Cys Phe Phe Leu Ser Ser Phe Phe Leu Ser
          115         120         125
Phe Phe Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe
          130         135         140
Phe Leu Ser Ser Phe Leu Pro Ser Leu Leu Pro Ser Phe Leu Ser Phe
145         150         155         160
Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Ser Leu Ser Phe
          165         170         175
Leu Ser Ala Ala Tyr Xaa Leu Gln Cys Ala Met Ile Ser Ile Cys Asn
          180         185         190
Ser Leu Val Tyr Asn Leu Phe Met Arg Pro Xaa Val Leu Ser Glu Pro
          195         200         205
Tyr Ser Trp Val Ile Leu Xaa Phe Ile Tyr Xaa Cys Val Asn Thr Leu
          210         215         220
Ser Ser Gly Ile Glu Thr Asp Thr Val Arg Arg Glu Thr Ser Cys Leu
225         230         235         240
Arg Val Arg Pro Ala Ala Pro Gly His Met Ser Val Ser Leu Glu Phe
          245         250         255
Phe Phe Cys Ser Gly Arg Val Tyr Leu Trp Gly Leu Pro Gln Thr Glu
          260         265         270
Leu Ile Pro Tyr Ala Xaa Leu Pro Val Gln Arg Pro Pro Val Leu Glu
          275         280         285
Glu Ser Leu Glu Gly Arg Arg Ala Arg Asn Val
          290         295

```

<210> 2352

<211> 339

<212> PRT

<213> Mus musculus (M80 8439916-20-13750-16634 2033-1016)

<220>

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400> 2352

```

Cys His Ser Phe Phe Leu Leu Leu Ile His Arg Leu Phe Xaa Arg Arg
 1           5           10           15
Met Gly Val Glu Asn Gly Ser Leu Val Thr Glu Phe Ile Leu Gln Gly
          20           25           30
Leu Thr Ser Asp Pro Asp Leu Gln Leu Pro Leu Phe Leu Phe Leu
          35           40           45
Leu Ile Tyr Thr Thr Thr Ala Leu Gly Asn Leu Ser Leu Ile Thr Leu
          50           55           60
Ile Ala Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Leu

```

```

65          70          75          80
Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
      85          90          95
Met Leu Met Asn Phe Leu Val Ser Lys Asn Phe Ile Ser Tyr Val Gly
      100        105        110
Cys Met Thr Gln Leu Tyr Leu Phe Val Phe Phe Ala Val Ser Glu Cys
      115        120        125
Cys Val Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      130        135        140
Pro Leu Leu Tyr Asn Ile Ala Met Ser Pro Gln Val Cys Ser Tyr Leu
145          150          155          160
Met Leu Gly Ser Tyr Ile Met Gly Phe Ser Gly Ala Met Ile His Thr
      165        170        175
Gly Trp Met Leu Arg Leu Thr Phe Cys Asp Arg Ser Ile Ile Asn His
      180        185        190
Tyr Phe Cys Asp Leu Leu Pro Leu Leu Gln Leu Ser Cys Thr Asn Thr
      195        200        205
Tyr Ala Asn Glu Ile Glu Ile Ile Ile Val Gly Gly Ile Asp Ile Ile
      210        215        220
Val Pro Ser Ile Ile Ile Phe Thr Ser Tyr Gly Phe Val Leu Ser Asn
225          230          235          240
Ile Phe Gln Met Arg Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr
      245        250        255
Cys Ser Ser His Ile Val Ala Val Ser Leu Phe Phe Gly Ser Gly Ala
      260        265        270
Phe Met Tyr Leu Gln Pro Ser Ser Pro Glu Ser Met Asp Gln Gly Lys
      275        280        285
Arg Ser Ser Val Phe Tyr Thr Ile Leu Val Pro Met Met Asn Pro Leu
290          295        300
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ile Ala Leu Lys Lys Thr
305          310        315          320
Phe Ser Thr Gln Ser Val Xaa Xaa Glu Ile Asn Val Tyr His Tyr Thr
      325        330        335
Tyr Ala Asn

```

<210> 2353

<211> 336

<212> PRT

<213> Mus musculus (M82 8439916-21-1-3132 1296-290)

<220>

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 2353

```

Asn Phe Ile Phe Phe Leu Pro Ile Asp Ser Leu Arg Glu Asp Met Ala
1      5      10      15
Leu Glu Asn Ala Ser Leu Val Thr Glu Phe Ile Leu Met Gly Leu Thr
      20      25      30
Asn Arg Pro Asp Leu Gln Ile Pro Leu Phe Leu Leu Phe Leu Val Met
      35      40      45
Tyr Val Ile Ala Thr Leu Gly Asn Leu Ala Leu Ile Met Leu Ile Ile
      50      55      60
Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Leu Asn Leu
65          70          75          80
Ser Cys Ile Asp Leu Phe Tyr Cys Ser Val Ile Thr Pro Lys Met Leu
      85          90          95
Met Asn Phe Val Leu Lys Lys Asn Val Ile Ser Tyr Glu Gly Cys Met
      100        105        110

```

Ala Gln Phe Tyr Phe Phe Ala Phe Phe Ala Ile Ser Glu Cys Tyr Val
 115 120 125
 Leu Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu
 130 135 140
 Leu Tyr Asn Ile Val Met Ser Pro Lys Leu Cys Ser Tyr Leu Met Met
 145 150 155 160
 Gly Thr Tyr Leu Met Gly Phe Ser Gly Ala Met Ile His Thr Gly Cys
 165 170 175
 Ile Leu Arg Leu Thr Phe Cys Asp Lys Asn Thr Ile Asn His Tyr Phe
 180 185 190
 Cys Asp Ile Leu Pro Leu Leu Gln Ile Ser Cys Thr Ser Thr Tyr Val
 195 200 205
 Asn Glu Ile Glu Leu Phe Ile Val Ala Gly Lys Asp Ile Ile Val Pro
 210 215 220
 Thr Val Ile Ile Phe Thr Ser Tyr Gly Phe Ile Leu Ser Ser Ile Leu
 225 230 235 240
 Lys Ile Ser Ser Thr Ala Gly Met Ser Lys Ala Phe Ser Thr Cys Ser
 245 250 255
 Ser His Ile Ile Ala Leu Cys Leu Phe Phe Gly Ser Cys Thr Phe Met
 260 265 270
 Tyr Leu Lys Pro Ser Ser Val Glu Ser Met Asp Gln Gly Lys Ile Ser
 275 280 285
 Ser Val Phe Tyr Asn Ile Val Val Pro Leu Met Asn Pro Leu Ile Tyr
 290 295 300
 Ser Leu Arg Asn Lys Asp Val Lys Ile Ala Ile Lys Lys Thr Ile Thr
 305 310 315 320
 Lys Gly Lys Phe Xaa Ser Glu Phe Val Ile Leu Phe Thr Phe Ser Tyr
 325 330 335

<210> 2354

<211> 316

<212> PRT

<213> Mus musculus (M84 8439916-22-16651-22211 2487-1540)

<400> 2354

Met Ala Leu Ala Asn Gly Ser Phe Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Gln Pro Asp Leu Gln Met Pro Leu Phe Leu Ile Phe Leu
 20 25 30
 Ile Ile Tyr Leu Ile Thr Ala Phe Gly Asn Leu Thr Leu Ile Ile Leu
 35 40 45
 Ile Val Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Leu Ile Thr Pro Lys
 65 70 75 80
 Met Leu Met Asn Phe Val Leu Glu Lys Asn Ile Ile Ser Tyr Met Gly
 85 90 95
 Cys Met Thr Gln Phe Tyr Phe Phe Gly Phe Phe Ala Ile Ser Glu Cys
 100 105 110
 Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Val Ala Met Ser Pro Lys Met Cys Ser Tyr Phe
 130 135 140
 Ile Leu Gly Ser Tyr Phe Met Gly Phe Ser Gly Ala Met Ile His Thr
 145 150 155 160
 Gly Cys Val Met Arg Leu Thr Phe Cys Asp Gly Asn Thr Ile Asn His
 165 170 175
 Tyr Phe Cys Asp Leu Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
 180 185 190
 Tyr Val Asn Glu Ile Glu Leu Phe Ile Val Thr Gly Lys Asp Ile Ile
 195 200 205

Val Pro Thr Val Ile Ile Phe Ala Ser Tyr Gly Phe Ile Leu Ser Asn
 210 215 220
 Ile Leu Lys Ile Arg Ser Thr Ser Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Ile Ile Ala Val Ser Met Phe Phe Gly Ser Ser Ala
 245 250 255
 Phe Met Tyr Leu Lys Pro Ser Ser Ala Val Ser Met Asn Glu Ala Lys
 260 265 270
 Phe Ser Ser Ile Phe Tyr Ser Ile Val Val Pro Met Met Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Gly Leu Lys Lys Thr
 290 295 300
 Leu Ser Arg Met Phe Ser His Asn Leu Ile Ser Leu
 305 310 315

<210> 2355

<211> 239

<212> PRT

<213> Mus musculus (M90 8567804-15-6071-7402 605-1319)

<220>

<221> VARIANT

<222> (1)...(239)

<223> Xaa = Any Amino Acid

<400> 2355

Asn Thr Glu Gly His Ser Leu Ile Leu Thr Tyr Asn Val Ser Asn Thr
 1 5 10 15
 Gln Ile Asn Cys Phe Cys Leu Ile Tyr Thr Xaa Tyr Asn Leu Leu Xaa
 20 25 30
 Phe Leu Glu Ile Tyr Phe Cys Pro Leu Leu Ile Pro Cys Val Ala Glu
 35 40 45
 Trp Ser Arg Gly Asp Cys Ile Glu Ile Leu Glu Tyr Asn Ile Cys Ile
 50 55 60
 Phe Ile Lys Leu Met Val Pro Thr Met Ser Ser Leu His Tyr Leu Met
 65 70 75 80
 Asn Ser Ser Val Xaa Tyr Leu Lys Ile Phe His Val Ser Lys Glu Leu
 85 90 95
 Tyr Gly Ser Phe Leu Gly Gly Ile Phe Phe Leu Ala Asn His Cys Arg
 100 105 110
 Glu Ile Glu Ile Ser Asn Arg Thr Thr Glu Met Arg Ile Lys Ala Leu
 115 120 125
 Gln Lys Gly Leu Arg Asp Ile Ser Phe Ile Thr Asn Ser Val Gly Ile
 130 135 140
 Val Ile Leu Ile Ile Ile Tyr Ala Arg Leu Gln Lys Ser Thr Glu Gly
 145 150 155 160
 Thr Val Lys Thr Ser Ser Asn Cys Gly Tyr His Ile Ile Ser Ile Tyr
 165 170 175
 Leu Phe Phe Leu Lys Phe Ala Phe Leu Tyr Ile Phe Lys Tyr Val Ser
 180 185 190
 Arg Met His Gln Gly Ser Val Ser Ser Val Phe Tyr Thr Asn Val Val
 195 200 205
 Pro Ile Cys Asn Thr Leu Ile Tyr Ser Leu Xaa Asn Asp Val Thr Ile
 210 215 220
 Ala Trp Met Asn Val Leu Met Lys Phe Gln Arg His Leu Phe Tyr
 225 230 235

<210> 2356

<211> 202

<212> PRT

<213> Mus musculus (M96 8567804-8-3023-3783 759-153)

<220>

<221> VARIANT

<222> (1)...(202)

<223> Xaa = Any Amino Acid

<400> 2356

```

Ile Leu Leu Gly Leu Thr Gln Gln Pro Glu Leu Gln Leu Pro Leu Phe
 1           5           10           15
Phe Gln Phe Leu Gly Ile Tyr Val Val Ser Ile Val Gly Asn Leu Gly
      20           25           30
Leu Ile Val Leu Ile Val Leu Asn Pro His Leu His Thr Pro Met Tyr
      35           40           45
Tyr Phe Leu Phe Asn Leu Ser Phe Thr Asp Leu Cys Tyr Ser Ser Ala
      50           55           60
Ile Thr Pro Lys Met Leu Val Gly Phe Val Asn Gln Asn Ile Ile Ala
      65           70           75           80
His Ala Glu Cys Leu Thr Gln Leu Phe Phe Cys Phe Phe Val Leu
      85           90           95
Asp Glu Cys Tyr Ile Cys Thr Glu Met Ala Tyr Asp Arg Tyr Ala Ala
      100          105          110
Ile Cys Lys Thr Leu Leu Asn Gln Val Thr Met Ser His Gln Val Cys
      115          120          125
Leu Glu Ile Thr Lys Gly Trp Ile Ile Leu Tyr Ser Glu Met Glu Lys
      130          135          140
Ser Lys Lys Ser Phe Xaa Met Tyr Ile Ser Ile Leu Leu Phe Phe Ser
      145          150          155          160
Leu Phe Gly Asp Ile Ile Ser Leu Lys Ser Phe Met Leu Ser Lys Cys
      165          170          175          180
Leu Thr Thr Asp Leu His Leu Lys Ser Arg His Ile Cys Lys Phe Cys
      180          185          190
Val Ala Val Ser Asp Asn Val Leu Leu Leu
      195          200

```

<210> 2357

<211> 123

<212> PRT

<213> Mus musculus (M98 8570471-14-891-2711 1429-1795)

<220>

<221> VARIANT

<222> (1)...(123)

<223> Xaa = Any Amino Acid

<400> 2357

```

Leu Cys Gly Ser Gly Thr Leu Ile Phe Ser Ser Glu Met Leu Phe Ile
 1           5           10           15
Phe Leu Gly Lys Xaa Phe Phe Gly Xaa Xaa Asp Leu Ile Val Ala Ile
      20           25           30
Phe Cys Ile Phe Asn Phe Leu Lys Leu Ser Leu Leu Thr Lys Val Pro
      35           40           45
Glu Cys Asp Phe Xaa Asn Lys Leu Ser Xaa Xaa Asn Glu Tyr Ile Xaa
      50           55           60
Asn Ile Val Pro Asp Ser Tyr Xaa Tyr Arg Asn Leu Tyr Trp Gly Asn
      65           70           75           80
Gly Asn Met Ser Ser Thr Gly Cys Met Leu Arg Leu Thr Ser Trp Asp
      85           90           95
Gly Asn Thr Ile Asn His Tyr Phe Cys Asp Leu Leu Pro Phe Leu Gln
      100          105          110
Leu Ser Cys Thr Ser Thr Tyr Val His Tyr Thr
      115          120

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<210> 2358
 <211> 179
 <212> PRT
 <213> Mus musculus (M99 8570471-17-1-2939 17-553)

<220>
 <221> VARIANT
 <222> (1)...(179)
 <223> Xaa = Any Amino Acid

<400> 2358
 Ile Cys Leu Asn Leu Met Leu Val Ser Tyr Phe Ile Ala Phe Ser Glu
 1 5 10 15
 Ser Val Ala His Thr Ala Cys Met Leu Arg Leu Thr Phe Cys Asp Ala
 20 25 30
 Asn Thr Ile Asn Tyr Tyr Phe Cys Asp Ile Pro Pro Leu Leu Gln Leu
 35 40 45
 Ser Cys Thr Thr Thr Arg Val Asn Glu Val Val Ile Phe Val Val Gly
 50 55 60
 Ser Ile Asn Ile Ile Ile Pro Thr Ser Thr Ile Phe Val Ser Tyr Gly
 65 70 75 80
 Phe Ile Leu Ser Ser Ile Phe Leu Ile Thr Ala Ser Glu Gly Arg Ser
 85 90 95
 Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Ala Ala Phe Leu Phe
 100 105 110
 Phe Gly Ser Gly Ala Ile Arg Tyr Phe Lys Pro Ser Ser Asp Gly Ser
 115 120 125
 Met Asp Glu Gly Lys Ile Ser Ser Val Phe Tyr Thr Asn Val Ile Pro
 130 135 140
 Met Ile Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Ile Lys Val
 145 150 155 160
 Ala Leu Arg Arg Thr Leu Arg Lys Arg Asn Phe Xaa Leu Ser Ser Val
 165 170 175
 Val Cys Val

<210> 2359
 <211> 324
 <212> PRT
 <213> Mus musculus (M100 8570471-17-6599-8104 424-1396)

<220>
 <221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 2359
 Ile Phe Cys Val Tyr Arg Phe Ser Gln Arg Arg Met Asp Ser Val Asn
 1 5 10 15
 Ile Ser Leu Val Thr Glu Phe Ile Leu Val Gly Leu Thr Asp Lys Pro
 20 25 30
 Tyr Leu Gln Ile Pro Leu Phe Phe Ile Phe Leu Ala Met Tyr Leu Val
 35 40 45
 Thr Ala Leu Gly Asn Leu Ser Leu Ile Ile Leu Thr Val Leu Asn Ser
 50 55 60
 His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Phe Val
 65 70 75 80
 Asp Phe Cys Tyr Ser Ser Val Phe Thr Pro Gln Met Leu Met Asn Phe
 85 90 95
 Ile Thr Arg Lys Asn Thr Ile Ser Tyr Met Glu Cys Met Ser Gln Leu

```

      100      105      110
Tyr Phe Phe Cys Phe Phe Val Ile Ser Glu Cys Tyr Val Leu Thr Ser
      115      120      125
Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Asn
      130      135      140
Leu Val Met Ser Ser Lys Leu Cys Leu Asn Leu Met Leu Val Ser Tyr
145      150      155      160
Phe Ile Ala Phe Ser Glu Ser Val Ala His Thr Val Cys Ile Met Arg
      165      170      175
Leu Asn Phe Cys Asp Ala Ser Lys Ile Asn His Tyr Phe Cys Asp Ile
      180      185      190
Pro Pro Leu Leu Gln Leu Ser Cys Thr Thr Thr Tyr Ile Asn Lys Leu
      195      200      205
Val Val Phe Val Ala Ser Ser Ile Asn Ile Ile Val Pro Ile Ser Thr
      210      215      220
Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser Ile Phe His Ile His
225      230      235      240
Ser Ser Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser His Ile
      245      250      255
Ile Ala Ala Phe Leu Phe Phe Gly Ser Gly Ala Phe Met Tyr Phe Gln
      260      265      270
Pro Ser Ser Ala Glu Ser Met Asp Glu Gly Lys Ile Ser Ser Val Phe
      275      280      285
Tyr Thr Asn Val Ile Pro Met Met Asn Pro Leu Leu Tyr Ser Leu Arg
      290      295      300
Asn Lys Asp Ile Lys Val Ala Leu Arg Lys Thr Leu Ser Lys Arg Asn
305      310      315      320
Ile Xaa Leu Tyr

```

<210> 2360

<211> 327

<212> PRT

<213> Mus musculus (M101 8570471-19-17517-20152 1114-134)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 2360

```

Leu Phe Ile Phe His Lys Ile Ser Tyr Arg Ser Met Ala Leu Ile Asn
1      5      10      15
Gly Ser Val Val Thr Glu Phe Ile Leu Leu Gly Leu Thr Asp Gln Pro
      20      25      30
Asp Leu Gln Val Pro Leu Phe Leu Val Phe Leu Leu Met Tyr Met Ile
      35      40      45
Thr Ala Leu Gly Asn Leu Thr Leu Ile Ile Leu Ile Val Leu Asn Ser
      50      55      60
His Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Phe Val
      65      70      75      80
Asp Phe Cys Tyr Ser Ser Val Ile Ile Pro Lys Met Leu Met Asn Phe
      85      90      95
Ile Leu Lys Lys Asn Phe Ile Ser Tyr Val Gly Cys Met Thr Gln Phe
      100      105      110
Tyr Leu Phe Gly Phe Cys Val Ile Leu Glu Cys Tyr Ile Leu Thr Ser
      115      120      125
Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Asn
      130      135      140
Ile Val Met Ser Pro Lys Met Cys Ser Tyr Leu Met Leu Gly Ser Tyr
145      150      155      160

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Leu Met Gly Phe Ser Gly Ala Met Ile His Thr Gly Cys Val Leu Arg
 165 170 175
 Leu Ser Phe Cys Asp Gly Asn Ile Ile Asn His Tyr Phe Cys Asp Leu
 180 185 190
 Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr Val Asn Glu Ile
 195 200 205
 Glu Val Leu Ile Val Ala Gly Lys Asp Ile Ile Val Pro Thr Val Ile
 210 215 220
 Ile Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser Ile Phe Gln Met Lys
 225 230 235 240
 Ser Thr Lys Gly Met Ser Lys Ala Phe Ser Thr Cys Ser Ser His Ile
 245 250 255
 Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys
 260 265 270
 Pro Asn Ser Thr Gly Thr Met Asn Asn Gly Lys Ile Pro Ser Ile Ile
 275 280 285
 Tyr Thr Ile Leu Ile Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg
 290 295 300
 Asn Lys Asp Val Lys Val Ala Leu Arg Lys Thr Leu Arg Lys Lys Ile
 305 310 315 320
 Leu Xaa Ser Glu Thr Val Ile
 325

<210> 2361

<211> 341

<212> PRT

<213> Mus musculus (M104 8570471-3-1-2271 2172-1151)

<220>

<221> VARIANT

<222> (1)...(341)

<223> Xaa = Any Amino Acid

<400> 2361

Asn Phe Ala Ile Phe Phe Ser Val His Arg Phe Ser Xaa Arg Arg Met
 1 5 10 15
 Ala Leu Val Asn Gly Ser Thr Val Thr Glu Phe Ile Leu Leu Gly Leu
 20 25 30
 Thr Asp Gln Pro Gly Leu Gln Met Pro Leu Phe Leu Leu Phe Leu Leu
 35 40 45
 Met Tyr Met Ile Thr Val Phe Gly Asn Leu Thr Leu Ile Phe Leu Ile
 50 55 60
 Leu Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Leu Asn
 65 70 75 80
 Leu Ser Phe Val Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys Met
 85 90 95
 Leu Met Asn Phe Ile Leu Lys Lys Asn Leu Ile Ser Tyr Met Gly Cys
 100 105 110
 Met Ser Gln Leu Tyr Phe Phe Cys Phe Phe Ile Ile Ser Glu Cys Tyr
 115 120 125
 Val Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 130 135 140
 Leu Leu Tyr Asn Thr Ala Met Ser Pro Arg Val Cys Ser Tyr Leu Met
 145 150 155 160
 Leu Gly Thr Tyr Leu Met Gly Phe Phe Asp Ala Met Ile His Thr Gly
 165 170 175
 Cys Met Leu Arg Leu Ser Phe Cys Asp Gly Asn Ile Ile Asn His Tyr
 180 185 190
 Phe Cys Asp Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr
 195 200 205
 Val Asn Glu Thr Glu Ile Phe Ile Val Gly Gly Lys Asp Ile Ile Leu

210	215	220
Pro Ser Ala Ile Ile Ph	Phe Ser Tyr Gly Phe	Ile Leu Ser Asn Ile
225	230	235
Phe Gln Ile Arg Ser	Thr Leu Gly Arg Ser	Lys Ala Phe Ser Thr Cys
245	250	255
Ser Ser His Ile Ile Ala	Val Ser Leu Phe Phe	Gly Ser Cys Gly Phe
260	265	270
Met Tyr Leu Lys Pro Ser	Ser Ala Val Ser Ile	Asp Gln Gly Lys Ile
275	280	285
Ser Ser Ile Phe Tyr Thr	Ile Val Val Pro Met	Met Asn Pro Leu Ile
290	295	300
Tyr Ser Leu Arg Asn Lys	Asp Val Lys Val Ala	Leu Arg Lys Thr Leu
305	310	315
Ser Arg Arg Lys Phe Leu	Lys Val Xaa Leu Gln	Ser Arg His Phe Leu
325	330	335
Cys Xaa Cys Thr Tyr		
340		

<210> 2362

<211> 337

<212> PRT

<213> Mus musculus (M106 8570471-9-3672-5945 1670-660)

<220>

<221> VARIANT

<222> (1)...(337)

<223> Xaa = Any Amino Acid

<400> 2362

Ile Asn Ile Phe Phe Leu	Leu Pro Thr Xaa Asn Met	Gln Val Gln Met
1	5	10
Ala Asp Thr Asn His Ser	Thr Val Thr Glu Phe Ile	Leu Ala Gly Leu
20	25	30
Thr Asp Lys Pro Glu Leu	Gln Leu Pro Leu Phe	Leu Leu Phe Leu Gly
35	40	45
Ile Tyr Leu Leu Thr Val	Leu Gly Asn Leu Gly	Met Ile Ile Leu Ile
50	55	60
Leu Leu Ser Ser His Leu	His Thr Pro Met Tyr	Phe Phe Leu Ser Ser
65	70	75
Leu Ser Phe Ile Asp Leu	Cys Tyr Ser Thr Val	Ile Thr Pro Lys Met
85	90	95
Leu Val Asn Phe Val Ala	Lys Lys Asn Val Ile	Ser Tyr Glu Glu Cys
100	105	110
Met Thr Gln Leu Tyr Phe	Phe Leu Ala Phe Val	Ile Ser Glu Cys His
115	120	125
Met Leu Ala Ala Met Ala	Tyr Asp Arg Tyr Val	Ala Ile Cys Asn Pro
130	135	140
Leu Leu Tyr Asn Val Thr	Met Ser Tyr Gln Ile	Cys Ser Trp Met Val
145	150	155
Gly Gly Val Tyr Gly Met	Gly Leu Ile Gly Ala	Ala Val His Thr Leu
165	170	175
Cys Met Leu Arg Val Val	Phe Cys Lys Ala Asn	Ile Ile Asn His Tyr
180	185	190
Phe Cys Asp Leu Phe Pro	Leu Met Glu Leu Ala	Cys Ser Ser Thr Tyr
195	200	205
Val Asn Glu Val Val Leu	Leu Cys Leu Ser Ala	Phe Asn Ile Phe Ile
210	215	220
Pro Thr Leu Thr Ile Leu	Gly Ser Tyr Ile Phe	Ile Ile Ile Ser Ile
225	230	235
Leu Arg Ile Lys Ser Thr	Glu Gly Arg Phe Lys	Ala Phe Ser Thr Cys
245	250	255

Ser Ser His Phe Ser Ala Val Ser Val Phe Phe Gly Ser Leu Ala Phe
 260 265 270
 Met Tyr Leu Gln Pro Phe Ser Val Ser Ser Lys Asp Lys Gly Lys Val
 275 280 285
 Ser Ser Val Phe Tyr Thr Thr Ile Val Pro Met Leu Asn Pro Met Ile
 290 295 300
 Tyr Ser Leu Arg Asn Arg Asp Val Lys Leu Ala Leu Asn Lys Leu Phe
 305 310 315 320
 Gln Lys Lys Phe His Val Xaa Arg Ser Ile Tyr Leu Arg Lys Thr Ile
 325 330 335
 Gln

<210> 2363

<211> 256

<212> PRT

<213> Mus musculus (M107 8571727-11-1262-2044 781-16)

<220>

<221> VARIANT

<222> (1)...(256)

<223> Xaa = Any Amino Acid

<400> 2363

Ile Leu Leu Gly Leu Thr Gln Gln Pro Glu Leu Gln Leu Pro Leu Phe
 1 5 10 15
 Phe Gln Phe Leu Gly Ile Tyr Val Val Ser Ile Val Gly Asn Leu Gly
 20 25 30
 Leu Ile Val Leu Ile Val Leu Asn Pro His Leu His Thr Pro Met Tyr
 35 40 45
 Tyr Phe Leu Phe Asn Leu Ser Phe Thr Asp Leu Cys Tyr Ser Ser Ala
 50 55 60
 Ile Thr Pro Lys Met Leu Val Gly Phe Val Asn Gln Asn Ile Ile Ala
 65 70 75 80
 His Ala Glu Cys Leu Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Leu
 85 90 95
 Asp Glu Cys Tyr Ile Cys Thr Glu Met Ala Tyr Asp Arg Tyr Ala Ala
 100 105 110
 Ile Cys Lys Thr Leu Leu Asn Gln Val Thr Met Ser His Gln Val Cys
 115 120 125
 Leu Gly Asn His Lys Arg Leu Asp Tyr Ile Ile Phe Arg Asn Gly Lys
 130 135 140
 Ile Lys Lys Ile Phe Leu Asn Val His Ile Tyr Phe Ile Ile Phe Xaa
 145 150 155 160
 Phe Val Cys Gly Thr Ser Tyr Pro Xaa Ser Leu Ser Cys Xaa Ala Ser
 165 170 175
 Val Xaa Pro Leu Thr Tyr Ile Leu Arg Val Gly Thr Phe Val Ser Phe
 180 185 190
 Val Trp Leu Ser Gln Thr Met Ser Tyr Tyr Phe Ile Ile Ala Asn Leu
 195 200 205
 Trp Asp Asn Leu Xaa Glu Ser Ser Phe Xaa Arg Leu Ile Cys Cys Ser
 210 215 220
 Lys Gly Xaa Ser Lys Glu Gly Lys Xaa Lys Leu Leu Ser Phe Trp Ser
 225 230 235 240
 Phe Phe Ile Val Leu Lys Gln Phe Arg Lys Glu Gly Leu Thr Ser Tyr
 245 250 255

<210> 2364

<211> 333

<212> PRT

<213> Mus musculus (M111 8571727-21-4956-7261 1151-153)

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 2364

```

Ile Leu Met Leu Xaa Leu Leu Leu Phe Leu Gln Glu Arg Met Val Leu
 1           5           10           15
Glu Asn Ser Ser Ser Val Lys Glu Phe Ile Leu Leu Gly Leu Thr Gln
          20           25           30
Gln Pro Glu Leu Gln Met Pro Leu Phe Phe Leu Phe Leu Gly Ile Tyr
 35           40           45
Ile Val Ser Met Val Gly Asn Leu Gly Leu Thr Val Leu Ile Val Leu
 50           55           60
Asn Pro His Leu His Asn Pro Met Tyr Tyr Phe Leu Phe Asn Leu Ser
 65           70           75           80
Phe Thr Asp Leu Cys Tyr Ser Thr Val Ile Thr Pro Arg Met Leu Val
          85           90           95
Gly Phe Val Lys Gln Asn Thr Ile Ser His Ala Glu Cys Met Thr Gln
          100          105          110
His Phe Phe Phe Cys Phe Phe Val Ile Asp Glu Cys Tyr Ile Leu Thr
          115          120          125
Ala Val Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Lys Pro Leu Leu Tyr
          130          135          140
Gln Val Thr Met Ser His Gln Val Cys Leu Leu Met Thr Val Gly Val
          145          150          155          160
Tyr Val Met Gly Phe Leu Glu Ala Ile Ala His Thr Gly Ser Met Val
          165          170          175
Ser Leu Thr Phe Cys Asp Gly Asn Ile Ile Asn His Tyr Ala Cys Asp
          180          185          190
Ile Leu Pro Leu Leu Lys Leu Ser Cys Thr Ser Thr Thr Ile Asn Glu
          195          200          205
Leu Val Val Phe Ile Val Val Gly Val Asn Val Ile Val Pro Thr Leu
          210          215          220
Thr Ile Phe Ile Ser Tyr Thr Leu Ile Leu Ser Asn Ile Leu Ser Ile
          225          230          235          240
His Ser Ala Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Gly Ser His
          245          250          255
Val Ile Ala Val Ser Leu Phe Phe Gly Ala Ala Ala Phe Met Tyr Leu
          260          265          270
Lys Pro Ser Ser Ala Ser Glu Asp Asp Asp Lys Val Ser Thr Ile Phe
          275          280          285
Tyr Thr Ile Val Gly Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg
          290          295          300
Asn Lys Asp Val Tyr Leu Ala Leu Arg Lys Thr Leu Met Lys Arg Ser
          305          310          315          320
Phe Thr Xaa Val Glu Ser Ile Phe Val Met Glu Leu Lys
          325          330

```

<210> 2365

<211> 344

<212> PRT

<213> Mus musculus (M112 8571727-22-3043-8090 3092-2061)

<220>

<221> VARIANT

<222> (1)...(344)

<223> Xaa = Any Amino Acid

<400> 2365

Ile Val Cys Phe Ile Ser Leu Phe Xaa Val Met Ser Gln Lys Arg Met
 1 5 10 15
 Ala Pro Arg Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Val Gly Phe
 20 25 30
 Ser Asn Gln Pro Ala Leu Gln Leu Pro Leu Phe Phe Val Phe Leu Gly
 35 40 45
 Ile Tyr Val Leu Thr Val Ile Gly Asn Leu Gly Leu Ile Thr Leu Ile
 50 55 60
 Gly Leu Asn Ser Ser Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn
 65 70 75 80
 Leu Ser Phe Ile Asp Phe Cys Tyr Ser Cys Val Phe Thr Pro Lys Met
 85 90 95
 Leu Ser Asp Phe Val Ser Glu Asn Ile Ile Ser Tyr Met Gly Cys Met
 100 105 110
 Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu Cys Tyr Val
 115 120 125
 Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu
 130 135 140
 Leu Tyr Thr Val Thr Met Ser Pro Gln Val Cys Thr Leu Leu Met Phe
 145 150 155 160
 Cys Ser Tyr Val Ile Gly Phe Ala Gly Ala Met Ala His Thr Gly Ser
 165 170 175
 Met Leu Thr Leu Thr Phe Cys Asp Ser Asn Met Ile His His Tyr Leu
 180 185 190
 Cys Glu Val Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr Ala
 195 200 205
 Asn Glu Leu Val Phe Phe Ile Val Val Gly Val Val Ile Thr Ala Ser
 210 215 220
 Ser Ile Ser Ile Phe Ile Ser Tyr Ala Leu Ile Leu Ser Asn Ile Leu
 225 230 235 240
 Lys Ile Pro Ser Ala Glu Gly Arg Ser Lys Ala Phe Gly Thr Trp Gly
 245 250 255
 Ser His Val Val Ala Val Ala Leu Phe Phe Gly Ser Gly Ala Phe Thr
 260 265 270
 Tyr Leu Thr Thr Ser Phe Pro Gly Ser Met Glu Glu Gly Arg Phe Ala
 275 280 285
 Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile Tyr
 290 295 300
 Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Asn Lys Thr Leu Lys
 305 310 315 320
 Arg Val Leu Phe Xaa Xaa Val Trp Cys Tyr His Trp Asn Xaa Ile Leu
 325 330 335
 Gly Lys His Thr Gln Ile His Phe
 340

<210> 2366

<211> 157

<212> PRT

<213> Mus musculus (M113 8571727-23-1650-2708 1059-589)

<220>

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400>2366

Ile Arg Phe Ala Gly Ser Ser Val His Thr Gly Cys Val Ph Leu Xaa
 1 5 10 15
 Gly His Ala Ile Asn His Xaa Leu Phe Asn Ile Leu Thr Leu Leu Gln
 20 25 30
 Leu Ser Xaa Ala Thr Thr Tyr Val Asn Val Val Ile Leu Ile Gly Val

```

      35              40              45
Tyr Ile Thr Val Pro Ser Phe Thr Ile Leu Ile Ser Tyr Val Phe Ile
  50              55              60
Phe Ile Asn Ile Leu Asn Ile Lys Ser Met Gln Arg Ile Ser Lys Asp
  65              70              75              80
Phe Ser Ile Cys Arg Phe His Ile Ala Ser Ile Tyr Val Phe Ile Glu
      85              90              95
Phe Thr Ala Phe Lys Cys Phe Lys Tyr Ser Tyr Gly Ser Ile Asp Gln
      100              105              110
Gly Phe Tyr Ser Ser Val Phe Tyr Thr Asp Val Ile Leu Ile Leu Asn
      115              120              125
Ile Ile Ile Tyr Ser Met Cys Ile Met Asp Val Glu Met Ala Leu Met
      130              135              140
Asp Ala Leu Met Lys Phe Gln Arg Asn Val Phe His Leu
  145              150              155

```

<210> 2367

<211> 127

<212> PRT

<213> Mus musculus (M114 8571727-23-3031-3453 387-9)

<220>

<221> VARIANT

<222> (1)...(127)

<223> Xaa = Any Amino Acid

<400>2367

```

His Ser Ile Gln Tyr Leu Asn Leu Ile Asn Leu Ser Tyr Ile Asp Leu
  1              5              10              15
Cys Tyr Ser Ser Val Pro Arg Ser Lys Met Leu Met Asn Phe Val Phe
      20              25              30
Glu Lys Asn Ala Ile Ser Phe Val Gly Cys Asp Ser Ile Gln Phe Ser
      35              40              45
Leu Val Pro Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe
      50              55              60
Leu Ser Phe Phe Leu Ser Phe Phe Leu Ser Phe Phe Leu Val Ile Phe
      65              70              75              80
Xaa Tyr Tyr Thr Leu Thr Ser Met Ala Tyr Asp Phe Tyr Val Ala Ile
      85              90              95
Cys Ser Ser Leu Val His Xaa Val Thr Pro Leu Leu Gln Val Cys Phe
      100              105              110
Phe Ser Phe Leu Leu Leu Phe Phe Phe Cys Pro Leu Phe Pro Met
      115              120              125

```

<210> 2368

<211> 133

<212> PRT

<213> Mus musculus (M115 8571727-24-1-1404 400-2)

<400>2368

```

Cys Asn Val Ile Thr Phe Thr Val Leu Thr Asp Met Asn Trp Gly Arg
  1              5              10              15
Met Ala Leu Gly Asn Asp Ser Ser Val Lys Glu Phe Ile Leu Leu Gly
      20              25              30
Leu Thr Gln Gln Pro Glu Leu Gln Leu Pro Leu Phe Phe Phe Phe Leu
      35              40              45
Gly Val Tyr Ile Phe Ser Val Val Gly Asn Leu Gly Leu Ile Val Leu
      50              55              60
Ile Val Leu Asn Pro His Leu Gln Thr Pro Met Tyr Tyr Phe Leu Phe
      65              70              75              80
Asn Leu Ser Phe Thr Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys

```



```

      85          90          95
Met Leu Val Ser Phe Val Lys Gln Asn Ile Ile Ser His Ala Glu Cys
      100          105          110
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Ile Asp Glu Cys Tyr
      115          120          125
Ile Leu Thr Ala Met
      130

```

<210> 2369

<211> 262

<212> PRT

<213> Mus musculus (M117 8571727-26-4808-6724 1497-715)

<220>

<221> VARIANT

<222> (1)...(262)

<223> Xaa = Any Amino Acid

<400>2369

```

Ser Ser Leu His Ala Ser His Ser His Glu Leu Xaa Lys Gly Ile Val
 1          5          10          15
Gly Leu Phe Xaa Ala Ala Ser Tyr Ser Thr Val Lys Leu Pro Lys Met
      20          25          30
Leu Val Ser Phe Val Lys Gln Asn Thr Ile Ser Tyr Ala Glu Cys Met
      35          40          45
Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Ile Asp Glu Cys Tyr Ile
      50          55          60
Leu Thr Ala Met Ala Tyr Asp Met Phe Ala Ala Ile Ser Lys Pro Leu
      65          70          75          80
Leu Tyr Gln Val Thr Met Ser His Trp Val Cys Leu Leu Met Ile Val
      85          90          95
Gly Val Tyr Val Ile Gly Phe Ser Gly Ser His Tyr Thr Ser Met Pro
      100          105          110
Asp Leu Xaa Trp Gln Arg His Tyr Met Cys Asp Ile Leu Leu Leu Leu
      115          120          125
Gln Leu Ser Cys Glu Ser Thr Ser Ile Asn Glu Leu Val Ile Tyr Arg
      130          135          140
Val Gly Phe Asn Val Thr Val Pro Ser Leu Thr Ile Phe Ile Ser Tyr
      145          150          155          160
Thr Leu Ile Leu Ser Asn Ile Pro Ser Ile His Ser Thr Glu Gly Arg
      165          170          175
Asn Cys Gly Ser His Val Ile Ala Leu Ser Leu Leu Tyr Gly Ile Val
      180          185          190
Ala Phe Thr Tyr Leu Lys Pro Ser Ser Val Ser Val Asp Asp Ala Asn
      195          200          205
Val Ser Thr Ile Phe Phe Tyr Thr Val Val Gly Pro Met Leu Asn Pro
      210          215          220
Phe Leu His Ser Ile Arg Asn Lys Asp Val His Thr Ala Leu Arg Lys
      225          230          235          240
Thr Leu Asn Lys Ser Ser Phe Thr Xaa Val Xaa Val Cys Ile Cys Tyr
      245          250          255
Glu Ser Lys Ile Leu Gly
      260

```

<210> 2370

<211> 329

<212> PRT

<213> Mus musculus (M119 8573058-17-2172-5249 1514-528)

<220>

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400>2370

Val	Met	Leu	Leu	Ala	Phe	Leu	Leu	Pro	Thr	Asp	Asp	Thr	Ile	Met	His
1				5					10					15	
Met	Ala	Met	Glu	Asn	Asp	Ser	Ser	Val	Thr	Glu	Phe	Val	Phe	Met	Gly
		20						25					30		
Leu	Thr	Glu	Gln	Pro	Glu	Leu	Arg	Leu	Pro	Leu	Phe	Phe	Val	Phe	Leu
		35					40					45			
Leu	Asn	Tyr	Thr	Ala	Thr	Val	Met	Gly	Asn	Leu	Ser	Leu	Met	Val	Leu
	50					55					60				
Ile	Cys	Leu	Asn	Ser	His	Leu	His	Asn	Pro	Met	Tyr	Phe	Phe	Leu	Phe
65					70					75					80
Asn	Leu	Ser	Leu	Val	Asp	Phe	Cys	Tyr	Ser	Phe	Val	Cys	Thr	Pro	Lys
			85						90					95	
Met	Leu	Met	Gly	Phe	Val	Ser	Glu	Lys	Ser	Ile	Ile	Ser	Tyr	Thr	Gly
			100					105					110		
Cys	Met	Thr	Gln	Leu	Phe	Phe	Phe	Cys	Phe	Phe	Val	Asn	Ser	Glu	Cys
		115					120					125			
Tyr	Val	Leu	Thr	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys
		130				135					140				
Pro	Leu	Val	Tyr	Ala	Ile	Leu	Met	Ser	Pro	Arg	Met	Cys	Ser	Leu	Leu
145					150					155					160
Met	Ile	Gly	Ser	Tyr	Leu	Met	Gly	Phe	Ala	Ser	Ala	Met	Ala	His	Thr
				165				170						175	
Gly	Cys	Met	Ile	Arg	Leu	Lys	Phe	Cys	Asp	Ser	Asn	Ile	Ile	Asn	His
		180						185					190		
Tyr	Met	Cys	Glu	Ile	Phe	Pro	Leu	Leu	Gln	Leu	Ser	Cys	Ser	Ser	Thr
		195					200					205			
Tyr	Ala	Asn	Glu	Leu	Val	Ser	Ser	Leu	Ile	Ala	Cys	Ile	Val	Val	Ile
		210				215					220				
Val	Ser	Gly	Leu	Val	Ile	Leu	Met	Ser	Tyr	Ala	Ser	Ile	Leu	Leu	Asn
225					230					235					240
Val	Val	Gln	Met	Ser	Ser	Ala	Thr	Gly	Trp	Ser	Lys	Ala	Met	Gly	Thr
			245						250					255	
Cys	Gly	Ser	His	Ile	Ile	Thr	Val	Ser	Leu	Phe	Tyr	Gly	Ser	Gly	Leu
			260					265					270		
Leu	Thr	Tyr	Val	Lys	Pro	Ala	Ser	Ala	Glu	Ser	Val	Asp	Gln	Gly	Lys
		275					280					285			
Phe	Phe	Ser	Val	Phe	Tyr	Thr	Leu	Met	Val	Pro	Met	Leu	Asn	Pro	Leu
		290				295					300				
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys	Leu	Ala	Ala	Lys	Arg	Thr
305					310				315						320
Met	Asn	Arg	Ile	Thr	Ile	Xaa	Gly	Lys							
				325											

<210> 2371

<211> 335

<212> PRT

<213> Mus musculus (M122 8573058-3-1-3007 1710-2714)

<220>

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400>2371

Val	Leu	Ile	Leu	Pro	Leu	His	Leu	Phe	Leu	Gln	Met	Ser	Leu	Asn	Ala
1				5					10					15	
Gln	Lys	Thr	Met	Glu	Asn	Asp	Ser	Ser	Val	Ser	Glu	Phe	Ile	Leu	Met

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<210> 2372
<211> 131
<212> PRT
<213> Mus musculus (M123 8573058-5-4486-4920 411-18)
```

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<220>  
<221> VARIANT  
<222> (1)...(131)  
<223> Xaa = Any Amino Acid
```

Leu	Gly	Gly	Glu	Asp	Arg	Phe	Ser	Leu	Asn	Asn	Glu	Ser	Leu	Ile	Asn
1				5				10						15	
Asn	Ser	Gly	Leu	Val	Pro	Cys	Thr	Phe	His	Ile	Leu	Thr	Ser	Phe	Cys
			20					25					30		
Lys	Ser	Arg	Ser	Xaa	Thr	Phe	Arg	Thr	Cys	Gly	Ser	His	Phe	Ile	Ala
		35					40					45			
Val	Ser	Leu	Phe	Tyr	Gly	Ala	Ser	Ala	Phe	Met	Tyr	Leu	Lys	Pro	Ser
	50					55					60				
Ser	Ala	Ser	Val	Asp	Asp	Lys	Ile	Ser	Thr	Ile	Phe	Tyr	Thr	Ile	
65				70					75					80	

Val Gly Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp
 85 90 95
 Val His Ile Ala Leu Arg Lys Tyr Phe Glu Glu Lys Ser Phe Ile Xaa
 100 105 110
 Glu Glu Leu Xaa Leu Ile Xaa Met Glu Asn Leu Met Val Cys Gln Ile
 115 120 125
 Tyr Asn Phe
 130

<210> 2373

<211> 167

<212> PRT

<213> Mus musculus (M124 8573058-8-1-894 16-516)

<400>2373

Leu Thr His Gly Ser Thr Pro Thr Gly Pro Ile Thr Ala Pro Ala Leu
 1 5 10 15
 Thr Val Cys Met Val Trp Leu Gln Phe Leu Asp Ser Pro Leu Thr Thr
 20 25 30
 Pro Tyr Met Cys His Ile Phe Pro Leu Leu Gln Val Ser Cys Ser Ser
 35 40 45
 Pro Tyr Val Asn Gln Leu Met Ser Tyr Ile Ala Val Gly Thr Ala Ile
 50 55 60
 Ile Leu Cys Ser Leu Ile Ile Leu Val Ser Tyr Ala Met Ile Leu Phe
 65 70 75 80
 Asn Ile Ile His Ile Ser Ser Gly Lys Gly Trp Ser Lys Ala Leu Gly
 85 90 95
 Thr Cys Gly Ser His Ile Ile Thr Val Ser Leu Phe Tyr Gly Ser Gly
 100 105 110
 Leu Leu Ala Tyr Val Asn Pro Ser Ser Ala Glu Thr Val Gly Gln Ala
 115 120 125
 Lys Phe Phe Ser Val Phe Tyr Thr Leu Leu Val Pro Met Leu Asn Pro
 130 135 140
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Met Lys Lys
 145 150 155 160
 Ser Trp Lys Arg Ile Thr Ser
 165

<210> 2374

<211> 337

<212> PRT

<213> Mus musculus (M126 8574266-10-448-5833 4192-5202)

<220>

<221> VARIANT

<222> (1)...(337)

<223> Xaa = Any Amino Acid

<400>2374

Leu Phe Ser Ser Cys Tyr His Lys Phe Ile Cys Lys Met Thr Ala Arg
 1 5 10 15
 Asn Met Thr Thr Met Ser Gly Phe Leu Leu Met Gly Phe Ser Asp Asn
 20 25 30
 His Glu Leu Gln Ile Leu Gln Ala Leu Leu Phe Leu Leu Thr Tyr Leu
 35 40 45
 Leu Gly Ser Ala Gly Asn Phe Ile Ile Ile Thr Ile Thr Thr Leu Asp
 50 55 60
 Pro Gln Leu Gln Ser Pro Met Tyr Tyr Phe Leu Lys Gln Leu Ser Thr
 65 70 75 80
 Leu Asp Leu Ser Ser Leu Ser Val Thr Val Pro Gln Tyr Val Ala Ser
 85 90 95

Ser Leu Ala Arg Ser Gly Tyr Ile Ser Tyr Gly Gln Cys Met Leu Gln
 100 105 110
 Ile Phe Phe Phe Thr Gly Leu Ala Trp Ser Glu Met Ala Thr Leu Thr
 115 120 125
 Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His Tyr
 130 135 140
 Glu Val Ile Met Ser Pro Arg Lys Cys Thr Trp Ala Val Ala Val
 145 150 155 160
 Trp Leu Ser Gly Gly Ile Ser Gly Thr Leu Phe Thr Ala Ser Thr Leu
 165 170 175
 Ser Ile Arg Phe Cys Gly Asp Lys Ile Ile His Gln Phe Phe Cys Asp
 180 185 190
 Ile Pro Gln Leu Leu Lys Leu Ser Cys Ser Asn Asp Tyr Phe Gly Val
 195 200 205
 Leu Glu Val Ser Thr Phe Met Ser Val Met Ala Phe Ala Cys Phe Val
 210 215 220
 Gly Ile Ala Phe Ser Tyr Gly Gln Ile Phe Ser Thr Val Leu Arg Met
 225 230 235 240
 Pro Ser Ala Glu Gly Arg Ser Lys Val Phe Ser Thr Cys Leu Pro His
 245 250 255
 Leu Phe Val Val Ser Phe Phe Leu Ser Thr Gly Ile Cys Ala Tyr Leu
 260 265 270
 Lys Pro Thr Ser Asp Ser Pro Thr Ala Leu Asp Leu Met Leu Ser Ile
 275 280 285
 Phe Tyr Thr Leu Leu Pro Pro Thr Leu Asn Pro Val Ile Tyr Ser Leu
 290 295 300
 Arg Asn Glu Ser Leu Lys Arg Ala Leu Lys Lys Leu Leu Leu Ser Glu
 305 310 315 320
 Glu Phe Ile Arg Lys Lys Cys Leu Phe Tyr Phe Xaa Cys Leu Leu Thr
 325 330 335
 Leu

<210> 2375

<211> 333

<212> PRT

<213> Mus musculus (M127 8574266-13-1078-2817 1563-564)

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400>2375

Leu Ser Phe Leu Ser Gly Asp Glu Tyr Gln Leu Leu Ser Val Gln Glu
 1 5 10 15
 Asn Ser Leu Ser Val Lys Arg Phe Ala Phe Ser Lys Phe Ser Glu Val
 20 25 30
 Pro Gly Glu Cys Phe Leu Leu Phe Thr Leu Ile Leu Leu Met Phe Leu
 35 40 45
 Val Ser Leu Thr Gly Asn Glu Leu Ile Val Ile Ala Ile Cys Thr Ser
 50 55 60
 Pro Ala Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser Leu
 65 70 75 80
 Leu Glu Ile Gly Tyr Thr Cys Ser Val Ile Pro Lys Met Leu Gln Ser
 85 90 95
 Leu Val Ser Glu Ala Arg Glu Ile Ser Arg Glu Gly Cys Ala Thr Gln
 100 105 110
 Met Phe Phe Phe Thr Phe Phe Gly Ile Thr Glu Cys Cys Leu Leu Ala
 115 120 125
 Ala Met Ala Tyr Asp Arg Cys Met Ala Ile Cys Ser Pro Leu His Tyr

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      130              135              140
Ala Thr Arg Met Ser His Gly Val Cys Ala His Leu Ala Ile Val Ser
145              150              155              160
Trp Gly Met Gly Cys Ile Val Gly Leu Gly Gln Thr Asn Phe Ile Phe
      165              170              175
Ser Leu Asn Phe Cys Gly Pro Cys Glu Ile Asp His Phe Phe Cys Asp
      180              185              190
Leu Pro Pro Val Leu Ala Leu Ala Cys Gly Asp Thr Ser Gln Asn Glu
      195              200              205
Ala Ala Ile Phe Val Ala Ala Ile Leu Cys Ile Ser Ser Pro Phe Leu
      210              215              220
Leu Ile Ile Tyr Ser Tyr Val Arg Ile Leu Val Ala Val Leu Val Met
225              230              235              240
Pro Ser Pro Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser His
      245              250              255
Leu Leu Val Val Thr Leu Phe Phe Gly Ser Gly Ser Ile Thr Tyr Leu
      260              265              270
Arg Pro Lys Ser Ser His Leu Pro Gly Met Asp Lys Leu Leu Ala Leu
      275              280              285
Phe Tyr Thr Ala Val Thr Ser Met Leu Asn Pro Ile Ile Tyr Ser Leu
      290              295              300
Arg Asn Lys Glu Val Lys Thr Ala Leu Arg Lys Thr Leu Ser Leu Lys
305              310              315              320
Thr Ser Arg Ala Ile Asn Arg Xaa Gln Asn Leu Ala Glu
      325              330

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<210> 2376

<211> 356

<212> PRT

<213> Mus musculus (M129 8574266-7-9797-11994 2006-942)

<220>

<221> VARIANT

<222> (1)...(356)

<223> Xaa = Any Amino Acid

<400>2376

```

Asn Phe Phe Leu Gln Ile Xaa Ser Gln Asn Tyr Gln Xaa Gly Xaa Leu
1      5      10      15
Lys Glu Ile Met Thr Lys Ser Asn Phe Ser Ser Pro Ile Cys Phe Arg
      20      25      30
Leu Pro Gly Phe Ser Asp His Leu Xaa Leu Asp Xaa Thr Leu Phe Leu
      35      40      45
Ala Thr Ser Val Ile Asp Ile Val Met Leu Thr Gln Asn Thr Met Ile
      50      55      60
Ile Leu Val Ser Phe Leu Asn Ser Arg Leu Gln Thr Pro Met Tyr Phe
65      70      75      80
Phe Leu Ser Asn Phe Phe Phe Leu Asp Leu Cys Phe Met Thr Asn Val
      85      90      95
Leu Xaa Ile Val Xaa Thr Ser Lys Gly Pro Glu Lys Ile Ile Ser Cys
      100      105      110
Cys Ala Ile His Val Tyr Ile Val Leu Xaa Leu Asp Phe Thr Lys Cys
      115      120      125
Val Leu Leu Thr Met Met Ala Tyr Asn Pro Val Thr Pro Ile Cys Trp
130      135      140
Pro Leu Xaa Tyr Pro Thr Thr His Pro Lys Phe Val Asp Ile His Pro
145      150      155      160
Lys Phe Pro Xaa Lys Pro Ala Ala Leu Ala Trp Ile Cys Ser Phe Met
      165      170      175
Val Phe Thr Ile Gln Thr Thr Leu Val Phe Gln Leu Ser Leu Cys Ser
      180      185      190

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His His Arg Met Asn Asp Phe Leu Cys Val Arg Asn Pro Pro Leu Val
 195 200 205
 Lys Ile Thr Phe Met Asp Thr Thr Ser Leu Glu Lys His Ile Ser Val
 210 215 220
 Phe Thr Phe Leu Xaa Ala Val Ile Pro Cys Gly Glu Tyr Ser Ile Ile
 225 230 235 240
 Tyr Leu Leu Val Leu Leu Lys Val Trp Leu Lys Ile Lys Phe Thr Gly
 245 250 255
 Arg Met Lys Thr Phe Gly Ser Cys Gly Phe His Leu Met Ala Ile Val
 260 265 270
 Leu Phe Phe Gly Asn Glu Ser Ser Val Tyr Met Val Tyr Met Tyr Pro
 275 280 285
 Arg Ala Asn Ala Cys Gln Tyr Arg Lys Phe Ser Val Phe Tyr Met Ile
 290 295 300
 Val Thr Pro Ser Ile Asn Pro Leu Ile Tyr Leu Arg Asn Lys Glu Phe
 305 310 315 320
 Arg Trp Ala Val Gln Arg Leu Val Thr Arg Asp Pro Ser Xaa Gly Lys
 325 330 335
 Ile Arg Gln Ser Leu Thr Ile Phe Gln Ala Phe Gly Ile Gly Arg His
 340 345 350
 Tyr Ile Tyr Cys
 355

<210> 2377

<211> 323

<212> PRT

<213> Mus musculus (M130 8574266-9-11171-19240 5578-6546)

<400>2377

Val Arg Ile Leu Thr Val Asn Thr Asn Met Trp Ile Asn Asn Gln Ser
 1 5 10 15
 Ser Val Asp Asp Phe Ile Leu Leu Gly Phe Ser Asp Arg Pro Trp Leu
 20 25 30
 Glu Thr Pro Leu Phe Val Ile Phe Leu Val Ala Tyr Ile Phe Ala Leu
 35 40 45
 Phe Gly Asn Ile Ser Ile Ile Leu Val Ser Arg Leu Asp Pro Gln Leu
 50 55 60
 Asp Ser Pro Met Tyr Phe Phe Val Ser Asn Leu Ser Leu Leu Asp Leu
 65 70 75 80
 Cys Tyr Thr Thr Ser Thr Val Pro Gln Met Leu Val Asn Leu Arg Gly
 85 90 95
 Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys Val Ala Gln Leu Tyr Ile
 100 105 110
 Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile Leu Leu Ala Ile Met Ala
 115 120 125
 Phe Asp Arg Phe Ala Ala Ile Cys Arg Pro Leu His Tyr Pro Ile Ile
 130 135 140
 Met Asn Gln Lys Arg Cys Ile His Met Ala Thr Gly Thr Trp Ile Ser
 145 150 155 160
 Gly Phe Ala Asn Ser Leu Val Gln Ser Thr Leu Thr Val Val Ala Pro
 165 170 175
 Arg Cys Gly Gln Arg Val Ile Asp His Phe Phe Cys Glu Val Pro Ala
 180 185 190
 Leu Leu Lys Leu Ala Cys Thr Asp Thr Ser Val Asn Glu Ala Glu Leu
 195 200 205
 Asn Val Leu Gly Ala Leu Leu Leu Val Pro Leu Ser Leu Ile Leu
 210 215 220
 Gly Thr Tyr Val Phe Ile Ala Gln Ala Val Leu Lys Leu Arg Ser Ala
 225 230 235 240
 Glu Ser Arg Arg Lys Ala Phe Asn Thr Cys Ala Ser His Leu Leu Val
 245 250 255

Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser Met Tyr Val Gln Pro Pro
 260 265 270
 Ser Ser Tyr Ser His Glu Arg Gly Lys Ile Met Ala Leu Phe Tyr Gly
 275 280 285
 Ile Val Thr Pro Thr Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys
 290 295 300
 Asp Val Lys Ala Ala Leu Arg Arg Ala Leu Thr Lys Glu Phe Trp Val
 305 310 315 320
 Lys Ala Arg

<210> 2378

<211> 329

<212> PRT

<213> Mus musculus (M131 8574266-9-30686-36974 2322-3308)

<220>

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400>2378

Leu Leu Ser Val Val Phe Phe Xaa Leu Phe Leu Asn Arg Val Ser Arg
 1 5 10 15
 Val Ile Ile Met Asn Val Ser Phe Lys Thr Gly Phe Leu Leu Met Gly
 20 25 30
 Phe Ser Asp Glu Arg Asn Leu Gln Ile Leu His Ala Val Leu Phe Leu
 35 40 45
 Ile Thr Tyr Leu Leu Ala Ile Met Gly Asn Leu Leu Ile Ile Thr Ile
 50 55 60
 Ile Thr Leu Asp Gln Arg Leu His Ser Pro Met Tyr Tyr Phe Leu Lys
 65 70 75 80
 His Leu Ser Phe Leu Asp Leu Cys Phe Ile Ser Val Thr Val Pro Gln
 85 90 95
 Ser Ile Ala Asn Ser Leu Met Asn Asn Gly Phe Ile Ser Leu Gly Gln
 100 105 110
 Cys Met Leu Gln Val Phe Phe Phe Ile Ala Leu Ala Ser Ser Glu Val
 115 120 125
 Ala Ile Leu Thr Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 130 135 140
 Pro Leu Gln Tyr Glu Thr Ile Met Asp Pro His Ala Cys Lys Cys Ala
 145 150 155 160
 Val Ile Ala Val Trp Met Ala Gly Gly Leu Ser Gly Leu Leu His Thr
 165 170 175
 Gly Val Asn Phe Ser Ile Pro Leu Cys Gly Lys Arg Ile Ile His Gln
 180 185 190
 Phe Phe Cys Asp Ile Pro Gln Met Leu Lys Leu Ala Cys Ser Tyr Glu
 195 200 205
 Phe Ile Asn Glu Ile Ala Val Ala Ala Phe Thr Thr Ser Thr Ala Phe
 210 215 220
 Val Cys Leu Ile Ala Ile Val Phe Ser Tyr Thr Gln Ile Phe Ser Thr
 225 230 235 240
 Val Met Arg Ile Pro Ser Ala Asp Ser Arg Thr Lys Val Phe Ser Thr
 245 250 255
 Cys Leu Pro His Leu Phe Val Val Met Phe Phe Leu Ser Ala Ala Gly
 260 265 270
 Phe Glu Phe Leu Arg Pro Pro Ser Asp Ser Leu Ser Ala Met Asp Leu
 275 280 285
 Val Phe Ser Ile Phe Tyr Thr Val Ile Pro Pro Thr Leu Asn Pro Leu
 290 295 300
 Ile Tyr Ser Leu Arg Asn Glu Ala Met Lys Ala Ala Leu Arg Lys Val


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<210> 2379
<211> 324
<212> PRT
<213> Mus musculus (M132 8574266-9-4118-8767 2921-3891)

<220>
<221> VARIANT
<222> (1)...(324)
<223> Xaa = Any Amino Acid
```

```
<210> 2380
<211> 341
<212> PRT
```

<213> Mus musculus (M133 8574277-10-1-1870 1597-577)

<220>

<221> VARIANT

<222> (1)...(341)

<223> Xaa = Any Amino Acid

<400>2380

```

Val Leu Leu Asn His Thr Phe Ile Thr Glu Phe Leu Leu Leu Gly Val
 1           5           10           15
Thr Asp Ile Gln Glu Leu Asn Pro Ile Leu Phe Val Met Val Leu Ala
          20           25           30
Met Tyr Phe Ile Asn Val Phe Gly Asn Gly Ala Ile Met Met Ile Val
          35           40           45
Ile Leu Asp Ser Arg Leu Tyr Ser Pro Met Tyr Phe Phe Leu Gly Asn
          50           55           60
Leu Ala Cys Leu Asp Ile Cys Phe Ser Thr Val Thr Val Pro Lys Met
          65           70           75           80
Leu Glu Asn Phe Phe Ser Thr Ser Lys Ala Ile Ser Phe Leu Gly Cys
          85           90           95
Ile Thr Gln Leu His Phe Phe His Phe Leu Gly Cys Thr Asp Ala Leu
          100          105          110
Leu Leu Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Arg Pro
          115          120          125
Leu His Tyr Pro Ser Ile Met Asn Arg Gln Val Cys Ile Gln Val Ala
          130          135          140
Ala Thr Ile Trp Ala Ile Pro Phe Leu His Ala Leu Val His Ser Ile
          145          150          155          160
Leu Thr Ser Gln Leu Asn Phe Cys Gly Ser Asn Arg Ile His His Phe
          165          170          175
Phe Cys Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Gly Asn Thr Glu
          180          185          190
Leu Asn Arg Trp Leu Leu Asn Thr Leu Ala Gly Thr Ile Gly Ile Gly
          195          200          205
Leu Phe Phe Leu Thr Phe Leu Ser Tyr Phe Tyr Ile Val Thr Tyr Leu
          210          215          220
Phe Leu Lys Thr His Ser Cys Ser Met Leu His Lys Ala Leu Ser Thr
          225          230          235          240
Cys Ala Ser His Phe Met Val Val Met Ile Phe Tyr Ala Pro Val Leu
          245          250          255
Phe Ile Tyr Ile Asn Pro Asp Ser Gly Ser Ser Leu Glu Lys Asp Arg
          260          265          270
Ile Ile Ala Val Met Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
          275          280          285
Ile Tyr Ala Leu Arg Asn Lys Glu Val Arg Cys Ala Leu Asn Arg Lys
          290          295          300
Leu Arg Ile Leu Ile Xaa Leu Gly Arg Asn Leu Val Ser Tyr Phe Val
          305          310          315          320
Ile Ser Gln His Lys Gln Leu Leu Xaa Lys Ser Met Cys Glu Ile Ser
          325          330          335
Xaa Phe Xaa Ile Cys
          340

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<210> 2381

<211> 284

<212> PRT

<213> Mus musculus (M136 8574277-13-1-992 974-124)

<220>

<221> VARIANT

<222> (1)...(284)

<223> Xaa = Any Amino Acid

<400>2381

Cys Ile Tyr Ile Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val
 1 5 10 15
 Cys Ile Ser Ile Cys Thr Tyr Leu His Ile Xaa Ile His Met Cys Val
 20 25 30
 Gln Val Val Ile Lys Leu Lys Val Lys Xaa Val Thr Trp Lys Glu Val
 35 40 45
 Xaa Lys Met Ser Val Glu Lys Arg Thr Gln Ser Arg Gln Lys Ser Gly
 50 55 60
 Tyr Leu Ala Asn Cys Phe Leu Gln Ser Phe Ile Leu Gly Ser Val Asp
 65 70 75 80
 Arg Asn Ile Cys Leu Leu Ile Val Met Val Tyr Asp His Tyr Leu Thr
 85 90 95
 Ile Cys His His Leu Xaa Tyr Pro Phe Leu Met Gly Pro Leu Trp Gly
 100 105 110
 Leu Gly Phe Gly Leu Thr Thr Ser Phe Val Val Asp Glu Leu Ile Val
 115 120 125
 Ala Leu Met Ala Gln Leu Arg Phe Cys Val Pro Lys Gln Ile Asp His
 130 135 140
 Phe Tyr Tyr Asp Phe Ser Pro Leu Val Val Leu Ala Tyr Thr Asp Thr
 145 150 155 160
 Gly Leu Val Gln Val Thr Thr Phe Val Leu Phe Val Val Phe Leu Thr
 165 170 175
 Val Pro Phe Gly Leu Val Leu Ile Ser Cys Ala Gln Ile Ala Val Thr
 180 185 190
 Val Leu Arg Val Pro Ser Arg Thr Arg Arg Asn Lys Ala Phe Ser Thr
 195 200 205
 Cys Ser Ser His Leu Asp Glu Val Ser Thr Phe Tyr Gly Ser Leu Met
 210 215 220
 Val Trp Tyr Thr Glu Pro Ser Ala Val His Ser Gln Ile Leu Ser Lys
 225 230 235 240
 Val Ile Ala Leu Leu Tyr Thr Val Val Thr Thr Ile Phe Asp Pro Gly
 245 250 255
 Ile Tyr Thr Leu Arg Asn Gln Glu Val Gln Gln Ser Leu Arg Arg His
 260 265 270
 Leu Tyr Cys Lys Pro Thr Glu Met Xaa Pro Lys Arg
 275 280

<210> 2382

<211> 314

<212> PRT

<213> Mus musculus (M143 8574277-22-875-4053 855-1796)

<400>2382

Tyr Pro Met Gly Ile Leu Ser Thr Gly Asn Gln Thr Val Thr Glu Phe
 1 5 10 15
 Val Leu Leu Gly Phe His Glu Val Pro Gly Leu His Leu Leu Phe Phe
 20 25 30
 Ser Val Phe Thr Ile Leu Tyr Ala Ser Ile Ile Thr Gly Asn Met Leu
 35 40 45
 Ile Ala Val Val Val Val Ser Gln Arg Leu His Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Val Asn Leu Ser Phe Ile Glu Ile Val Tyr Thr Ser Thr
 65 70 75 80
 Val Val Pro Lys Met Leu Glu Gly Phe Leu Gln Glu Ala Thr Ile Ser
 85 90 95
 Val Ala Gly Cys Leu Leu Gln Phe Phe Val Phe Gly Ser Leu Ala Thr
 100 105 110
 Asp Glu Cys Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala

115	120	125
Ile Cys His Pro Leu Arg Tyr	Pro His Leu Met Gly	Pro Gln Trp Cys
130	135	140
Leu Gly Leu Val Leu Thr Val Trp	Leu Ser Gly Phe Met Val Asp Gly	
145	150	155
Leu Val Val Ala Leu Met Ala Gln	Leu Arg Phe Cys Gly Pro Asn Leu	
165	170	175
Val Asp His Phe Tyr Cys Asp Phe	Ser Pro Leu Met Val Leu Ala Cys	
180	185	190
Ser Asp Thr Gln Val Ala Gln Val	Thr Thr Phe Val Leu Ser Val Val	
195	200	205
Phe Leu Thr Val Pro Phe Gly Leu	Val Leu Ile Ser Tyr Ala Gln Ile	
210	215	220
Val Val Thr Val Leu Arg Val Pro	Ser Gly Thr Arg Arg Thr Lys Ala	
225	230	235
Phe Ser Thr Cys Ser Ser His Leu	Ala Val Val Ser Thr Phe Tyr Gly	
245	250	255
Thr Leu Met Val Leu Tyr Ile Val	Pro Ser Ala Val His Ser Gln Leu	
260	265	270
Leu Ser Lys Val Ile Ala Leu Leu	Tyr Thr Val Val Thr Pro Ile Phe	
275	280	285
Asn Pro Val Ile Tyr Thr Leu Arg	Asn Gln Glu Val Gln Gln Ala Leu	
290	295	300
Arg Arg Leu Leu Tyr Cys Lys Pro	Thr Glu	
305	310	

<210> 2383

<211> 107

<212> PRT

<213> Mus musculus (M144 8574277-30-676-1123 424-104)

<220>

<221> VARIANT

<222> (1)...(107)

<223> Xaa = Any Amino Acid

<400>2383

Ser Gly Val Leu Gly Asn Lys Leu	Ser Leu Cys Leu Xaa Val Xaa Arg
1	5 10 15
Val Phe Phe Ser Cys Gly Xaa Val	Pro Ser Ala Gln Gly Lys Arg Lys
20	25 30
Ser Leu Ala Thr Cys Ser Ser His	Leu Ser Val Val Leu Leu Phe Tyr
35	40 45
Ser Thr Val Phe Ala Thr Tyr Leu	Lys Pro Pro Ser Thr Ser His Ser
50	55 60
Ser Ala Glu Val Val Ala Ala Val	Met Tyr Thr Leu Val Thr Pro Thr
65	70 75 80
Leu Asn Pro Phe Ile Tyr Ser Leu	Arg Asn Lys Asp Val Lys Ser Ser
85	90 95
Leu Arg Lys Ile Leu Asn Met Asp	Lys Phe Gln
100	105

<210> 2384

<211> 232

<212> PRT

<213> Mus musculus (M148 8574277-5-2944-4486 2-698)

<220>

<221> VARIANT

<222> (1)...(232)

<223> Xaa = Any Amino Acid

<400>2384

```

Lys Ser Leu Ala Thr Leu Ala Gly Cys Leu Leu Gln Phe Leu Thr Phe
 1           5           10           15
Thr Ser Leu Asp Ala Asp Glu Tyr Phe Leu Leu Thr Leu Met Ala His
          20           25           30
Asp His Cys Leu Ala Ile Phe Tyr Ser Leu Xaa Tyr Pro Arg Leu Met
          35           40           45
Arg Pro Gln Trp Cys Leu Gly Leu Val Ile Ile Val Trp Leu Ser Gly
          50           55           60
Phe Met Glu Ala Gly Leu Val Val Ala Leu Thr Ala Gln Leu Arg Phe
65           70           75           80
Cys Gly Pro Asn Leu Ile Asp His Phe Tyr Cys Asp Phe Ser Pro Leu
          85           90           95
Met Ile Leu Ala Cys Ser Asp Thr Xaa Val Ala Gln Met Thr Thr Phe
          100          105          110
Val Leu Phe Val Val Phe Leu Pro Val Leu Ser Gly Leu Ile Leu Met
          115          120          125
Ser Tyr Ala Gln Phe Val Val Ile Val Leu Arg Ile Pro Ser Gly Ala
          130          135          140
Arg Arg Thr Lys Ala Phe Phe Thr Cys Ser Ser His Leu Ala Met Met
145          150          155          160
Phe Thr Phe Tyr Gly Ser Leu Met Val Trp Tyr Thr Ala Pro Ser Ala
          165          170          175
Val Leu Ser Leu Gln Leu Leu Ser Lys Val Ile Ala Leu Leu Tyr Thr
          180          185          190
Val Phe Ala Pro Ile Phe Asn Ser Val Ile Tyr Thr Leu Arg Asn Leu
          195          200          205
Asp Met Gln Lys Ala Leu Arg Arg Leu Leu Tyr Cys Lys Ser Thr Glu
210          215          220
Met Xaa Pro Lys Lys Glu Gly Ser
225          230

```

<210> 2385

<211> 326

<212> PRT

<213> Mus musculus (M149 8574277-6-4252-5644 1059-82)

<220>

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400>2385

```

Tyr Ile Val Phe Thr Pro Ile Ser Ser Xaa Asn Thr Arg Pro Thr Met
 1           5           10           15
Asn Cys Ser Gln Ala Pro Thr Phe Ile Leu Leu Gly Leu Ser Ser Asp
          20           25           30
Ala Glu Lys Trp Gln Pro Leu Phe Ser Ile Phe Leu Val Leu Tyr Leu
          35           40           45
Leu Gly Leu Leu Gly Asn Leu Leu Leu Leu Leu Ala Ile Gly Thr Asp
          50           55           60
Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Gln Leu Ser Leu
65           70           75           80
Val Asp Leu Cys Phe Ile Thr Thr Thr Ala Pro Lys Met Leu Glu Ala
          85           90           95
Leu Trp Thr Gly Asp Gly Ser Ile Ser Phe Ser Gly Cys Leu Thr Gln
          100          105          110
Leu Tyr Phe Phe Ala Val Phe Ala Asp Met Asp Asn Leu Leu Leu Ala
          115          120          125
Val Met Ala Ile Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Leu Tyr

```

130		135		140
Pro Leu Leu Met Thr	Pro Cys Arg Cys Arg	Val Leu Val Ser Gly Ser		
145	150	155	160	
Trp Gly Val Ala His	Cys Val Ser Leu Thr His	Thr Leu Leu Phe Ser		
	165	170	175	
Lys Leu Tyr Phe His	Asn Asn Gln Glu Ile Pro	His Phe Phe Cys Asp		
	180	185	190	
Phe Gly Pro Leu Leu Leu	Leu Ser Cys Ser Asp Thr	Tyr Leu Asn Glu		
	195	200	205	
Ser Leu Met Met Ala Leu	Ser Gly Leu Leu Ala Ile	Ser Ala Phe Leu		
	210	215	220	
Cys Ile Val Ser Ser Tyr	Gly Cys Ile Phe Tyr Ala	Val Ala Lys Val		
225	230	235	240	
Pro Ser Ala Gln Gly Lys	Arg Lys Ala Leu Ala Thr	Cys Ser Ser His		
	245	250	255	
Leu Ser Val Val Leu Leu	Phe Tyr Ser Thr Val Phe	Ala Thr Tyr Leu		
	260	265	270	
Lys Pro Pro Ser Ser Ser	His Ser Ser Gln Glu Val	Val Ala Ala Val		
	275	280	285	
Met Tyr Thr Leu Val Thr	Pro Thr Leu Asn Pro Phe	Ile Tyr Ser Leu		
	290	295	300	
Arg Asn Lys Asp Val Lys	Ser Ser Leu Arg Arg Ile	Leu Asn Met Val		
305	310	315	320	
Lys Ser Gln Asp Xaa Gly				
	325			

<210> 2386

<211> 321

<212> PRT

<213> Mus musculus (M152 8574277-7-18987-20418 1032-73)

<220>

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400>2386

Cys Gly Leu Ser Cys Ser	Gln Arg Ser Arg Arg	Asn Val Leu Ile Ser
1	5	10
Leu Xaa Xaa Leu Asn Phe	Phe Leu Met Gly Phe	Ser Arg Lys Leu Glu
	20	25
Val Glu His Asn Phe Ile	Leu Ala Leu Gly Leu Val	Ile Leu Ile Ala
	35	40
Asn Val Phe Ile Ile Ala	Ala Ile Ser Leu Glu Tyr	His Leu Cys Ser
	50	55
Leu Arg His Phe Leu Leu	Glu Gln Leu Phe Cys	Leu Asp Leu Cys Tyr
65	70	75
Ile Ser Met Ile Val Leu	Ser Thr Ile Lys Ser	Ile Cys Arg Ser Phe
	85	90
Met Tyr Ser Ala Tyr Ile	Ser Leu Ile Glu Cys Thr	Leu Gln Gly Phe
	100	105
Ala Phe Thr Leu Cys Ser	Tyr Thr Ser Met Ala Ile	Leu Thr Val Met
	115	120
Ser Cys His Cys Tyr Val	Ile Met Cys Tyr Lys	Val Ile Ile Ser Val
	130	135
Ser Leu Cys Met His Lys	Val Leu Ala Val Trp	Ala Ser Gly Cys Gly
145	150	155
Ile Asn Phe Gly Val Met	His Thr Ala Val Asn	Phe Ser Ile Ser Leu
	165	170
Cys Gly Ala Ser Val Ile	His Xaa Phe Cys	Asn Val Leu Leu Val Leu
	180	185
		190

Lys Leu Ser Cys Ser Asn Asp Cys Val Ser Glu Leu Ser Ile Ile Gly
 195 200 205
 Phe Pro Thr Cys Arg His Phe Ile Ser Ile Ser Phe Ala Tyr Glu His
 210 215 220
 Ile Leu Ser Pro Glu Leu Arg Met Pro Ser Val Lys Gly Arg Thr Arg
 225 230 235 240
 Val Phe Ser Thr Cys Leu Cys His Ile Ser Val Val Ile Leu Phe Ile
 245 250 255
 Pro Thr Gly Val Phe Glu Phe Leu Asn Pro His Ser Lys Ser Pro Thr
 260 265 270
 Xaa Ile Leu His Xaa Thr Leu Phe Leu Val Phe His Thr Phe Leu Ser
 275 280 285
 Ser Thr Leu Asn Pro Glu Ile Asn Ser Leu Arg Asn Glu Ala Thr Glu
 290 295 300
 His His Ser Lys Glu Asn Val Ser Leu Phe Ile Ser Thr Ile Ser Ser
 305 310 315 320
 Leu

<210> 2387

<211> 327

<212> PRT

<213> Mus musculus (M154 8575572-1-103679-105172 492-1471)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400>2387

His Xaa Met Gly Ala Leu Asn Gln Thr Arg Val Thr Glu Phe Ile Phe
 1 5 10 15
 Leu Gly Leu Thr Asp Asn Trp Val Leu Glu Ile Leu Phe Phe Val Pro
 20 25 30
 Phe Thr Val Thr Tyr Met Leu Thr Leu Leu Gly Asn Phe Leu Ile Val
 35 40 45
 Val Thr Ile Val Phe Thr Pro Arg Leu His Asn Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Ser Phe Ile Asp Ile Cys His Ser Ser Val Thr Val
 65 70 75 80
 Pro Lys Met Leu Glu Gly Leu Leu Leu Glu Arg Lys Thr Ile Ser Phe
 85 90 95
 Asp Asn Cys Ile Ala Gln Leu Phe Phe Leu His Leu Phe Ala Cys Ser
 100 105 110
 Glu Ile Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Ile Pro Leu His Tyr Ser Asn Val Met Asn Met Lys Val Cys Val
 130 135 140
 Gln Leu Val Phe Ala Leu Trp Leu Gly Gly Thr Ile His Ser Leu Val
 145 150 155 160
 Gln Thr Phe Leu Thr Ile Arg Leu Pro Tyr Cys Gly Pro Asn Ile Ile
 165 170 175
 Asp Ser Tyr Phe Cys Asp Val Pro Pro Val Ile Lys Leu Ala Cys Thr
 180 185 190
 Asp Thr Tyr Leu Thr Gly Ile Leu Ile Val Ser Asn Ser Gly Thr Ile
 195 200 205
 Ser Leu Val Cys Phe Leu Ala Leu Val Thr Ser Tyr Thr Val Ile Leu
 210 215 220
 Phe Ser Leu Arg Lys Lys Ser Ala Glu Gly Arg Arg Lys Ala Leu Ser
 225 230 235 240
 Thr Cys Ser Ala His Phe Met Val Val Thr Leu Phe Phe Gly Pro Cys

```

                245                250                255
Ile Phe Leu Tyr Thr Arg Pro Asp Ser Ser Phe Ser Ile Asp Lys Val
                260                265                270
Val Ser Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu Ile
                275                280                285
Tyr Thr Leu Arg Asn Glu Glu Val Lys Thr Ala Met Lys His Leu Arg
                290                295                300
Gln Arg Arg Ile Cys Ser Xaa Asn His Val Cys Val Trp Leu Val Xaa
305                310                315                320
Cys Cys Asp Asn Ser His Gly
                325

```

<210> 2388

<211> 330

<212> PRT

<213> Mus musculus (M157 8575572-1-144835-147600 2426-1439)

<220>

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400>2388

```

Met Glu Lys Ala Val Leu Ile Asn Gln Thr Ser Val Met Ser Phe Arg
 1                5                10                15
Leu Thr Gly Leu Ser Thr Asn Pro Lys Val Gln Met Ala Ile Phe Phe
                20                25                30
Ile Phe Leu Ile Phe Tyr Val Leu Thr Leu Val Gly Asn Ile Leu Ile
                35                40                45
Val Val Thr Ile Ile His Asp His Arg Leu His Thr Pro Met Tyr Phe
                50                55                60
Phe Leu Ser Asn Leu Ser Phe Ile Asp Val Cys His Ser Thr Val Thr
65                70                75                80
Val Pro Lys Met Leu Ser Asp Thr Phe Ser Glu Glu Lys Leu Ile Ser
                85                90                95
Phe Asp Asp Cys Val Val Gln Ile Phe Phe Leu His Leu Phe Ala Cys
                100                105                110
Thr Glu Ile Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala
                115                120                125
Ile Cys Lys Pro Leu Arg Tyr Met Thr Ile Met Asn Trp Lys Val Cys
130                135                140
Met Val Leu Gly Gly Ala Met Trp Thr Ala Gly Thr Ile His Ser Ile
145                150                155                160
Ser Phe Thr Ser Leu Thr Ile Lys Leu Pro Tyr Cys Gly Pro Asn Glu
                165                170                175
Leu Asp Ser Phe Phe Cys Asp Val Pro Gln Val Ile Glu Leu Ala Cys
                180                185                190
Thr Asp Thr Arg Ile Thr Glu Ile Leu Val Val Ser Asn Ser Gly Met
195                200                205
Ile Ser Met Val Cys Phe Val Ile Ile Val Val Ser Tyr Ala Val Ile
210                215                220
Leu Val Ser Leu Arg Gln Gln Ile Ser Asp Gly Lys Arg Lys Ala Leu
225                230                235                240
Ser Thr Cys Ala Ala His Leu Thr Val Val Thr Leu Phe Leu Gly His
                245                250                255
Cys Ile Phe Ile Tyr Ser Arg Pro Ala Ile Ser Leu Pro Glu Asp Lys
                260                265                270
Ile Val Ser Ala Phe Phe Thr Ala Ile Thr Pro Leu Leu Asn Pro Ile
275                280                285
Ile Tyr Thr Phe Arg Asn Glu Asp Met Lys Ser Ala Leu Lys Lys Leu
290                295                300

```


Ile Arg Arg Lys Glu Gly Lys Glu Lys Xaa Lys Cys Ile Ser Ser Leu
 305 310 315 320
 Gly Phe Leu Val Ile Xaa Ile Lys Glu Ala
 325 330

<210> 2389

<211> 331

<212> PRT

<213> Mus musculus (M158 8575572-1-18114-22131 1498-507)

<220>

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400>2389

Cys Leu Ser Ala Ser Leu Asp Ile Ser Lys Met Glu Arg Ile Asn Tyr
 1 5 10 15
 Thr Val Leu Thr Glu Phe Ile Leu Thr Gly Val Pro His Pro Pro Arg
 20 25 30
 Leu Arg Thr Phe Leu Phe Val Phe Phe Leu Leu Ile Tyr Ile Leu Thr
 35 40 45
 Gln Leu Gly Asn Ala Leu Ile Leu Ile Thr Val Cys Ala Asp Thr Gln
 50 55 60
 Leu His Ala Arg Pro Met Tyr Ile Phe Leu Gly Ala Leu Ser Val Ile
 65 70 75 80
 Asp Met Gly Ile Ser Thr Ile Ile Val Pro Arg Leu Met Met Asn Phe
 85 90 95
 Thr Pro Gly Ile Lys Pro Ile Pro Phe Gly Gly Cys Val Ala Gln Leu
 100 105 110
 Tyr Phe Tyr His Phe Leu Gly Ser Ser Gln Cys Phe Leu Tyr Thr Thr
 115 120 125
 Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro
 130 135 140
 Val Leu Met Ser Ala Lys Leu Ser Ile Leu Leu Val Ala Gly Ala Trp
 145 150 155 160
 Val Ala Gly Ser Ile His Gly Ala Ile Gln Ala Ile Leu Thr Phe Arg
 165 170 175
 Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile
 180 185 190
 Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Thr Val Asn Glu Leu
 195 200 205
 Val Thr Phe Val Asp Ile Gly Val Val Val Ala Ser Cys Phe Ser Leu
 210 215 220
 Ile Leu Leu Ser Tyr Ile Tyr Ile Ile Arg Ala Ile Leu Arg Ile Arg
 225 230 235 240
 Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser Thr Cys Gly Ala His Val
 245 250 255
 Thr Ile Val Thr Val Tyr Tyr Val Pro Cys Ala Phe Ile Tyr Leu Arg
 260 265 270
 Pro Asp Ser His Ser Ile Leu Asp Gly Ala Ala Ala Leu Phe Pro Thr
 275 280 285
 Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln
 290 295 300
 Glu Val Lys Leu Ala Leu Arg Arg Met Val Gly Ser Gln Ser Thr Lys
 305 310 315 320
 Ser Glu Val Xaa Ala Pro Leu Leu Phe Xaa Gly
 325 330

<210> 2390

<211> 324

<212> PRT

<213> Mus musculus (M160 8575572-1-54180-57203 1450-479)

<220>

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400>2390

```

Ile Leu Thr Asp Xaa Asp Met Arg Arg Thr Arg Asn Thr Ser Leu Asp
 1           5           10           15
Ala Val Val Thr Asp Phe Leu Leu Leu Gly Leu Ala His Pro Pro Asn
 20           25           30
Leu Arg Ala Phe Leu Phe Leu Val Phe Phe Leu Ile Tyr Ile Leu Thr
 35           40           45
Gln Leu Gly Asn Leu Leu Ile Leu Leu Thr Val Trp Ala Asp Pro Lys
 50           55           60
Leu His Ala Arg Pro Met Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu
 65           70           75           80
Asp Met Trp Leu Ser Ser Val Ile Val Pro Arg Leu Ile Leu Asn Phe
 85           90           95
Thr Pro Ala Ser Lys Ala Ile Pro Phe Gly Gly Cys Val Ala Gln Leu
100           105           110
Tyr Phe Phe His Phe Leu Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu
115           120           125
Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro
130           135           140
Val Leu Met Asn Gly Lys Leu Cys Thr Ile Leu Val Ser Gly Ala Trp
145           150           155           160
Val Ala Gly Ser Ile His Gly Ser Ile Gln Thr Thr Leu Thr Phe Arg
165           170           175
Leu Pro Tyr Cys Gly Pro Asn Gln Ile Asp Tyr Phe Ile Cys Asp Ile
180           185           190
Pro Ala Val Leu Arg Leu Ala Cys Ala Asp Thr Thr Val Asn Glu Leu
195           200           205
Val Thr Phe Val Asp Ile Gly Val Val Ala Ala Ser Cys Phe Met Leu
210           215           220
Ile Leu Leu Ser Tyr Ala Asn Ile Val His Ala Ile Leu Lys Ile Arg
225           230           235           240
Thr Ala Asp Gly Arg Lys Arg Ala Phe Ser Thr Cys Gly Ser His Leu
245           250           255
Thr Val Val Thr Val Tyr Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg
260           265           270
Ala Gly Ser Lys Ser Pro Phe Asp Gly Ala Val Ala Val Phe Tyr Thr
275           280           285
Val Val Thr Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Gln
290           295           300
Glu Val Lys Ser Ala Leu Lys Arg Leu Thr Ala Gly Arg Arg Asp Val
305           310           315           320
Gly Gly Glu Lys

```

<210> 2391

<211> 329

<212> PRT

<213> Mus musculus (M162 8576192-11-46369-50310 3151-2165)

<220>

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400>2391

```

Phe Ser Xaa Ser His Tyr Arg Gln Asn Met Thr Gly Asn Asn Gln Thr
 1           5           10           15
Leu Ile Ser Lys Phe Leu Leu Leu Gly Leu Pro Ile Leu Ser Glu Tyr
 20           25           30
His Phe Leu Phe Tyr Ala Leu Phe Leu Ala Met Tyr Leu Thr Thr Ile
 35           40           45
Leu Gly Asn Leu Leu Ile Ile Ala Leu Val Arg Leu Asp Ser His Leu
 50           55           60
His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu
 65           70           75           80
Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln Asn Met Gln Ser
 85           90           95
Gln Val Pro Ser Ile Ser Tyr Val Gly Cys Leu Thr Gln Leu Tyr Phe
100           105           110
Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu Val Val Met Ala
115           120           125
Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ser Ile
130           135           140
Met Ser Thr Lys Phe Cys Thr Ser Leu Val Leu Leu Trp Met Leu
145           150           155           160
Thr Thr Ser Asn Ala Leu Met His Thr Leu Leu Met Ala Arg Leu Ser
165           170           175
Phe Cys Glu Lys Asn Val Ile Leu Arg Phe Phe Cys Asp Ile Ser Ala
180           185           190
Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Val Asn Glu Leu Met Ile
195           200           205
Phe Ile Met Gly Gly Ile Ile Ile Ile Ile Pro Phe Leu Leu Ile Val
210           215           220
Met Ser Tyr Val Arg Ile Phe Phe Ser Ile Leu Lys Val Pro Ser Thr
225           230           235           240
Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val
245           250           255
Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser
260           265           270
Ser Asn Asn Ser Thr Val Lys Glu Ser Ala Met Ala Met Met Tyr Thr
275           280           285
Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg
290           295           300
Asp Met Lys Arg Ala Leu Ile Arg Val Ile Cys Ser Lys Lys Ile Ser
305           310           315           320
Leu Xaa Trp Lys Tyr Phe Arg Met Ile
325

```

<210> 2392

<211> 275

<212> PRT

<213> Mus musculus (M163 8576192-5-7971-9031 1060-236)

<220>

<221> VARIANT

<222> (1)...(275)

<223> Xaa = Any Amino Acid

<400>2392

```

Ile Ile Ile Leu Ile Ile Leu Asp Phe His Leu His Thr Pro Ile Tyr
 1           5           10           15
Leu Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val
 20           25           30
Thr Met Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Asp Thr Thr Ile

```

```

      35      40      45
Ser Tyr Val Gly Cys Leu Thr Gln Met Tyr Phe Pro Asn Val Phe Ala
  50      55      60
Asn Leu Glu Asn Phe Leu Leu Met Phe Met Ala Tyr Asp Arg Tyr Val
  65      70      75      80
Ala Ile Cys Tyr Pro Leu Arg Tyr Thr Ser Ile Met Ser Pro Ile Leu
      85      90      95
Cys Val Cys Met Val Phe Met Ser Trp Leu Leu Thr Met Leu Asn Ser
      100      105      110
Thr Leu His Thr Val Leu Ile Val Lys Leu Ser Phe Cys Glu Asp Asn
      115      120      125
Val Ile Pro His Phe Phe Cys Asp Ile Ser Ala Val Leu Lys Leu Ala
      130      135      140
Cys Ser Asp Ile Tyr Ile Asn Glu Leu Thr Ile Phe Ile Thr Gly Ala
      145      150      155      160
Phe Ile Ile Val Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Gln
      165      170      175
Ile Val Cys Ser Ile Leu Lys Phe Ser Ser Thr Arg Gly Ile Ala Lys
      180      185      190
Ile Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
      195      200      205
Gly Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser Thr Asn Asn Ser Thr
      210      215      220
Val Lys Asp Thr Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met
      225      230      235      240
Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala
      245      250      255
Leu Ile Arg Val Leu Cys Lys Lys Glu Ile Ser Leu Xaa Trp Gln Tyr
      260      265      270
Leu His Leu
      275

```

<210> 2393

<211> 327

<212> PRT

<213> Mus musculus (M165 8576192-7-12279-14147 678-1658)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400>2393

```

Trp Arg Ile Arg Met Ile Ile Asn Asn Gln Thr Ala Ile Pro Gln Phe
  1      5      10      15
Ile Leu Leu Gly Leu Pro Ile Leu Pro Glu Gln Gln Met Phe Tyr
      20      25      30
Ala Leu Phe Leu Ala Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile
      35      40      45
Ile Ile Ile Leu Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr
      50      55      60
Leu Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val
      65      70      75      80
Thr Met Pro Lys Leu Leu Gln Asn Ile Gln Ser Gln Asp Pro Ser Ile
      85      90      95
Ser Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Phe Met Val Phe Ala
      100      105      110
Asn Thr Glu Asn Val Leu Leu Val Met Ala Tyr Asp Arg Tyr Val
      115      120      125
Ala Ile Cys Phe Pro Leu His Tyr Thr Ser Ile Met Ser Pro Lys Leu
      130      135      140

```

Cys Val Ser L u Val Val Leu Thr Trp Val Phe Thr Val Leu Tyr Ser
 145 150 155 160
 Met Leu His Thr Leu L u Leu Ala Arg Leu Ser Phe Cys Glu Asp Asn
 165 170 175
 Val Ile Thr His Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ala
 180 185 190
 Cys Ser Asp Thr Tyr Ile Asnⁿ Glu Leu Met Ile Phe Ile Leu Gly Thr
 195 200 205
 Leu Asp Thr Val Val Pro Phe Leu Leu Ile Val Val Ser Tyr Val Gln
 210 215 220
 Ile Val Cys Ser Ile Leu Lys Phe Ser Thr Lys Gln Gly Ile Ala Lys
 225 230 235 240
 Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
 245 250 255
 Gly Thr Ile Ile Gly Val Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr
 260 265 270
 Val Lys Glu Ile Val Met Ala Leu Met Tyr Thr Val Val Thr Pro Met
 275 280 285
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Glu Ala
 290 295 300
 Leu Ile Arg Val Leu Cys Lys Lys Gln Ile Pro Leu Xaa Cys Leu Tyr
 305 310 315 320
 Trp Asn Phe Xaa Ile Xaa Ile
 325

<210> 2394

<211> 316

<212> PRT

<213> Mus musculus (M166 8576192-8-1-1469 247-1198)

<400>2394

Arg Gly Arg Met Val Met Asn Asn Gln Thr Val Ile Ser Gln Leu Leu
 1 5 10 15
 Leu Val Gly Leu His Ile Pro Pro Asp His Gln Gln Gly Phe Tyr Thr
 20 25 30
 Leu Phe Leu Ala Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile
 35 40 45
 Ile Pro Leu Ile Ile Met Asp Ser Pro Phe Pro Thr His Pro Met Tyr
 50 55 60
 Leu Phe Leu Ile Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val
 65 70 75 80
 Thr Val Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Asp Thr Ser Ile
 85 90 95
 Ser Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Leu Met Val Phe Gly
 100 105 110
 Asp Met Glu Ser Phe Leu Leu Val Met Ala Tyr Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Phe Pro Leu His Tyr Thr Ser Thr Met Ser Pro Lys Phe
 130 135 140
 Cys Val Cys Val Gly Ala Leu Ser Trp Val Phe Thr Ile Met Tyr Ser
 145 150 155 160
 Met Val His Thr Leu Leu Ser Arg Leu Ser Phe Cys Glu Asp Asn
 165 170 175
 Val Ile Pro His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ala
 180 185 190
 Cys Ser Asp Ile Phe Ile Asn Glu Leu Met Ile Phe Ile Leu Gly Gly
 195 200 205
 Pro Val Val Ala Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Arg
 210 215 220
 Ile Val Ser Ser Ile Leu Lys Val Ser Ser Ser Gln Gly Ile His Lys
 225 230 235 240

```

<210> 2395
<211> 244
<212> PRT
<213> Mus musculus (M167 8576192-8-6530-9303 730-2)

<220>
<221> VARIANT
<222> (1)...(244)
<223> Xaa = Any Amino Acid

```

```
<210> 2396
<211> 338
<212> PRT
<213> Mus musculus (M168 8576195-11-1440-4165 2456-1443)
<220>
```

<221> VARIANT

<222> (1)...(338)

<223> Xaa = Any Amino Acid

<400>2396

Cys Xaa Xaa His Phe Ile Leu Ser Leu Leu Gln Met Lys Val Met Lys
 1 5 10 15
 Gln Met Val Thr Glu Ser Asn Ser Ser Val Thr Glu Phe Ile Leu Met
 20 25 30
 Gly Leu Thr Val Gln Lys Glu Leu Gln Leu Pro Leu Phe Ile Leu Phe
 35 40 45
 Leu Leu Asn Tyr Thr Ala Thr Val Val Gly Asn Leu Ser Leu Met Asn
 50 55 60
 Leu Ile Cys Leu Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Ile
 65 70 75 80
 Phe Asn Leu Ser Cys Ile Asp Phe Cys Tyr Ser Phe Val Ser Asn Pro
 85 90 95
 Thr Met Leu Arg Ser Phe Val Thr Glu Gln Asn Thr Ile Ser Tyr Glu
 100 105 110
 Gly Cys Met Ser Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser Glu
 115 120 125
 Cys Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 130 135 140
 His Pro Leu Lys Tyr Thr Thr Val Met Ser Pro Lys Ile Cys Cys Leu
 145 150 155 160
 Leu Val Phe Gly Ser Tyr Leu Met Gly Phe Ala Gly Ala Leu Thr His
 165 170 175
 Thr Gly Phe Met Ile Arg Leu Ser Phe Cys Asn Ser Asn Ile Ile Asn
 180 185 190
 His Tyr Met Cys Asp Ile Phe Pro Leu Leu Gln Leu Ser Cys Thr Ser
 195 200 205
 Thr Tyr Val Asn Glu Leu Val Ser Ser Ala Val Val Gly Thr Ile Ile
 210 215 220
 Ile Leu Ser Ser Ile Ile Ile Leu Val Ser Tyr Ala Met Ile Leu Ser
 225 230 235 240
 Asn Ile Leu His Met Ser Ser Ser Lys Gly Trp Ser Lys Ala Leu Gly
 245 250 255
 Thr Cys Gly Ser His Ile Ile Thr Val Ser Leu Phe Tyr Gly Ser Gly
 260 265 270
 Leu Leu Ala Tyr Ile Lys Pro Thr Ser Ala Glu Thr Val Asp Gln Gly
 275 280 285
 Lys Phe Leu Ser Ile Phe Tyr Thr Leu Val Val Pro Met Leu Asn Pro
 290 295 300
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Lys Arg
 305 310 315 320
 Thr Met Lys Arg Val Thr Thr Xaa Met Asn Ser Cys Ala Phe Ile Val
 325 330 335
 Leu Pro

<210> 2397

<211> 340

<212> PRT

<213> Mus musculus (M169 8576195-13-2329-4897 1250-2268)

<220>

<221> VARIANT

<222> (1)...(340)

<223> Xaa = Any Amino Acid

<400>2397

```

Ile Ser Cys Leu Val Val Ser Pro S r Ile Leu Gln Thr Ser His Thr
 1          5          10          15
Lys Gln Ile Thr Met Glu Asn Asp Ser Phe Val Ser Glu Phe Ile Leu
      20          25          30
Met Gly Leu Thr Asp His Pro Glu Leu Gln Leu Ser Leu Phe Val Leu
      35          40          45
Phe Leu Met Asn Tyr Thr Ala Ile Val Met Gly Asn Leu Ser Leu Met
      50          55          60
Ile Leu Ile Phe Leu Asn Ser Asn Leu His Thr Pro Met Tyr Phe Phe
65          70          75          80
Ile Phe Asn Leu Ser Phe Ile Asp Phe Cys Tyr Ser Phe Val Phe Thr
      85          90          95
Pro Lys Met Leu Met Ser Phe Phe Leu Glu Lys Asn Thr Ile Ser Phe
      100          105          110
Arg Gly Cys Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Asn Ser
      115          120          125
Glu Ser Tyr Val Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile
      130          135          140
Cys Lys Pro Leu Leu Tyr Lys Thr Ile Met Val Pro Arg Ile Cys Cys
145          150          155          160
Leu Leu Met Phe Val Ser Tyr Leu Ile Gly Phe Thr Ser Ala Met Ile
      165          170          175
Leu Thr Gly Leu Met Phe Arg Leu Asn Phe Cys Asn Asn His Ile Ile
      180          185          190
Asn His Tyr Met Cys Asp Ile Phe Pro Val Ile Gln Ile Ser Cys Ser
      195          200          205
Asp Thr Tyr Leu Asn Glu Leu Val Ser Thr Ala Val Val Gly Thr Gly
      210          215          220
Ile Ile Leu Cys Ser Leu Leu Ile Leu Met Ser Tyr Ala Leu Ile Leu
225          230          235          240
Phe Asn Ile Leu Asn Met Ser Ser Gly Lys Gly Trp Ser Lys Ala Met
      245          250          255
Gly Thr Cys Gly Ser His Ile Ile Thr Val Ser Leu Phe Tyr Gly Ser
      260          265          270
Gly Leu Leu Ala Tyr Val Lys Pro Ser Ser Ala Glu Thr Val Gly Gln
      275          280          285
Gly Lys Phe Phe Ser Leu Phe Tyr Thr Phe Leu Val Pro Met Leu Asn
      290          295          300
Pro Leu Ile Tyr Ser Leu Gln Asn Lys Asp Val Lys Val Ala Val Lys
305          310          315          320
Lys Thr Leu Lys Arg Ile Ser Asn Xaa Leu Glu Pro Leu Ala Leu His
      325          330          335
Arg Thr Leu Ser
      340

```

<210> 2398

<211> 336

<212> PRT

<213> Mus musculus (M171 8576195-15-1361-3546 1172-2177)

<220>

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400>2398

```

Phe Xaa Leu Met Leu Leu Gln Met Gln His Met Lys Gln Met Ile Met
 1          5          10          15
Glu Asn Asp Ser Ser Val Ser Glu Phe Ile Leu Met Gly Leu Thr Tyr
      20          25          30
Gln Pro Glu Leu Trp Trp Pro Leu Phe Val Leu Ph Leu Val Asn Tyr

```



```

      35      40      45
Thr Ala Thr Val Met Gly Asn Leu Ser Leu Met Thr Leu Ile Cys Leu
  50      55      60
Asn Ser His Leu His Thr Pro Met Tyr Phe Phe Ile Leu Asn Leu Ser
  65      70      75      80
Phe Ile Asp Phe Cys Tyr Ser Phe Val Phe Thr Pro Lys Met Leu Met
      85      90      95
Gly Phe Val Ser Glu His Asn Thr Ile Ser Phe Thr Gly Cys Met Thr
      100      105      110
Gln Leu Phe Phe Phe Cys Leu Phe Val Asn Ser Glu Cys Tyr Val Leu
      115      120      125
Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu Leu
      130      135      140
Tyr Thr Val Val Met Ser Pro Arg Ala Cys Ser Leu Leu Met Leu Ala
      145      150      155      160
Ala His Leu Met Gly Val Ser Ser Ala Val Val His Thr Gly Cys Ile
      165      170      175
Ile Gln Leu Arg Phe Cys Gly Ser Lys Val Ile Asn His Tyr Met Cys
      180      185      190
Asp Thr Phe Pro Leu Leu Glu Leu Ser Cys Gly Ser Ser His Val Asn
      195      200      205
Glu Leu Val Ser Ser Val Ser Val Ala Val Val Val Val Ile Ser Ser
      210      215      220
Leu Ile Ile Val Ser Ser Tyr Ala Leu Ile Leu Val Asn Val Ile His
      225      230      235      240
Leu Ser Ser Ser Lys Gly Trp Ser Lys Ala Val Ser Thr Cys Ser Ser
      245      250      255
His Ile Ile Thr Val Ala Leu Phe Tyr Gly Phe Gly Leu Leu Ala His
      260      265      270
Ile Lys Pro Ser Ser Ala Glu Ser Val Val Gln Arg Lys Phe Phe Ser
      275      280      285
Val Val Tyr Thr Phe Val Leu Pro Leu Leu Asn Pro Leu Ile Tyr Ser
      290      295      300
Ser Gly Asn Lys Asp Phe Lys Leu Leu Gly Thr Ile Asp Arg Leu Ala
      305      310      315      320
Gly Ser Asn Leu Ala Ser Phe Phe Phe Leu Ser Pro Leu Leu Ser Lys
      325      330      335

```

<210> 2399

<211> 326

<212> PRT

<213> Mus musculus (M172 8576195-20-3387-5132 199-1176)

<220>

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400>2399

```

Ile Leu Thr Asp Met Thr Xaa Glu Gly Met Ala Ser Gly Asn Asp Ser
  1      5      10      15
Thr Thr Val Lys Glu Phe Ile Leu Leu Gly Leu Thr Gln Gln Pro Glu
      20      25      30
Leu Gln Leu Pro Phe Phe Phe Leu Phe Leu Gly Ile Tyr Val Val Ser
      35      40      45
Ile Val Gly Asn Leu Gly Leu Ile Val Leu Ile Val Leu Asn Pro His
      50      55      60
Leu His Thr Pro Met Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp
      65      70      75      80
Phe Cys Tyr Ser Ser Val Ile Thr Pro Lys Met Leu Val Gly Phe Val
      85      90      95

```

Lys Gln Asn Ile Ile Ser His Ala Glu Cys Met Thr Gln Leu Phe Phe
 100 105 110
 Phe Ala Phe Phe Val Ile Asp Glu Cys Cys Ile Leu Thr Ala Met Ser
 115 120 125
 Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Lys Val Thr
 130 135 140
 Met Ser Tyr Gln Val Cys Phe Met Met Thr Val Ser Val Tyr Met Met
 145 150 155 160
 Gly Phe Val Gly Ala Ile Ala His Thr Ile Cys Met Leu Arg Leu Thr
 165 170 175
 Phe Cys Asp Gly Asn Ile Ile Asn His Tyr Met Cys Asp Ile Pro Pro
 180 185 190
 Leu Leu Lys Leu Ser Cys Thr Asn Thr Ser Val Asn Glu Leu Val Val
 195 200 205
 Phe Ile Val Val Gly Val Asn Val Ile Gly Pro Thr Leu Ile Ile Phe
 210 215 220
 Thr Ser Tyr Thr Leu Ile Ile Phe Asn Ile Ser His Ile Arg Ser Thr
 225 230 235 240
 Glu Gly Arg Ser Lys Ala Ile Ser Thr Cys Ser Ser His Ile Ile Ala
 245 250 255
 Val Ser Ile Phe Phe Gly Ala Ser Ala Phe Met Tyr Leu Lys Pro Ser
 260 265 270
 Pro Val Gly Ser Val Gly Glu Asp Lys Val Ser Thr Val Phe Tyr Thr
 275 280 285
 Ile Val Gly Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys
 290 295 300
 Asp Val His Ile Ala Leu His Lys Thr Leu Lys Lys Ser Met Leu Ile
 305 310 315 320
 Xaa Ile Glu Thr Phe Phe
 325

<210> 2400

<211> 337

<212> PRT

<213> Mus musculus (M174 8576195-24-446-3721 1969-959)

<220>

<221> VARIANT

<222> (1)...(337)

<223> Xaa = Any Amino Acid

<400>2400

Leu Leu Phe Leu Gln Arg Pro Ser Met Lys Gln Met Ala Thr Lys Asn
 1 5 10 15
 Asp Ser Ser Val Ser Glu Phe Ile Leu Met Gly Leu Thr Asp Gln Pro
 20 25 30
 Glu Leu Gln Leu Pro Leu Phe Phe Leu Phe Leu Leu Asn His Thr Val
 35 40 45
 Ile Val Val Gly Asn Leu Ser Leu Met Ser Leu Ile Ile Leu Asn Ser
 50 55 60
 Asn Leu His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Phe Ile
 65 70 75 80
 Asp Phe Cys Tyr Ser Phe Val Phe Thr Pro Lys Met Leu Met Ser Phe
 85 90 95
 Val Ser Glu Lys Asn Ile Ile Pro Phe Thr Gly Cys Met Thr Gln Leu
 100 105 110
 Phe Phe Phe Cys Phe Phe Ala His Ser Glu Ser Trp Val Leu Thr Val
 115 120 125
 Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Lys
 130 135 140
 Ala Ile Met Leu Pro Arg Ile Cys Cys Leu Leu Met Phe Val Ser Tyr

```

145          150          155          160
Leu Ile Gly Phe Ala Ser Ala Met Val Leu Ala Gly Leu Met Ile Arg
          165          170          175
Leu Asn Phe Cys Asn Asn Asn Ile Ile Asn His Tyr Met Cys Asp Ile
          180          185          190
Phe Pro Val Leu Arg Ile Ser Cys Ser Asn Thr Tyr Leu Asn Glu Leu
          195          200          205
Val Ser Thr Ala Val Val Gly Thr Ala Ile Ile Leu Cys Ser Leu Ile
          210          215          220
Ile Phe Ile Ser Tyr Ala Met Ile Leu Phe Asn Ile Val His Met Ser
225          230          235          240
Ser Gly Lys Gly Trp Ser Lys Ala Leu Gly Thr Cys Gly Ser His Ile
          245          250          255
Ile Thr Val Ser Phe Phe Tyr Gly Ser Gly Leu Leu Ala Tyr Val Lys
          260          265          270
Pro Ser Ser Ala Glu Thr Val Gly Gln Gly Lys Phe Phe Ser Val Phe
          275          280          285
Tyr Thr Phe Leu Val Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg
          290          295          300
Asn Lys Asp Val Lys Val Ala Val Lys Lys Thr Ile Lys Arg Ile Thr
305          310          315          320
Ser Xaa Leu Lys Gln Phe Glu Leu Val Cys Phe His Phe Leu Ser Ile
          325          330          335
Ile

```

<210> 2401

<211> 325

<212> PRT

<213> Mus musculus (M175 8576195-26-1-5230 3083-4056)

<220>

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400>2401

```

Leu Phe Ser Ser Arg Phe Ser Met Ile Ser Met Leu Ala Gly Asn Gly
1          5          10          15
Ser Ser Val Thr Glu Phe Val Leu Ala Gly Leu Thr Asp Arg Pro Glu
          20          25          30
Leu Gln Leu Pro Leu Phe Tyr Leu Phe Leu Ile Ile Tyr Ile Ile Thr
          35          40          45
Val Val Gly Asn Leu Gly Leu Ile Ile Leu Ile Gly Leu Asn Pro His
          50          55          60
Leu His Thr Pro Met Tyr Tyr Phe Leu Phe Asn Leu Ser Phe Ile Asp
65          70          75          80
Leu Cys Tyr Ser Ser Val Phe Ser Pro Lys Met Leu Ile Asn Phe Val
          85          90          95
Ser Glu Lys Asn Ser Ile Ser Tyr Ala Gly Cys Met Thr Gln Leu Phe
          100          105          110
Leu Phe Leu Phe Phe Val Ile Ser Glu Cys Tyr Met Leu Thr Ser Met
          115          120          125
Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Lys Val
          130          135          140
Thr Met Ser Pro Gln Ile Cys Ser Val Ile Ser Phe Ala Ala Tyr Gly
145          150          155          160
Met Gly Phe Ala Gly Ser Ser Ala His Thr Gly Cys Met Leu Arg Leu
          165          170          175
Thr Phe Cys Asn Val Asn Val Ile Asn His Tyr Leu Cys Asp Ile Leu
          180          185          190

```

Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr Tyr Val Asn Glu Val Val
 195 200 205
 Val Leu Ile Val Val Gly Ile Asn Ile Thr Val Pro Ser Phe Thr Ile
 210 215 220
 Leu Ile Ser Tyr Val Phe Ile Leu Ala Asn Ile Leu Asn Ile Lys Ser
 225 230 235 240
 Thr Gln Gly Arg Ala Lys Ala Phe Ser Thr Cys Ser Ser His Ile Met
 245 250 255
 Ala Ile Ser Leu Phe Phe Gly Ser Ala Ala Phe Met Tyr Leu Lys Tyr
 260 265 270
 Ser Ser Gly Ser Met Glu Gln Gly Lys Ile Ser Ser Val Phe Tyr Thr
 275 280 285
 Asn Val Gly Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys
 290 295 300
 Asp Val Lys Val Ala Leu Arg Lys Ser Leu Ile Lys Ile Gln Arg Lys
 305 310 315 320
 Asp Arg Phe Xaa Leu
 325

<210> 2402

<211> 204

<212> PRT

<213> Unknown (p124-dir-0-7 conceptual translation of range 2-613)

<400>2402

Phe Leu Glu Phe Ala Phe Thr Pro Ala Cys Ile Leu Arg Phe Pro Val
 1 5 10 15
 Thr Ile Val Thr Gly Asp Arg Thr Ile Ser Phe Ser Asn Cys Phe Phe
 20 25 30
 Phe Gln Leu Phe Phe Ile Phe Leu Gly Val Met Glu Phe Phe Leu Leu
 35 40 45
 Ala Pro Thr Ser Tyr Asp Cys Tyr Val Ala Ile Cys Arg Pro Leu His
 50 55 60
 His Ser Thr Val Met Thr Arg Gly Val Cys Thr Leu Leu Val Leu Ser
 65 70 75 80
 Ser Phe Leu Ser Thr Tyr Leu Asn Leu Phe Pro Pro Val Val Met Asp
 85 90 95
 Phe Trp Leu Asp Cys Cys Asp Pro Asn Ile Leu Lys His Phe Ile Cys
 100 105 110
 Asp Ser Ser Ser Val Met Glu Leu Leu Cys Thr Asp Thr Arg Phe Leu
 115 120 125
 Glu Leu Met Thr Phe Pro Leu Ser Leu Val Leu Met Thr Ala Ser Tyr
 130 135 140
 Thr Ala Ile Ile Cys Ala Ile Leu Arg Leu Pro Tyr Ala Gln Gln Arg
 145 150 155 160
 Arg Lys Val Phe Ser Ile Cys Ser Ser His Arg Val Gly Phe Ser Ile
 165 170 175
 Thr Tyr Gly Ser Cys Ile Phe Met Tyr Ile Asn Thr Val Ala Asp Lys
 180 185 190
 Asp Arg Val Gly Val Arg Gln Gly Leu Gly Gly Pro
 195 200

<210> 2403

<211> 312

<212> PRT

<213> Unknown (OR2B8)

<400>2403

Met Asp Gln Lys Asn Gly Ser Ser Phe Thr Gly Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Pro Gln Leu Glu Leu Val Leu Phe Val Val Phe Leu

```

      20      25      30
Ile Phe Tyr Ile Phe Thr Leu Leu Gly Asn Lys Thr Ile Ile Val Leu
      35      40      45
Ser His Leu Asp Pro His Leu His Asn Pro Met Tyr Phe Phe Phe Ser
      50      55      60
Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Gly Ile Val Pro Gln
      65      70      75      80
Leu Leu Val Asn Leu Arg Gly Ala Asp Lys Ser Ile Ser Tyr Gly Gly
      85      90      95
Cys Val Val Gln Leu Tyr Ile Ser Leu Gly Leu Gly Ser Thr Glu Cys
      100      105      110
Val Leu Leu Gly Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Arg
      115      120      125
Pro Leu His Tyr Thr Val Val Met His Pro Cys Leu Tyr Val Leu Met
      130      135      140
Ala Ser Thr Ser Trp Val Ile Gly Phe Ala Asn Ser Leu Leu Gln Thr
      145      150      155      160
Val Leu Ile Leu Leu Thr Leu Cys Gly Arg Asn Lys Leu Glu His
      165      170      175
Phe Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Val Asp Thr
      180      185      190
Thr Met Asn Glu Ser Glu Leu Phe Phe Val Ser Val Ile Ile Leu Leu
      195      200      205
Val Pro Val Ala Leu Ile Ile Phe Ser Tyr Ser Gln Ile Val Arg Ala
      210      215      220
Val Val Arg Ile Lys Ser Ala Thr Gly Gln Arg Lys Val Phe Gly Thr
      225      230      235      240
Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
      245      250      255
Tyr Ala Tyr Leu Gln Pro Gly Asn Asn Tyr Ser Gln Asp Gln Gly Lys
      260      265      270
Phe Ile Ser Leu Phe Tyr Thr Ile Ile Thr Pro Met Ile Asn Pro Leu
      275      280      285
Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Lys Val
      290      295      300
Leu Trp Lys Asn Tyr Asp Ser Arg
      305      310

```

<210> 2404

<211> 315

<212> PRT

<213> Unknown (OR12D3)

<400>2404

```

Met Glu Asn Val Thr Thr Met Asn Glu Phe Leu Leu Leu Gly Leu Thr
      1      5      10      15
Gly Val Gln Glu Leu Gln Pro Phe Phe Gly Ile Phe Leu Ile Ile
      20      25      30
Tyr Leu Ile Asn Leu Ile Gly Asn Gly Ser Ile Leu Val Met Val Val
      35      40      45
Leu Glu Pro Gln Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu
      50      55      60
Ser Cys Leu Asp Ile Ser Tyr Ser Ser Val Thr Leu Pro Lys Leu Leu
      65      70      75      80
Val Asn Leu Val Cys Ser Arg Arg Ala Ile Ser Phe Leu Gly Cys Ile
      85      90      95
Thr Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Ile Leu
      100      105      110
Leu Ala Ile Met Ala Phe Asp Arg Phe Val Ala Ile Cys Asn Pro Leu
      115      120      125
Arg Tyr Thr Val Ile Met Asn Pro Gln Val Cys Ile Leu Leu Ala Ala

```

```

      130              135              140
Ala Ala Trp Leu Ile Ser Phe Phe Tyr Ala Leu Met His Ser Val Met
145              150              155              160
Thr Ala His Leu Ser Phe Cys Gly Ser Gln Lys Leu Asn His Phe Phe
      165              170              175
Tyr Asp Val Lys Pro Leu Leu Glu Leu Ala Cys Ser Asp Thr Leu Leu
      180              185              190
Asn Gln Trp Leu Leu Ser Ile Val Thr Gly Ser Ile Ser Met Gly Ala
      195              200              205
Phe Phe Leu Thr Leu Leu Ser Cys Phe Tyr Val Ile Gly Phe Leu Leu
      210              215              220
Phe Lys Asn Arg Ser Cys Arg Ile Leu His Lys Ala Leu Ser Thr Cys
225              230              235              240
Ala Ser His Phe Met Val Val Cys Leu Phe Tyr Gly Pro Val Gly Phe
      245              250              255
Thr Tyr Ile Arg Pro Ala Ser Ala Thr Ser Met Ile Gln Asp Arg Ile
      260              265              270
Met Ala Ile Met Tyr Ser Ala Val Thr Pro Val Leu Asn Pro Leu Ile
      275              280              285
Tyr Thr Leu Arg Asn Lys Glu Val Met Met Ala Leu Lys Lys Ile Phe
      290              295              300
Gly Arg Lys Leu Phe Lys Asp Trp Gln Gln His
305              310              315

```

<210> 2405

<211> 115

<212> PRT

<213> Unknown (3273654-dir-0-5 conceptual translation of range 1-345)

<400>2405

```

Leu Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ser Cys Ser Asn Thr
1      5      10      15
Phe Ser Asp Asn Ile Val Lys Tyr Phe Leu Gly Ala Leu Tyr Gly Leu
      20      25      30
Phe Pro Ile Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Ile Ser Ser
      35      40      45
Ile Leu Arg Ile Pro Ser Leu Gly Gly Lys Tyr Lys Ala Phe Ser Thr
      50      55      60
Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Leu Val Thr Ala Ser
65      70      75      80
Thr Val Tyr Leu Gly Ser Val Ala Ser His Ser Pro Arg Asn Asp Val
      85      90      95
Val Ala Ser Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      100      105      110
Ile Cys Ser
      115

```

<210> 2406

<211> 139

<212> PRT

<213> Unknown (3810857-dir-0-6 conceptual translation of range 1-417)

<220>

<221> VARIANT

<222> (1)...(139)

<223> Xaa = Any Amino Acid

<400>2406

```

Met Ala Xaa Asp Arg Phe Val Ala Ile Cys His Pro Leu Asn Tyr Thr
1      5      10      15
Val Ile Met Asn Pro Arg Ile Cys Gly Leu Leu Val Leu Leu Ser Trp

```

```

      20      25      30
Ile Ile Met Phe Trp Val Ser Leu Ile His Met Leu Leu Met Lys Gln
      35      40      45
Leu Asn Phe Ser Thr Ser Thr Glu Ile Pro His Phe Phe Cys Glu Leu
      50      55      60
Thr Glu Leu Leu Arg Val Gly Arg Ser Asp Thr Phe Thr Gln Asn Ile
65      70      75      80
Phe Leu Tyr Leu Gly Tyr Cys Arg Ala Gly Met Phe Pro Val Ile Gly
      85      90      95
Ile Ala Phe Ser Tyr Phe His Ile Val Ser Ala Leu Met Lys Met Ser
      100      105      110
Ser Ile Lys Asn Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu
      115      120      125
Cys Val Val Ser Met Phe Tyr Gly Thr Gly Leu
      130      135

```

<210> 2407

<211> 211

<212> PRT

<213> Unknown (p106-dir-0-8 conceptual translation of range 2-633)

<220>

<221> VARIANT

<222> (1)...(211)

<223> Xaa = Any Amino Acid

<400>2407

```

Leu Val Asp Leu Cys Leu Val Thr Thr Leu Val Pro Lys Met Leu Val
1      5      10      15
Asn Leu Leu Thr His Ser Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
      20      25      30
Gln Met Phe Phe Phe Met Val Phe Ala Cys Ser Asn Thr Leu Leu Leu
      35      40      45
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Pro Leu Ser
      50      55      60
Tyr Val Thr Ile Met Arg Pro Gln Phe Cys Gly Leu Leu Ala Leu Leu
65      70      75      80
Ser Trp Thr Ile Ser Leu Leu Asn Ala Val Leu His Ser Pro Leu Val
      85      90      95
Met Arg Leu Leu Phe Cys Thr Glu Arg Glu Ile Pro Leu Phe Tyr His
      100      105      110
Asp Leu Thr Xaa Val Leu Arg Leu Ser Cys Thr Asp Met Leu Ile Asn
      115      120      125
Asp Ile Leu Val Tyr Leu Leu Thr Ala Leu Leu Ser Ile Phe Pro Phe
      130      135      140
Thr Gly Ile Leu Phe Ser Tyr Thr Gln Ile Cys Ser Ser Ile Val Lys
145      150      155      160
Ile Pro Ser Thr Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
      165      170      175
Tyr Leu Cys Val Val Leu Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
      180      185      190
Leu Ser Ser Ser Val Thr Lys Ser Ser Trp Lys Ser Ser Val Ala Ser
      195      200      205
Val Ile Cys
      210

```

<210> 2408

<211> 159

<212> PRT

<213> Unknown (4877338-dir-0-6 conceptual translation of range 2-478)

<220>

<221> VARIANT

<222> (1)...(159)

<223> Xaa = Any Amino Acid

<400>2408

```

Ile Cys His Pro Leu Arg Tyr Thr Val Ser Met Asn Pro Arg Leu Cys
 1           5           10           15
Val Gln Leu Ile Leu Leu Ser Leu Phe Ile Ser Ile Ala Asp Ala Leu
          20           25           30
Leu His Ser Leu Met Val Leu Gln Leu Ser Phe Cys Thr Asp Leu Glu
          35           40           45
Ile Ser Leu Phe Cys Glu Val Val Gln Val Ile Lys Arg Ala Cys Ser
          50           55           60
Asp Thr Leu Ile Asn Asn Ile Leu Val Tyr Phe Ala Ala Gly Ile Phe
          65           70           75           80
Ala Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ile Gln Ile Val
          85           90           95
Ser Ser Ile Leu Xaa Met Pro Ser Ser Gly Arg Lys Xaa Lys Ala Phe
          100          105          110
Ser Thr Cys Glu Ser His Leu Ser Val Val Ser Phe Phe Tyr Gly Thr
          115          120          125
Ala Phe Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser Ser Arg Lys
          130          135          140
Thr Ala Val Ala Ser Leu Met Tyr Thr Val Val Thr Pro Val Met
          145          150          155

```

<210> 2409

<211> 310

<212> PRT

<213> Unknown (p22-dir-0-11 conceptual translation of range 1-930)

<400>2409

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1           5           10           15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
          20           25           30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
          35           40           45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
          50           55           60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
          65           70           75           80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
          85           90           95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
          100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
          115          120          125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
          130          135          140
Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
          145          150          155          160
Phe Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
          165          170          175
Leu Phe Cys Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr
          180          185          190
His Ile Ile His Thr Ala Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
          195          200          205
Thr Leu Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
          210          215          220

```


Ile Leu Gln Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
 245 250 255
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu
 290 295 300
 Trp Arg Pro Phe Gln Arg
 305 310

<210> 2410

<211> 310

<212> PRT

<213> Unknown (p23-dir-0-11 conceptual translation of range 1-930)

<400>2410

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1 5 10 15
 Ile Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys Cys
 115 120 125
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
 145 150 155 160
 Phe Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
 165 170 175
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr
 180 185 190
 His Ile Ile His Thr Ala Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
 210 215 220
 Ile Leu Gln Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
 245 250 255
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Arg Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu
 290 295 300
 Trp Arg Pro Phe Gln Arg
 305 310

<210> 2411

<211> 215

<212> PRT

<213> Unknown (p139-dir-0-8 conceptual translation of range 2-646)

<400>2411

```

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1          5          10          15
Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
      20          25          30
Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn Leu Ile Leu
      35          40          45
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
      50          55          60
Cys Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu Leu Ser Leu
      65          70          75          80
Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr Phe Leu Leu
      85          90          95
Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr Leu Phe Cys
      100          105          110
Asp Met Tyr Ile Leu Leu Trp Leu Ala Cys Ser Asn Thr His Ile Ile
      115          120          125
His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu Thr Pro Leu
      130          135          140
Gly Phe Met Thr Lys Ser Tyr Val Arg Ile Val Arg Thr Ile Leu Gln
      145          150          155          160
Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr Cys Ala Ser
      165          170          175
His Leu Gly Val Val Ser Leu Phe Tyr Gly Met Leu Ala Met Val Tyr
      180          185          190
Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
      195          200          205
Met Tyr Ala Val Val Thr Pro
      210          215

```

<210> 2412

<211> 312

<212> PRT

<213> Unknown (p182-dir-0-11 conceptual translation of range 1-936)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2412

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1          5          10          15
Ile Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
      20          25          30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
      35          40          45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50          55          60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
      65          70          75          80
Met Leu Val Asn Pro Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
      85          90          95
Cys Leu Thr Gln Leu Xaa Phe Leu Val Ser Leu Val Thr Leu Asp Asn
      100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
      115          120          125

```

Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
 145 150 155 160
 Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
 165 170 175
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr
 180 185 190
 His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Cys Ile Val Arg Thr
 210 215 220
 Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
 245 250 255
 Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Val Leu
 290 295 300
 Arg Arg Leu Phe Gln Arg Pro Lys
 305 310

<210> 2413

<211> 312

<212> PRT

<213> Unknown (p184-dir-0-11 conceptual translation of range 1-936)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2413

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1 5 10 15
 Ile Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Pro Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Xaa Phe Leu Val Ser Leu Val Thr Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
 145 150 155 160
 Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His His
 165 170 175
 Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr
 180 185 190
 His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu

195	200	205
Thr Pro Leu Gly Phe Met	Thr Thr Ser His Val Cys	Ile Val Arg Thr
210	215	220
Ile Leu Gln Ile Pro Ser Ala	Ser Lys Lys Tyr Lys Ala Phe	Ser Thr
225	230	235
Cys Ala Ser His Leu Gly Val	Val Ser Leu Phe Tyr Gly Thr	Leu Ala
245	250	255
Met Val Tyr Leu Gln Pro Leu His	Thr Tyr Ser Met Lys Asp	Ser Val
260	265	270
Ala Thr Val Met Tyr Ala Val	Val Thr Pro Met Met Asn	Pro Phe Ile
275	280	285
Tyr Ser Leu Arg Asn Lys Asp	Met His Gly Ala Leu Gly	Arg Val Leu
290	295	300
Arg Arg Leu Phe Gln Arg	Pro Lys	
305	310	

<210> 2414

<211> 312

<212> PRT

<213> Unknown (p183-dir-0-11 conceptual translation of range 1-936)

<400>2414

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly	
1	5 10 15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu	
20	25 30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala	
35	40 45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala	
50	55 60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys	
65	70 75 80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly	
85	90 95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn	
100	105 110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys	
115	120 125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu	
130	135 140
Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr	
145	150 155 160
Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr	
165	170 175
Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr	
180	185 190
His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu	
195	200 205
Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Cys Ile Val Arg Thr	
210	215 220
Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr	
225	230 235 240
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala	
245	250 255
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val	
260	265 270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile	
275	280 285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Val Leu	
290	295 300
Arg Arg Leu Phe Gln Arg Pro Lys	

305

310

<210> 2415

<211> 312

<212> PRT

<213> Unknown (p186-dir-0-11 conceptual translation of range 1-936)

<400>2415

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1          5          10          15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
          20          25          30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
          35          40          45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
          50          55          60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
65          70          75          80
Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
          100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
          115          120          125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
          130          135          140
Leu Ser Leu Cys Trp Gly Leu Ser Val Phe Tyr Gly Leu Leu Leu Thr
          145          150          155          160
Leu Leu Leu Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
          165          170          175
Leu Phe Cys Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr
          180          185          190
His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
          195          200          205
Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr
          210          215          220
Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr
          225          230          235          240
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
          245          250          255
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
          260          265          270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
          275          280          285
His Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Val Leu
          290          295          300
Arg Arg Leu Phe Gln Arg Pro Lys
305          310

```

<210> 2416

<211> 215

<212> PRT

<213> Unknown (p140-dir-0-8 conceptual translation of range 2-646)

<400>2416

```

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1          5          10          15
Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
          20          25          30
Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn Leu Ile Leu
          35          40          45

```

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
 50 55 60
 Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu Ser Leu
 65 70 75 80
 Cys Trp Gly Leu Ser Val Phe Tyr Gly Leu Leu Leu Thr Leu Leu
 85 90 95
 Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr Phe Phe Cys
 100 105 110
 Asp Met Tyr Ile Leu Leu Arg Leu Ala Cys Ser Asn Thr His Ile Ile
 115 120 125
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Thr Pro Leu
 130 135 140
 Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr Ile Leu Gln
 145 150 155 160
 Ile Pro Ser Ala Ser Lys Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala Met Val Cys
 180 185 190
 Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met Tyr Ala Val Val Thr Pro
 210 215

<210> 2417

<211> 215

<212> PRT

<213> Unknown (p141-dir-0-8 conceptual translation of range 2-646)

<400>2417

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Asn Met Leu Val
 1 5 10 15
 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Lys Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn Leu Ile Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
 50 55 60
 Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu Leu Ser Leu
 65 70 75 80
 Gly Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr Leu Leu Met
 85 90 95
 Thr Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr Leu Phe Cys
 100 105 110
 Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asn Thr His Ile Ile
 115 120 125
 His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Thr Pro Leu
 130 135 140
 Gly Phe Met Thr Thr Ser Tyr Val Arg Ile Val Arg Thr Ile Leu Gln
 145 150 155 160
 Met Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala Met Val Tyr
 180 185 190
 Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met Tyr Ala Val Val Thr Pro
 210 215

<210> 2418

<211> 312

<212> PRT

<213> Unknown (p187-dir-0-11 conceptual translation of range 1-936)

<400>2418

```

Met Asp Gly Asp Asn Gln Ser Glu Asn Ser Gln Phe Leu Leu Leu Gly
 1          5          10          15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20          25          30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
 35          40          45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50          55          60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65          70          75          80
Met Leu Val Asn Phe Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Glu
 85          90          95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Thr Leu Asp Asn
 100         105         110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115         120         125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu
 130         135         140
Leu Ser Leu Cys Trp Gly Leu Ser Val Leu Tyr Gly Leu Leu Leu Thr
 145         150         155         160
Leu Leu Met Asn Arg Val Thr Phe Cys Gly Pro Arg Glu Ile His Tyr
 165         170         175
Leu Phe Cys Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asn Thr
 180         185         190
His Ile Ile His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
 195         200         205
Thr Pro Leu Gly Phe Met Thr Thr Ser Tyr Val His Ile Val Arg Thr
 210         215         220
Ile Leu Gln Ile Pro Ser Ala Ser Lys Lys Tyr Lys Thr Phe Ser Thr
 225         230         235         240
Cys Ala Ser His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Ala
 245         250         255
Met Val Tyr Leu Gln Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val
 260         265         270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275         280         285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Val Leu Gly Arg Val Leu
 290         295         300
Gly Arg Pro Phe Gln Arg Pro Lys
 305         310

```

<210> 2419

<211> 211

<212> PRT

<213> Unknown (p167-dir-0-8 conceptual translation of range 2-634)

<400>2419

```

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1          5          10          15
Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
 20          25          30
Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu
 35          40          45
Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His Tyr
 50          55          60
Val Thr Ala Met Ser Pro Gly Leu Cys Val Leu Leu Leu Cys Leu Cys
 65          70          75          80
Trp Ser Val Leu Tyr Gly Leu Leu Leu Thr Leu Leu Met Thr Thr Val

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```
<210> 2420
<211> 210
<212> PRT
<213> Unknown (p168-dir-0-8 conceptual translation of range 2-632)
```

```
<210> 2421
<211> 313
<212> PRT
<213> Unknown (p145-dir-0-11 conceptual translation of range 1-937)
```

1467


```

Ile Ser Glu Ser Pro Glu Gln Gln Gln Met Leu Phe Trp Met Phe Leu
      20      25      30
Val Arg Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala
      35      40      45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50      55      60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
      65      70      75      80
Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly
      85      90      95
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
      100      105      110
Leu Asn Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
      115      120      125
Pro Leu His Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu
      130      135      140
Leu Ser Leu Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile
      145      150      155      160
Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr
      165      170      175
Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile
      180      185      190
His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
      195      200      205
Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala Arg Ile Val Arg Ala
      210      215      220
Ile Leu Gln Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr
      225      230      235      240
Cys Ala Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly
      245      250      255
Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val
      260      265      270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Ile Asn Pro Phe Ile
      275      280      285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Arg
      290      295      300
Gln Gly Lys Ala Phe Gln Lys Leu Thr
305      310

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<210> 2422

<211> 214

<212> PRT

<213> Unknown (3831606-dir-0-8 conceptual translation of range 2-642)

<400>2422

```

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
      1      5      10      15
Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Thr Gly Cys Leu Thr
      20      25      30
Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Asn Leu
      35      40      45
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His
      50      55      60
Tyr Val Thr Ala Met Ile Pro Gly Leu Cys Ile Leu Leu Leu Ser Leu
      65      70      75      80
Cys Trp Val Phe Ser Ala Leu Tyr Gly Leu Ile His Ile Leu Leu Met
      85      90      95
Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr Leu Phe Cys
      100      105      110
Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile His Val Asn
      115      120      125

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His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Leu
 130 135 140
 Gly Phe Met Ile Thr Ser Asn Ala Arg Ile Val Arg Ala Ile Leu Gln
 145 150 155 160
 Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly Met Val Tyr
 180 185 190
 Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met His Ala Val Val Thr
 210

<210> 2423

<211> 319

<212> PRT

<213> Unknown (p35-dir-0-11 conceptual translation of range 1-954)

<400>2423

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Val Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Ser Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Met Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Ile Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Gly Phe Ser Ala Leu Tyr Gly Leu Ile His Ile
 145 150 155 160
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr
 165 170 175
 Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile
 180 185 190
 His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala His Ile Val Arg Ala
 210 215 220
 Ile Leu Gln Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Ser Ala Ser His Leu Ala Val Val Phe Leu Phe Tyr Gly Thr Leu Gly
 245 250 255
 Met Val Tyr Leu Gln Pro Leu His Asn Leu Gln Pro Leu Gln Thr Tyr
 260 265 270
 Ser Met Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr Pro
 275 280 285
 Met Ile Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met His Gly
 290 295 300
 Ala Leu Gly Arg Leu Arg Gln Gly Lys Ala Phe Gln Lys Leu Thr
 305 310 315

<210> 2424

<211> 313

<212> PRT

<213> Unknown (p34-dir-0-11 conceptual translation of range 1-937)

<400>2424

```

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
          20           25           30
Val Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Leu Ala
      35           40           45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50           55           60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
65           70           75           80
Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
          85           90           95
Cys Leu Met Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
          100          105          110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
          115          120          125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Gly Leu Cys Ile Leu Leu
          130          135          140
Leu Ser Leu Cys Trp Gly Phe Ser Ala Leu Tyr Gly Leu Ile His Ile
145          150          155          160
Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Gln Lys Ile His Tyr
          165          170          175
Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile
          180          185          190
His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu
          195          200          205
Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala His Ile Val Arg Ala
          210          215          220
Ile Leu Gln Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Ala Val Val Phe Leu Phe Tyr Gly Thr Val Gly
          245          250          255
Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val
          260          265          270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Ile Asn Pro Phe Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Arg
          290          295          300
Gln Gly Lys Ala Phe Gln Lys Leu Thr
305           310

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<210> 2425

<211> 313

<212> PRT

<213> Unknown (p87-dir-0-11 conceptual translation of range 1-937)

<400>2425

```

Met Asp Gly Asp Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Arg Gly
 1           5           10           15
Ile Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
          20           25           30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Phe Ile Ile Leu Ala
      35           40           45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ala
 50           55           60
Asn Phe Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys

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65					70					75				80
Met	Pro	Val	Asn	Leu	Gln	Ser	Gln	Asn	Lys	Ala	Ile	Ser	Tyr	Ala
				85					90					95
Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Leu	Val	Ser	Leu	Val	Ala	Leu	Asp
			100					105					110	Asn
Leu	Ile	Pro	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys
		115					120					125		Arg
Pro	Leu	His	Tyr	Val	Thr	Ala	Met	Ser	Pro	Gly	Leu	Cys	Ile	Leu
		130				135					140			Leu
Leu	Ser	Met	Cys	Trp	Val	Phe	Ser	Ala	Leu	Tyr	Gly	Leu	Ile	His
		145			150					155				160
Leu	Leu	Met	Thr	Arg	Val	Thr	Phe	Cys	Gly	Ser	Gln	Lys	Ile	His
			165						170				175	Tyr
Leu	Phe	Cys	Glu	Met	Tyr	Phe	Leu	Leu	Arg	Leu	Ala	Cys	Ser	Asn
		180						185					190	Ile
His	Val	Asn	His	Thr	Val	Leu	Val	Ala	Met	Gly	Cys	Phe	Ile	Phe
		195					200					205		Leu
Ile	Pro	Leu	Gly	Phe	Met	Ile	Thr	Ser	Tyr	Ala	Arg	Ile	Val	Arg
		210				215					220			Ala
Ile	Leu	Gln	Ile	Pro	Pro	Ala	Thr	Gly	Lys	Tyr	Lys	Ala	Phe	Ser
		225				230				235				240
Cys	Ala	Ser	His	Leu	Ala	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Leu
			245					250					255	Gly
Ile	Val	Tyr	Leu	Gln	Pro	Pro	Gln	Thr	Tyr	Ser	Met	Lys	Asp	Ser
		260						265					270	Val
Ala	Thr	Val	Met	Tyr	Val	Val	Val	Thr	Pro	Met	Ile	Asn	Pro	Phe
		275					280					285		Ile
Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Met	His	Gly	Asp	Leu	Gly	Arg	Leu
		290				295					300			Arg
Gln	Gly	Lys	Ala	Phe	Gln	Lys	Leu	Thr						
		305				310								

<210> 2426

<211> 313

<212> PRT

<213> Unknown (p136-dir-0-11 conceptual translation of range 1-939)

<400>2426

Met	Asp	Gly	Gly	Asn	Gln	Ser	Lys	Gly	Ser	Glu	Phe	Leu	Leu	Leu
1				5					10				15	
Met	Ser	Glu	Ser	Pro	Glu	Gln	Gln	Arg	Ile	Leu	Phe	Trp	Met	Phe
		20						25				30		Leu
Ser	Met	Tyr	Leu	Val	Thr	Val	Val	Gly	Asn	Ala	Leu	Ile	Ile	Leu
		35					40					45		Ala
Ile	Thr	Ser	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
		50				55					60			Val
Asn	Leu	Ser	Phe	Thr	Asp	Leu	Phe	Phe	Val	Thr	Asn	Thr	Ile	Pro
		65			70				75					Lys
Met	Leu	Val	Asn	Leu	Gln	Ser	Gln	Asn	Lys	Ala	Ile	Ala	Tyr	Ala
			85						90				95	Gly
Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Leu	Val	Ser	Leu	Val	Ala	Leu	Asp
		100						105					110	Asn
Leu	Ile	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys
		115					120					125		His
Pro	Leu	His	Tyr	Val	Thr	Ala	Met	Ser	Pro	Gly	Leu	Cys	Ile	Leu
		130				135					140			Leu
Leu	Ser	Leu	Cys	Trp	Val	Phe	Ser	Val	Leu	Tyr	Gly	Leu	Ile	His
		145			150					155				160
Leu	Leu	Met	Thr	Arg	Val	Thr	Phe	Cys	Gly	Ser	Arg	Lys	Ile	His
			165						170				175	Tyr
Leu	Phe	Cys	Glu	Met	Tyr	Val	Leu	Leu	Gln	Leu	Ala	Cys	Ser	Asn
														Ile

180	185	190
His Val Asn His Thr Val Leu Val Ala Thr Gly Cys Phe Ile Phe Leu		
195	200	205
Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala Arg Ile Val Arg Ala		
210	215	220
Ile Leu Arg Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr		
225	230	235
Cys Ala Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly		
245	250	255
Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Met Lys Asp Ser Val		
260	265	270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile		
275	280	285
Tyr Ser Leu Lys Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu		
290	295	300
Gln Gly Lys Ala Phe Trp Lys Leu Thr		
305	310	

<210> 2427

<211> 313

<212> PRT

<213> Unknown (p163-dir-0-11 conceptual translation of range 1-939)

<400>2427

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly		
1	5	10
Met Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu		
20	25	30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Val Leu Ile Ile Leu Ala		
35	40	45
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ala		
50	55	60
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys		
65	70	75
Met Leu Val Asn Leu Gln Ser Gln Asp Lys Ala Ile Ser Tyr Ala Gly		
85	90	95
Cys Leu Thr Gln Leu Tyr Phe Leu Leu Ser Leu Val Thr Leu Asp Asn		
100	105	110
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys		
115	120	125
Pro Leu His Tyr Val Thr Ala Met Ser Pro Arg Leu Cys Ile Leu Leu		
130	135	140
Leu Ser Leu Cys Trp Val Phe Ser Val Leu Tyr Gly Leu Ile His Thr		
145	150	155
Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr		
165	170	175
Leu Phe Cys Glu Met Tyr Phe Leu Leu Arg Leu Ala Cys Ser Asn Ile		
180	185	190
Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu		
195	200	205
Ile Pro Leu Gly Phe Met Ile Thr Ser Tyr Ala Arg Ile Val Arg Ala		
210	215	220
Ile Leu Arg Ile Pro Ser Ala Thr Gly Lys Tyr Lys Ala Phe Ser Thr		
225	230	235
Cys Ala Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Gly		
245	250	255
Met Val Tyr Leu Gln Pro Leu Gln Thr Tyr Ser Thr Lys Asp Ser Val		
260	265	270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile		
275	280	285
Tyr Ser Leu Arg Asn Lys Asp Ile His Gly Ala Leu Gly Arg Leu Leu		

290 295 300
 Gln Gly Lys Ala Phe Gln Lys Leu Thr
 305 310

<210> 2428

<211> 312

<212> PRT

<213> Unknown (p18-dir-0-11 conceptual translation of range 1-936)

<400>2428

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Leu Gln Ser His Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125
 Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr
 145 150 155 160
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
 165 170 175
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile
 180 185 190
 Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys
 245 250 255
 Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
 290 295 300
 Asp Lys His Phe Lys Arg Leu Thr
 305 310

<210> 2429

<211> 312

<212> PRT

<213> Unknown (p32-dir-0-11 conceptual translation of range 1-936)

<400>2429

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu
 20 25 30

Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Asn Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125
 Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu
 130 135 140
 Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr
 145 150 155 160
 Ile Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
 165 170 175
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile
 180 185 190
 Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys
 245 250 255
 Met Val Tyr Leu Lys Pro Leu His Thr Phe Ser Val Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
 290 295 300
 Asp Thr His Phe Lys Arg Leu Thr
 305 310

<210> 2430

<211> 312

<212> PRT

<213> Unknown (p130-dir-0-11 conceptual translation of range 1-936)

<400>2430

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Met Ser Glu Ser Pro Glu Gln Gln Arg Ile Leu Phe Trp Met Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ser Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn
 100 105 110
 Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125
 Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu
 130 135 140

Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr
 145 150 155 160
 Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr
 165 170 175
 Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile
 180 185 190
 Gln Thr Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu
 195 200 205
 Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Leu Ser Lys Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys
 245 250 255
 Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val
 260 265 270
 Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
 290 295 300
 Asp Lys His Phe Lys Arg Leu Thr
 305 310

<210> 2431

<211> 215

<212> PRT

<213> Unknown (p143-dir-0-8 conceptual translation of range 2-646)

<400>2431

Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
 1 5 10 15
 Ser Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Pro Gly Cys Leu Thr
 20 25 30
 Gln Leu Phe Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60
 Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu Ile Leu
 65 70 75 80
 Cys Trp Ala Leu Ser Ile Leu Tyr Gly Leu Ile His Thr Leu Leu Met
 85 90 95
 Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr Ile Phe Cys
 100 105 110
 Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asn Thr His Ile Asn
 115 120 125
 His Met Met Leu Ile Ala Thr Gly Cys Phe Val Phe Leu Val Pro Phe
 130 135 140
 Gly Phe Met Ile Met Ser Tyr Ile Cys Ile Val Arg Ala Ile Leu Lys
 145 150 155 160
 Ile Pro Ser Ala Ser Asn Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Ala Val Val Ala Leu Phe Tyr Gly Thr Leu Cys Met Val Tyr
 180 185 190
 Leu Lys Pro Leu His Thr Tyr Ser Met Lys Asp Ser Val Ala Thr Val
 195 200 205
 Met Tyr Ala Val Val Thr Pro
 210 215

<210> 2432

<211> 312

<212> PRT

<213> Unknown (p89-dir-0-11 conceptual translation of range 1-935)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2432

```

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
 1           5           10           15
Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
      20           25           30
Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
      35           40           45
Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala
      50           55           60
Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
      65           70           75           80
Met Leu Ala Asn His Leu Ser Gly Ser Lys Ser Ile Ser Phe Gly Gly
      85           90           95
Cys Leu Thr Gln Met Tyr Phe Met Ile Asp Leu Gly Asn Thr Asp Ser
      100           105           110
Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg
      115           120           125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
      130           135           140
Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
      145           150           155           160
Leu Leu Thr Ala Ser Leu Ser Phe Xaa Gly Asn Gln Glu Val Ala Asn
      165           170           175
Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
      180           185           190
Arg Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Pro Val
      195           200           205
Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
      210           215           220
Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
      225           230           235           240
Gly Ser His Leu Thr Val Val Cys Phe Val Tyr Gly Thr Val Met Gly
      245           250           255
Met Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
      260           265           270
Thr Val Met Cys Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
      275           280           285
Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Asn
      290           295           300
Lys Arg Ile Ser Ser Xaa Pro Met
305           310

```

<210> 2433

<211> 312

<212> PRT

<213> Unknown (p88-dir-0-11 conceptual translation of range 1-936)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2433

```

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly

```

```

1           5           10           15
Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
20           25           30
Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
35           40           45
Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala
50           55           60
Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
65           70           75           80
Met Leu Ala Asn His Leu Ser Gly Ser Lys Ser Ile Ser Phe Gly Gly
85           90           95
Cys Leu Thr Gln Met Tyr Phe Met Ile Asp Leu Gly Asn Thr Asp Ser
100          105          110
Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg
115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
130          135          140
Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
145          150          155          160
Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
165          170          175
Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
180          185          190
His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val
195          200          205
Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
210          215          220
Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly
245          250          255
Met Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
260          265          270
Thr Val Met Cys Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
275          280          285
Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Asn
290          295          300
Lys Arg Ile Ser Ser Xaa Pro Met
305          310

```

<210> 2434

<211> 312

<212> PRT

<213> Unknown (p33-dir-0-11 conceptual translation of range 1-936)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2434

```

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
1           5           10           15
Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
20           25           30
Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Ile Leu Ala
35           40           45
Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala
50           55           60
Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
65           70           75           80

```

Met Leu Ala Asn His Leu Ser Gly Ser Lys Ser Ile Ser Phe Gly Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Met Ile Asp Leu Gly Asn Thr Asp Ser
 100 105 110
 Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg
 115 120 125
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
 130 135 140
 Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
 145 150 155 160
 Leu Leu Thr Ala Ser Leu Ser Phe Xaa Gly Asn Gln Glu Val Ala Asn
 165 170 175
 Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
 180 185 190
 His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val
 195 200 205
 Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
 210 215 220
 Phe Gln Gly Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ser His Leu Thr Val Val Ser Leu Asp Tyr Gly Thr Val Lys Gly
 245 250 255
 Lys Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
 260 265 270
 Thr Val Met Cys Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
 275 280 285
 Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Gln Lys Leu Phe Asn
 290 295 300
 Lys Arg Ile Ser Ser Xaa Pro Met
 305 310

<210> 2435

<211> 312

<212> PRT

<213> Unknown (p43-dir-0-11 conceptual translation of range 1-936)

<220>

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400>2435

Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Val Thr Gly Gln Gln Glu Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
 20 25 30
 Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
 35 40 45
 Ile Cys Ser Asp Val Arg Leu His Asn Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ala Asn His Leu Leu Gly Ser Lys Ser Ile Ser Phe Gly Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Met Ile Ala Leu Gly Asn Thr Asp Ser
 100 105 110
 Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser His
 115 120 125
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
 130 135 140
 Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr

145 150 155 160
 Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
 165 170 175
 Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
 180 185 190
 His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val
 195 200 205
 Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
 210 215 220
 Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly
 245 250 255
 Thr Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile
 260 265 270
 Thr Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
 275 280 285
 Ser Leu Arg Asn Arg Asp Met Lys Ala Ala Leu Arg Lys Leu Phe Asn
 290 295 300
 Lys Arg Ile Ser Ser Xaa Pro Met
 305 310

<210> 2436
 <211> 309
 <212> PRT
 <213> Unknown (p180-dir-0-11 conceptual translation of range 1-927)

<400>2436
 Met Arg Glu Asn Asn Gln Ser Ser Thr Leu Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Val Thr Gly Gln Gln Glu Asp Phe Phe Tyr Ile Leu Phe Leu
 20 25 30
 Phe Ile Tyr Pro Ile Thr Leu Ile Gly Asn Leu Leu Ile Val Leu Ala
 35 40 45
 Ile Cys Ser Asp Val His Leu His Asn Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ala Asn His Leu Leu Gly Ser Lys Ser Ile Ser Phe Gly Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Met Ile Ala Leu Gly Asn Thr Asp Ser
 100 105 110
 Tyr Ile Leu Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg
 115 120 125
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Arg Ser Cys Ile Trp Leu
 130 135 140
 Ile Ala Gly Ser Trp Val Ile Gly Asn Ala Asn Ala Leu Pro His Thr
 145 150 155 160
 Leu Leu Thr Ala Ser Leu Ser Phe Cys Gly Asn Gln Glu Val Ala Asn
 165 170 175
 Phe Tyr Cys Asp Ile Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Ile
 180 185 190
 His Phe His Val Lys Met Met Tyr Leu Gly Val Gly Ile Phe Ser Val
 195 200 205
 Pro Leu Leu Cys Ile Ile Val Ser Tyr Ile Arg Val Phe Ser Thr Val
 210 215 220
 Phe Gln Val Pro Ser Thr Lys Gly Val Leu Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ser His Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly
 245 250 255
 Met Tyr Phe Arg Pro Leu Thr Asn Tyr Ser Leu Lys Asp Ala Val Ile

[illegible]

<210> 2437

<211> 309

<212> PRT

<213> Unknown (p204-dir-0-11 conceptual translation of range 1-927)

<400>2437

[illegible]

<210> 2438

<211> 214

<212> PRT

<213> Unknown (p179-dir-0-8 conceptual translation of range 2-643)

<400>2438

Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys Met Leu Ala
 1 5 10 15
 Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala
 20 25 30
 Gln Met Tyr Phe Met Ile Ser Leu Gly Asn Thr Asp Ser Tyr Ile Leu
 35 40 45
 Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His
 50 55 60
 Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly
 65 70 75 80
 Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr
 85 90 95
 Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys
 100 105 110
 Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn
 115 120 125
 Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu
 130 135 140
 Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val
 145 150 155 160
 Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His
 165 170 175
 Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe
 180 185 190
 Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met
 195 200 205
 Tyr Thr Ala Val Thr Pro
 210

<210> 2439

<211> 214

<212> PRT

<213> Unknown (p191-dir-0-8 conceptual translation of range 2-643)

<400>2439

Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys Met Leu Ala
 1 5 10 15
 Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala
 20 25 30
 Gln Met Tyr Phe Met Ile Gly Leu Ala Asn Thr Asp Ser Tyr Ile Leu
 35 40 45
 Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His
 50 55 60
 Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly
 65 70 75 80
 Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr
 85 90 95
 Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys
 100 105 110
 Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn
 115 120 125
 Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu
 130 135 140
 Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val
 145 150 155 160
 Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His
 165 170 175
 Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe
 180 185 190
 Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met
 195 200 205

Tyr Thr Ala Val Thr Pro
210

<210> 2440

<211> 222

<212> PRT

<213> Unknown (3983387-dir-0-8 conceptual translation of range 1-666)

<400>2440

Ala	Asn	Leu	Ser	Phe	Val	Asp	Val	Cys	Phe	Thr	Thr	Asn	Leu	Ile	Pro
1				5					10					15	
Arg	Leu	Leu	Ala	Gly	His	Val	Ala	Gly	Thr	Arg	Thr	Ile	Ser	Tyr	Val
			20					25					30		
His	Cys	Leu	Thr	Gln	Thr	Tyr	Phe	Leu	Ile	Ser	Phe	Ala	Asn	Val	Asp
		35					40					45			
Thr	Phe	Leu	Leu	Ala	Ala	Met	Ala	Leu	Asp	Arg	Phe	Val	Ala	Ile	Cys
	50					55					60				
Tyr	Pro	Leu	Gln	Tyr	His	Thr	Ile	Ile	Thr	Pro	Gln	Leu	Cys	Val	Gly
65					70					75					80
Leu	Ala	Ala	Val	Val	Trp	Met	Cys	Ser	Ala	Leu	Ile	Ser	Leu	Met	His
			85						90					95	
Thr	Leu	Leu	Met	Ser	Arg	Leu	Ser	Phe	Cys	Ser	Ser	Ile	Pro	Glu	Ile
			100					105					110		
Ser	His	Phe	Tyr	Cys	Asp	Ala	Tyr	Leu	Leu	Met	Lys	Leu	Ala	Cys	Ser
		115					120					125			
Asp	Thr	Arg	Val	Asn	Gln	Leu	Val	Phe	Leu	Gly	Ala	Val	Val	Leu	Phe
		130				135					140				
Val	Ala	Pro	Cys	Ile	Leu	Ile	Val	Val	Ser	Tyr	Val	Arg	Ile	Thr	Met
145					150					155					160
Val	Val	Leu	Gln	Ile	Pro	Ser	Ala	Lys	Gly	Arg	His	Lys	Thr	Phe	Ser
			165						170					175	
Thr	Cys	Ser	Ser	His	Leu	Ser	Val	Val	Thr	Leu	Phe	Tyr	Gly	Thr	Val
		180						185					190		
Leu	Gly	Ile	Tyr	Ile	Arg	Pro	Pro	Asp	Ser	Phe	Ser	Thr	Gln	Asp	Thr
		195					200					205			
Val	Ala	Thr	Ile	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn		
		210					215					220			

<210> 2441

<211> 314

<212> PRT

<213> Unknown (205837-dir-0-11 conceptual translation of range 1-942)

<400>2441

Met	Thr	Arg	Arg	Asn	Gln	Thr	Ala	Ile	Ser	Gln	Phe	Phe	Leu	Leu	Gly
1				5					10					15	
Leu	Pro	Phe	Pro	Pro	Glu	Tyr	Gln	His	Leu	Phe	Tyr	Ala	Leu	Phe	Leu
			20					25					30		
Ala	Met	Tyr	Leu	Thr	Thr	Leu	Leu	Gly	Asn	Leu	Ile	Ile	Ile	Ile	Leu
		35					40					45			
Ile	Leu	Leu	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu	Ser
		50				55					60				
Asn	Leu	Ser	Phe	Ala	Asp	Leu	Cys	Phe	Ser	Ser	Val	Thr	Met	Pro	Lys
65					70					75					80
Leu	Leu	Gln	Asn	Met	Gln	Ser	Gln	Val	Pro	Ser	Ile	Pro	Tyr	Ala	Gly
			85						90					95	
Cys	Leu	Ala	Gln	Ile	Tyr	Phe	Phe	Leu	Phe	Phe	Gly	Asp	Leu	Gly	Asn
		100						105					110		
Phe	Leu	Leu	Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe
		115					120					125			
Pro	Leu	His	Tyr	Met	Ser	Ile	Met	Ser	Pro	Lys	Leu	Cys	Val	Ser	Leu

130	135	140
Val Val Leu Ser Trp	Val Leu Thr Thr Phe His Ala Met Leu His Thr	
145	150	155
Leu Leu Met Ala Arg	Leu Ser Phe Cys Glu Asp Ser Val Ile Pro His	160
165	170	175
Tyr Phe Cys Asp Met Ser Thr Leu Leu Lys Val Ala Cys Ser Asp Thr		
180	185	190
His Asp Asn Glu Leu Ala Ile Phe Ile Leu Gly Gly Pro Ile Val Val		
195	200	205
Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala Arg Ile Val Ser Ser		
210	215	220
Ile Phe Lys Val Pro Ser Ser Gln Ser Ile His Lys Ala Phe Ser Thr		
225	230	235
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile		
245	250	255
Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr		
260	265	270
Val Met Ser Leu Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe		
275	280	285
Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Asp Ala Leu Glu Lys Ile		
290	295	300
Met Cys Lys Lys Gln Ile Pro Ser Phe Leu		
305	310	

<210> 2442

<211> 221

<212> PRT

<213> Unknown (3769630-dir-0-8 conceptual translation of range 1-663)

<400>2442

Leu Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Ser Val Thr Met Pro	
1	5
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala	10
20	25
Gly Cys Leu Ala Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly	30
35	40
Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys	45
50	55
Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser	60
65	70
Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His	75
85	90
Thr Leu Leu Met Ala Arg Leu Ser Phe Arg Glu Asp Ser Val Ile Pro	95
100	105
His Tyr Phe Cys Asp Met Ser Thr Leu Leu Lys Val Ala Cys Pro Asp	110
115	120
Thr His Asp Asn Glu Leu Ala Ile Phe Ile Leu Gly Gly Pro Ile Val	125
130	135
Val Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala Arg Ile Val Ser	140
145	150
Ser Ile Phe Lys Val Pro Ser Ser Gln Ser Ile His Lys Ala Phe Ser	155
165	170
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Ile Tyr Gly Thr Val	175
180	185
Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu	190
195	200
Thr Val Met Ser Leu Met Tyr Thr Met Val Thr Pro Met	205
210	215
	220

<210> 2443

<211> 314

<212> PRT

<213> Unknown (1504111-dir-0-11 conceptual translation of range 1-942)

<400>2443

```

Met Thr Glu Arg Asn Gln Thr Val Il Ser Gln Phe Leu Leu Leu Gly
 1          5          10          15
Leu Pro Ile Pro Pro Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
          20          25          30
Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
          35          40          45
Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65          70          75          80
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly
          85          90          95
Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn
          100          105          110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
          115          120          125
Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
          130          135          140
Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
145          150          155          160
Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His
          165          170          175
Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
          180          185          190
Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu Val
          195          200          205
Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser
          210          215          220
Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
          245          250          255
Gly Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu Thr
          260          265          270
Val Met Ser Leu Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Ala Met Glu Arg Ile
          290          295          300
Phe Cys Lys Arg Lys Ile Gln Leu Asn Leu
305          310

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<210> 2444

<211> 221

<212> PRT

<213> Unknown (3769633-dir-0-8 conceptual translation of range 1-663)

<400>2444

```

Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro
 1          5          10          15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala
          20          25          30
Gly Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly
          35          40          45
Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          50          55          60
Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser
65          70          75          80

```

Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His
 85 90 95
 Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro
 100 105 110
 His Ph Phe Cys Asp Thr Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp
 115 120 125
 Thr Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu
 130 135 140
 Val Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser
 145 150 155 160
 Ser Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Glu Ala Phe Ser
 165 170 175
 Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val
 180 185 190
 Ile Gly Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu
 195 200 205
 Thr Val Met Ser Leu Met Tyr Thr Val Val Thr Pro Met
 210 215 220

<210> 2445

<211> 221

<212> PRT

<213> Unknown (3769632-dir-0-8 conceptual translation of range 1-663)

<400>2445

Gly Asn Met Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro
 1 5 10 15
 Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Val
 20 25 30
 Gly Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly
 35 40 45
 Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys
 50 55 60
 Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser
 65 70 75 80
 Leu Val Val Leu Ser Trp Val Arg Thr Thr Phe His Ala Met Leu His
 85 90 95
 Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro
 100 105 110
 His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp
 115 120 125
 Thr Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu
 130 135 140
 Val Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser
 145 150 155 160
 Ser Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser
 165 170 175
 Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val
 180 185 190
 Ile Gly Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu
 195 200 205
 Thr Val Met Ser Leu Met Tyr Thr Ala Val Thr Pro Met
 210 215 220

<210> 2446

<211> 157

<212> PRT

<213> Unknown (902347-dir-0-6 conceptual translation of range 2-472)

<400>2446

Ile Cys Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Ser Leu Cys

```

1           5           10           15
Val Ser Leu Val Leu Leu Ser Trp Val Leu Thr Thr Phe His Ala Met
20           25           30
Leu His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val
35           40           45
Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ser Cys
50           55           60
Ser Asp Thr His Val Asn Glu Leu Val Ile Phe Val Thr Gly Gly Leu
65           70           75           80
Ile His Val Ile Pro Leu Val Leu Ile Leu Val Ser Tyr Ala Gln Ile
85           90           95
Val Ser Ser Ile Leu Lys Val Pro Ser Ala Arg Gly Ile Arg Lys Ala
100          105          110
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly
115          120          125
Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asp Asn Ser Thr Val
130          135          140
Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr
145          150          155

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<210> 2447

<211> 157

<212> PRT

<213> Unknown (902682-dir-0-6 conceptual translation of range 2-472)

<400>2447

```

Ile Cys Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Ser Leu Cys
1           5           10           15
Val Ser Leu Val Leu Leu Ser Trp Val Leu Thr Thr Phe His Ala Met
20           25           30
Leu His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val
35           40           45
Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ser Cys
50           55           60
Ser Asp Thr His Val Asn Glu Leu Val Ile Phe Val Thr Gly Gly Leu
65           70           75           80
Ile Leu Val Ile Pro Phe Val Leu Ile Leu Val Ser Tyr Ala Gln Ile
85           90           95
Val Ser Ser Ile Leu Lys Val Pro Ser Ala Arg Gly Ile Arg Lys Ala
100          105          110
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly
115          120          125
Thr Ile Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asp Asn Ser Thr Val
130          135          140
Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr
145          150          155

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<210> 2448

<211> 221

<212> PRT

<213> Unknown (3769627-dir-0-8 conceptual translation of range 1-663)

<400>2448

```

Gly Asn Ile Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro
1           5           10           15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala
20           25           30
Gly Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu
35           40           45
Ser Phe Leu Leu Glu Ala Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys
50           55           60

```

Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser
 65 70 75 80
 Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His
 85 90 95
 Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro
 100 105 110
 His Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp
 115 120 125
 Thr His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile
 130 135 140
 Val Ile Pro Phe Val Leu Ile Ile Val Ser Tyr Ala Arg Val Val Ala
 145 150 155 160
 Ser Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser
 165 170 175
 Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile
 180 185 190
 Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu
 195 200 205
 Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met
 210 215 220

<210> 2449

<211> 221

<212> PRT

<213> Unknown (3769629-dir-0-8 conceptual translation of range 1-663)

<220>

<221> VARIANT

<222> (1)...(221)

<223> Xaa = Any Amino Acid

<400>2449

Ser Asn Ile Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro
 1 5 10 15
 Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala
 20 25 30
 Gly Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu
 35 40 45
 Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
 50 55 60
 Phe Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser
 65 70 75 80
 Leu Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His
 85 90 95
 Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro
 100 105 110
 His Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp
 115 120 125
 Arg His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile
 130 135 140
 Val Ile Pro Phe Val Leu Ile Ile Val Ser Xaa Ala Arg Val Val Ala
 145 150 155 160
 Ser Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser
 165 170 175
 Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile
 180 185 190
 Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu
 195 200 205
 Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met
 210 215 220

<210> 2450

<211> 314

<212> PRT

<213> Unknown (205845-dir-0-11 conceptual translation of range 1-942)

<400>2450

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Met Thr Glu Glu Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Phe
 1           5           10           15
Leu Pro Ile Pro Ser Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
 20           25           30
Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
 35           40           45
Ile His Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50           55           60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65           70           75           80
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Phe Ala Gly
 85           90           95
Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu Ser
 100          105          110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115          120          125
Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
 130          135          140
Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145          150          155          160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His
 165          170          175
Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
 180          185          190
His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile Val
 195          200          205
Ile Pro Phe Val Leu Ile Ile Val Ser Tyr Ala Arg Val Val Ala Ser
 210          215          220
Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser Thr
 225          230          235          240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245          250          255
Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr
 260          265          270
Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Ile Arg Val
 290          295          300
Leu Cys Lys Lys Lys Ile Thr Phe Cys Leu
 305          310

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<210> 2451

<211> 192

<212> PRT

<213> Unknown (2921663-dir-1-7 conceptual translation of range 101-676)

<400>2451

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Met Tyr Phe Phe Leu Tyr Phe Thr Asp Leu Glu Ser Phe Leu Leu Val
 1           5           10           15
Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Met His Tyr
 20           25           30
Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile Met Ser Pro Met
 35           40           45
Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 50           55           60

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Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 65 70 75 80
 Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 85 90 95
 Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
 100 105 110
 Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 115 120 125
 Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 130 135 140
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 145 150 155 160
 Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser
 165 170 175
 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 180 185 190

<210> 2452

<211> 323

<212> PRT

<213> Unknown (p25-dir-0-11 conceptual translation of range 1-969)

<400>2452

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile
 130 135 140
 Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu
 145 150 155 160
 Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys
 165 170 175
 Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala
 180 185 190
 Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile
 195 200 205
 Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu
 210 215 220
 Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser
 225 230 235 240
 Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val
 245 250 255
 Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser
 260 265 270
 Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr
 275 280 285
 Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg
 290 295 300

Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro
 305 310 315 320
 Phe Leu Leu

<210> 2453

<211> 314

<212> PRT

<213> Unknown (p181-dir-0-11 conceptual translation of range 1-942)

<400>2453

Met Met Glu Gln Asn Gln Thr Ser Thr Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Val
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
 260 265 270
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Glu Arg Val
 290 295 300
 Ile Cys Lys Arg Lys Asn Pro Phe Leu Ile
 305 310

<210> 2454

<211> 149

<212> PRT

<213> Unknown (p166-dir-0-6 conceptual translation of range 2-448)

<400>2454

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
 1 5 10 15
 Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Val Asp Cys Leu Thr

```

      20      25      30
Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
      35      40      45
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      50      55      60
Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu Val Ala Leu
      65      70      75      80
Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
      85      90      95
Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Val Pro His Phe Phe Cys
      100      105      110
Asp Met Pro Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn
      115      120      125
Glu Ser Gly Ile Phe Ile Thr Gly Gly Leu Ile Leu Gly Ile Pro Phe
      130      135      140
Leu Leu Ile Leu Gly
145

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<210> 2455

<211> 314

<212> PRT

<213> Unknown (p17-dir-0-11 conceptual translation of range 1-942)

<400>2455

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Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1      5      10      15
Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
      20      25      30
Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
      35      40      45
Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
      65      70      75      80
Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
      85      90      95
Cys Leu Thr Gln Met Tyr Phe Phe Leu Phe Gly Asp Leu Glu Ser
      100      105      110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
      115      120      125
Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu
      130      135      140
Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
      145      150      155      160
Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
      165      170      175
Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr
      180      185      190
Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val
      195      200      205
Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
      210      215      220
Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
      225      230      235      240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
      245      250      255
Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
      260      265      270
Val Met Ala Met Met Tyr Thr Val Thr Pro Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val

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290 295 300
 Ile His Gln Lys Lys Thr Phe Phe Ser Leu
 305 310

<210> 2456

<211> 314

<212> PRT

<213> Unknown (p90-dir-0-11 conceptual translation of range 1-942)

<400>2456

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met His Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Val
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Phe Lys Gly Ile Cys Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
 260 265 270
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Glu Arg Val
 290 295 300
 Ile Cys Lys Arg Lys Asn Pro Phe Leu Leu
 305 310

<210> 2457

<211> 314

<212> PRT

<213> Unknown (p175-dir-0-11 conceptual translation of range 1-942)

<400>2457

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30

Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Val
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
 260 265 270
 Val Met Ala Met Ile Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val
 290 295 300
 Ile His Gln Lys Lys Thr Phe Phe Ser Leu
 305 310

<210> 2458

<211> 314

<212> PRT

<213> Unknown (p170-dir-0-11 conceptual translation of range 1-942)

<400>2458

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Leu
 130 135 140

Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Glu Thr
 260 265 270
 Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Glu Arg Val
 290 295 300
 Ile Cys Lys Arg Lys Asn Pro Phe Leu Leu
 305 310

<210> 2459

<211> 314

<212> PRT

<213> Unknown (p31-dir-0-11 conceptual translation of range 1-942)

<400>2459

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Ala Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ser Leu
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Val Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255

Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr Leu Lys Glu Thr
 260 265 270
 Val M t Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gly Asp Met Lys Gly Ala Leu Ser Arg Val
 290 295 300
 Ile His Gln Lys Lys Thr Phe Phe Ser Leu
 305 310

<210> 2460

<211> 324

<212> PRT

<213> Unknown (890-dir-5-12 conceptual translation of range 642-1613)

<220>

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400>2460

Arg Gln Ser Met Thr Glu Lys Asn Gln Thr Val Val Ser Glu Phe Val
 1 5 10 15
 Leu Leu Gly Leu Pro Ile Asp Pro Asp Gln Arg Asp Leu Phe Tyr Ala
 20 25 30
 Leu Phe Leu Ala Met Tyr Val Thr Thr Ile Leu Gly Asn Leu Leu Ile
 35 40 45
 Ile Val Leu Ile Gln Leu Asp Ser His Leu His Thr Pro Met Tyr Leu
 50 55 60
 Phe Leu Ser Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr
 65 70 75 80
 Met Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro
 85 90 95
 Tyr Ala Gly Cys Leu Thr Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp
 100 105 110
 Leu Glu Ser Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys Phe Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Leu Cys
 130 135 140
 Phe Ser Leu Leu Val Leu Ser Trp Val Leu Thr Met Phe His Ala Val
 145 150 155 160
 Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asn Thr Ile
 165 170 175
 Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser
 180 185 190
 Asp Thr Gln Val Asn Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile
 195 200 205
 Leu Val Ile Pro Phe Leu Leu Ile Ile Thr Ser Tyr Ala Arg Ile Val
 210 215 220
 Ser Ser Ile Leu Lys Val Pro Ser Ala Ile Gly Ile Cys Lys Val Phe
 225 230 235 240
 Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr
 245 250 255
 Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys
 260 265 270
 Glu Thr Ile Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn
 275 280 285
 Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg
 290 295 300
 Arg Val Ile Cys Arg Lys Lys Ile Thr Phe Ser Val Xaa Trp Xaa His
 305 310 315 320
 Leu Ile Leu Leu

<210> 2461

<211> 162

<212> PRT

<213> Unknown (4877306-dir-0-6 conceptual translation of range 2-487)

<400>2461

Val	Ala	Ile	Cys	Phe	Pro	Leu	His	Tyr	Thr	Thr	Ile	Met	Ser	Pro	Arg
1				5					10					15	
Leu	Cys	Leu	Phe	Leu	Val	Leu	Leu	Pro	Trp	Ile	Leu	Thr	Thr	Phe	His
		20						25					30		
Ala	Met	Leu	His	Thr	Leu	Leu	Met	Ala	Arg	Leu	His	Phe	Cys	Glu	Asp
		35					40					45			
Asn	Val	Ile	Pro	His	Phe	Phe	Cys	Asp	Ser	Ser	Ala	Leu	Leu	Lys	Leu
	50					55					60				
Ser	Cys	Ser	Asp	Thr	Arg	Val	Asn	Glu	Leu	Val	Ile	Phe	Phe	Val	Gly
65					70					75					80
Gly	Leu	Ile	Ile	Ile	Ile	Pro	Phe	Leu	Leu	Ile	Ile	Met	Ser	Tyr	Ala
			85						90					95	
Arg	Ile	Val	Ser	Ser	Ile	Leu	Lys	Val	Pro	Ser	Ala	Lys	Gly	Ile	Cys
		100						105					110		
Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Thr	Val	Val	Ser	Leu	Phe
		115					120					125			
Tyr	Gly	Thr	Ile	Ile	Gly	Leu	Tyr	Leu	Cys	Pro	Ser	Ala	His	Asn	Ser
	130					135					140				
Thr	Val	Lys	Glu	Thr	Val	Met	Ser	Met	Met	Tyr	Thr	Val	Val	Ala	Pro
145					150					155					160
Met	Leu														

<210> 2462

<211> 216

<212> PRT

<213> Unknown (p194-dir-0-8 conceptual translation of range 2-649)

<400>2462

Phe	Thr	Asp	Leu	Cys	Phe	Ser	Thr	Val	Thr	Met	Pro	Asn	Phe	Leu	Gln
1				5					10					15	
Asn	Met	Gln	Ser	Gln	Val	Ser	Ser	Ile	Pro	Tyr	Ala	Gly	Cys	Leu	Ala
		20						25					30		
Gln	Met	Tyr	Phe	Phe	Leu	Phe	Phe	Gly	Asp	Val	Glu	Ser	Leu	Leu	Leu
		35					40					45			
Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe	Pro	Leu	His
	50					55					60				
Tyr	Thr	Arg	Ile	Met	Ser	Pro	Asn	Leu	Cys	Val	Ser	Met	Val	Leu	Leu
65				70						75					80
Ser	Trp	Ala	Leu	Thr	Thr	Leu	Cys	Ala	Met	Leu	His	Thr	Leu	Leu	Leu
			85						90				95		
Thr	Arg	Leu	Ser	Phe	Cys	Lys	Asn	Asn	Val	Ile	Pro	His	Phe	Phe	Cys
		100						105					110		
Asp	Leu	Ser	Ala	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Asp	Ile	His	Ile	Asn
		115					120					125			
Glu	Leu	Met	Ile	Met	Ile	Ile	Gly	Ala	Leu	Val	Val	Ile	Leu	Pro	Phe
	130					135					140				
Leu	Leu	Ile	Ile	Val	Ser	Tyr	Ala	His	Ile	Val	Ser	Ser	Ile	Leu	Lys
145					150					155					160
Val	Pro	Ser	Thr	Arg	Gly	Ile	His	Lys	Val	Phe	Ser	Thr	Cys	Gly	Ser
				165					170					175	
His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly	Ser	Val	Ile	Val	Leu	Tyr
			180					185					190		

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser
 195 200 205
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2463

<211> 157

<212> PRT

<213> Unknown (902674-dir-0-6 conceptual translation of range 2-472)

<400>2463

Ile Cys Phe Pro Leu His Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys
 1 5 10 15
 Val Ser Met Val Leu Leu Ser Trp Ala Leu Thr Thr Leu Cys Ala Met
 20 25 30
 Leu Arg Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Lys Asn Asn Val
 35 40 45
 Ile Pro His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys
 50 55 60
 Ser Asp Ile His Ile Asn Glu Leu Met Ile Met Ile Ile Gly Ala Leu
 65 70 75 80
 Val Val Ile Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala His Ile
 85 90 95
 Val Ser Ser Ile Leu Lys Val Pro Ser Thr Arg Gly Ile His Lys Val
 100 105 110
 Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly
 115 120 125
 Ser Val Ile Val Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val
 130 135 140
 Lys Asp Thr Val Met Ser Met Met Tyr Thr Val Val Thr
 145 150 155

<210> 2464

<211> 216

<212> PRT

<213> Unknown (p197-dir-0-8 conceptual translation of range 2-649)

<220>

<221> VARIANT

<222> (1)...(216)

<223> Xaa = Any Amino Acid

<400>2464

Phe Thr Asp Leu Xaa Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15
 Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Tyr Phe Leu Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
 35 40 45
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60
 Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
 65 70 75 80
 Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
 85 90 95
 Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
 100 105 110
 Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
 115 120 125
 Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
 130 135 140

Leu Leu Ile Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
 145 150 155 160
 Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190
 Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser
 195 200 205
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2465

<211> 216

<212> PRT

<213> Unknown (p195-dir-0-8 conceptual translation of range 2-650)

<400>2465

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Leu
 1 5 10 15
 Asn Met Gln Ser Gln Ile Pro Ser Ile Ser Tyr Ala Ser Cys Leu Ala
 20 25 30
 Gln Met Tyr Phe Phe Leu Phe Phe Gly Ala Leu Glu Asn Phe Leu Leu
 35 40 45
 Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60
 Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Met Val Val Met
 65 70 75 80
 Cys Trp Val Leu Thr Thr Phe Asp Ala Met Leu His Thr Leu Leu Met
 85 90 95
 Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys
 100 105 110
 Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
 115 120 125
 Glu Val Val Ile Phe Ile Ile Gly Gly Leu Gly Val Val Leu Pro Phe
 130 135 140
 Leu Leu Ile Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
 145 150 155 160
 Val Pro Ser Thr Gln Gly Ile Gln Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190
 Leu Gly Pro Ser Ala Tyr Tyr Ser Thr Leu Lys Asp Thr Val Met Ser
 195 200 205
 Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2466

<211> 157

<212> PRT

<213> Unknown (902672-dir-0-6 conceptual translation of range 2-472)

<400>2466

Ile Cys Phe Pro Leu His Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys
 1 5 10 15
 Val Ser Met Val Val Met Cys Arg Val Leu Thr Thr Phe Asp Ala Met
 20 25 30
 Leu His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val
 35 40 45
 Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ser Cys
 50 55 60
 Ser Asp Thr His Val Asn Glu Val Val Ile Phe Ile Ile Gly Gly Leu

```

65          70          75          80
Gly Val Val Leu Pro Phe Leu Leu Ile Thr Val Ser Tyr Ala Arg Ile
      85          90          95
Ile Ser Ser Ile Leu Lys Val Pro Ser Thr Gln Gly Ile Gln Lys Val
      100         105         110
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly
      115         120         125
Thr Ile Ile Gly Leu Tyr Leu Gly Pro Ser Ala Tyr Tyr Ser Thr Leu
      130         135         140
Lys Asp Thr Val Met Ser Met Met Tyr Thr Val Val Thr
145          150          155

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<210> 2467

<211> 216

<212> PRT

<213> Unknown (p196-dir-0-8 conceptual translation of range 2-649)

<400>2467

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Phe Ser Asp Phe Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
1      5      10      15
Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
      20      25      30
Gln Met Tyr Phe Phe Leu Leu Phe Ala Asp Leu Glu Ser Phe Leu Leu
      35      40      45
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      50      55      60
Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Leu Cys Leu Val Ala Leu
65      70      75      80
Ser Trp Leu Leu Thr Thr Val Ile Ser Leu Ser His Thr Leu Leu Met
      85      90      95
Ala Arg Leu Ser Phe Cys Ala Asn Asn Val Ile Pro His Phe Phe Cys
      100     105     110
Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Gln Ile Asn
      115     120     125
Lys Leu Met Ile Phe Ile Leu Gly Gly Leu Val Ile Ile Val Pro Phe
      130     135     140
Leu Leu Ile Phe Ser Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
145     150     155     160
Val Pro Ser Ser Arg Ser Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
      165     170     175
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
      180     185     190
Leu Cys Pro Ser Ala Asn Asn Ser Thr Ile Lys Glu Thr Val Met Ala
      195     200     205
Val Met Tyr Thr Val Val Thr Pro
210          215

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<210> 2468

<211> 216

<212> PRT

<213> Unknown (p91-dir-0-8 conceptual translation of range 2-649)

<400>2468

```

Phe Ser Asp Met Cys Phe Ser Ser Val Ser Ile Pro Lys Leu Leu Val
1      5      10      15
Asn Met Gln Ser Lys Lys Pro Ala Ile Pro Tyr Ala Gly Cys Leu Ser
      20      25      30
Gln Met Tyr Phe Phe Leu Phe Phe Ala Asp Leu Glu Ser Phe Leu Leu
      35      40      45
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
50          55          60

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Tyr Ile Val Ile Met Ser Pro Lys Leu Cys Ser Ser Leu Val Val Leu
 65 70 75 80
 Ser Trp Val Leu Thr Ala Phe His Ala Leu Leu His Thr Leu Leu Met
 85 90 95
 Ser Arg Leu Ser Phe Cys Ala Asn Asn Val Ile Pro His Phe Phe Cys
 100 105 110
 Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Gln Pro Asn
 115 120 125
 Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Val Pro Phe
 130 135 140
 Leu Leu Ile Ile Thr Ser Tyr Ala His Ile Ile Ser Ser Ile Leu Arg
 145 150 155 160
 Val Pro Ser Val Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr
 180 185 190
 Leu Cys Pro Ser Thr Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser
 195 200 205
 Ile Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2469

<211> 314

<212> PRT

<213> Unknown (p29-dir-0-11 conceptual translation of range 1-942)

<400>2469

Met Met Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Arg Asn Leu Phe Tyr Ala Leu Phe Leu
 20 25 30
 Ala Val Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Val Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Cys Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp
 85 90 95
 Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Cys Cys Leu Gly Leu
 130 135 140
 Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Thr Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Glu Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asn Thr
 180 185 190
 Gln Val Asn Gly Trp Val Met Phe Phe Met Gly Gly Leu Ile Leu Val
 195 200 205
 Ile Pro Phe Leu Leu Leu Ile Met Ser Cys Ala Arg Ile Val Ser Thr
 210 215 220
 Ile Leu Arg Val Pro Ser Thr Gly Gly Ile Gln Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Pro His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Leu Thr Asn His Asn Thr Val Lys Asp Thr
 260 265 270

Val Met Ala Val Met Tyr Thr Gly Val Thr His Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Arg Gly Thr Leu Gly Arg Val
 290 295 300
 Phe Ser Thr Lys Lys Ile Phe Leu Ser Leu
 305 310

<210> 2470

<211> 314

<212> PRT

<213> Unknown (p132-dir-0-11 conceptual translation of range 1-942)

<400>2470

Met Thr Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Phe Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Cys Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp
 85 90 95
 Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu Gln Tyr Thr Thr Ile Met Ser Ser Lys Gly Cys Leu Ala Leu
 130 135 140
 Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Arg Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Gln Val Asn Gly Trp Val Met Phe Phe Thr Gly Gly Leu Ile Leu Val
 195 200 205
 Ile Pro Phe Leu Leu Leu Ile Met Ser Tyr Ala Arg Ile Leu Ser Thr
 210 215 220
 Ile Leu Arg Val Pro Cys Ala Gly Gly Ile Gln Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Pro His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Thr Asn His Asn Thr Val Lys Asp Thr
 260 265 270
 Val Met Ala Val Met Tyr Thr Gly Val Thr His Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Arg Gly Asn Pro Gly Gln Ser
 290 295 300
 Leu Gln His Lys Glu Asn Phe Phe Val Phe
 305 310

<210> 2471

<211> 310

<212> PRT

<213> Unknown (205831-dir-0-11 conceptual translation of range 1-930)

<400>2471

Met Asn Asn Gln Thr Phe Ile Thr Gln Phe Leu Leu Leu Gly Leu Pro

```

1           5           10           15
Ile Pro Glu Glu His Gln His Leu Phe Tyr Ala Leu Phe Leu Val Met
20           25           30
Tyr Leu Thr Thr Ile Leu Gly Asn Leu Leu Ile Ile Val Leu Val Gln
35           40           45
Leu Asp Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu
50           55           60
Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu
65           70           75           80
Gln Asn Met Arg Ser Gln Asp Thr Ser Ile Pro Tyr Gly Gly Cys Leu
85           90           95
Ala Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu
100          105          110
Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu
115          120          125
His Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Thr Cys Leu Val Leu
130          135          140
Leu Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu
145          150          155          160
Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Val Leu Asn Phe Phe
165          170          175
Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Ile
180          185          190
Asn Glu Leu Met Ile Phe Ile Met Ser Thr Leu Leu Ile Ile Ile Pro
195          200          205
Phe Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu
210          215          220
Lys Val Pro Ser Thr Gln Gly Ile Cys Lys Val Phe Ser Thr Cys Gly
225          230          235          240
Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu
245          250          255
Tyr Leu Cys Pro Ala Gly Asn Asn Ser Thr Val Lys Glu Met Val Met
260          265          270
Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
275          280          285
Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val Ile Cys
290          295          300
Ser Met Lys Ile Thr Leu
305          310

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<210> 2472

<211> 221

<212> PRT

<213> Unknown (3769635-dir-0-8 conceptual translation of range 1-663)

<400>2472

```

Gly Asn Met Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Leu
1           5           10           15
Lys Leu Leu Gln Asn Ile Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala
20           25           30
Gly Cys Leu Thr Gln Ile Phe Phe Leu Leu Phe Gly Tyr Leu Gly
35           40           45
Asn Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
50           55           60
Phe Pro Leu His Tyr Thr Asn Ile Met Ser His Lys Leu Cys Thr Cys
65           70           75           80
Leu Leu Leu Val Phe Trp Ile Met Thr Ser Ser His Ala Met Val His
85           90           95
Thr Leu Leu Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Leu Leu
100          105          110
Asn Phe Phe Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp

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115	120	125
Thr Tyr Val Asn Glu Leu Met Ile His Ile Met Gly Val Ile Ile Ile		
130	135	140
Val Ile Pro Phe Val Leu Ile Val Ile S r Tyr Ala Lys Ile Ile Ser		
145	150	155
Ser Ile Leu Lys Val Pro Ser Thr Gln Ser Ile His Lys Val Phe Ser		160
	165	170
Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile		175
	180	185
Ile Gly Leu Tyr Leu Cys Pro Ser Gly Asp Asn Phe Ser Leu Lys Gly		190
	195	200
Ser Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met		205
210	215	220

<210> 2473

<211> 221

<212> PRT

<213> Unknown (3769637-dir-0-8 conceptual translation of range 1-663)

<400>2473

Gly Asn Met Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro		
1	5	10
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala		15
	20	25
Gly Cys Leu Thr Gln Leu Tyr Phe Phe Met Val Phe Ala Asp Met Glu		30
	35	40
Ser Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys		45
	50	55
Phe Pro Leu His Tyr Thr Thr Ile Met Ser Thr Lys Val Cys Ala Ser		60
65	70	75
Leu Leu Ile Leu Leu Trp Met Leu Thr Thr Ser His Ala Leu Leu His		80
	85	90
Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu		95
	100	105
His Phe Phe Cys Asp Ile Thr Ala Leu Leu Lys Leu Ser Cys Ser Asp		110
	115	120
Thr Tyr Val Asn Glu Met Met Met His Ile Leu Gly Gly Leu Ile Ser		125
	130	135
Val Ile Pro Phe Leu Phe Ile Val Met Ser Tyr Val Arg Ile Phe Phe		140
145	150	155
Ser Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile His Lys Val Phe Ser		160
	165	170
Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile		175
	180	185
Phe Gly Leu Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Glu		190
	195	200
Ile Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met		205
210	215	220

<210> 2474

<211> 221

<212> PRT

<213> Unknown (3769639-dir-0-8 conceptual translation of range 1-663)

<220>

<221> VARIANT

<222> (1)...(221)

<223> Xaa = Any Amino Acid

<400>2474

Gly Asn Phe Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro

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1           5           10           15
Lys Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala
20           25           30
Gly Cys Leu Thr Gln Leu Tyr Phe Phe Met Val Phe Ala Asp Met Glu
35           40           45
Ser Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
50           55           60
Phe Pro Leu His Tyr Thr Thr Ile Met Ser Thr Lys Val Cys Ala Ser
65           70           75           80
Leu Leu Ile Leu Leu Xaa Met Leu Thr Thr Ser His Ala Pro Leu His
85           90           95
Thr Leu Leu Met Ala Arg Leu Pro Phe Tyr Glu Lys Asn Val Ile Leu
100          105          110
His Phe Phe Cys Asp Val Thr Ala Leu Leu Lys Leu Ser Cys Ser Asp
115          120          125
Thr Tyr Val Asn Glu Met Met Met Tyr Ile Leu Gly Gly Leu Ile Ser
130          135          140
Val Ile Pro Phe Leu Phe Ile Val Met Ser Tyr Val Arg Ile Phe Phe
145          150          155          160
Ser Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile His Lys Val Phe Ser
165          170          175
Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile
180          185          190
Phe Gly Leu Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Glu
195          200          205
Ile Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met
210          215          220

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<210> 2475

<211> 312

<212> PRT

<213> Unknown (205843-dir-0-11 conceptual translation of range 1-936)

<400>2475

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Met Thr Gly Asn Asn Gln Thr Leu Ile Leu Glu Phe Leu Leu Leu Gly
1           5           10           15
Leu Pro Ile Pro Ser Glu Tyr His Leu Leu Phe Tyr Ala Leu Phe Leu
20           25           30
Ala Met Tyr Leu Thr Ile Ile Leu Gly Asn Leu Leu Ile Ile Val Leu
35           40           45
Val Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Phe Leu Ser
50           55           60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65           70           75           80
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Ser Tyr Thr Gly
85           90           95
Cys Leu Thr Gln Leu Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser
100          105          110
Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
115          120          125
Pro Leu Arg Tyr Thr Thr Ile Met Ser Thr Lys Phe Cys Ala Ser Leu
130          135          140
Val Leu Leu Leu Trp Met Leu Thr Met Thr His Ala Leu Leu His Thr
145          150          155          160
Leu Leu Ile Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu His
165          170          175
Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile
180          185          190
Tyr Val Asn Glu Leu Met Ile Tyr Ile Leu Gly Gly Leu Ile Ile Ile
195          200          205
Ile Pro Phe Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser

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      210              215              220
Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile Tyr Lys Val Phe Ser Thr
225              230              235              240
Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Phe
      245              250              255
Gly Ile Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Glu Ile
      260              265              270
Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val
      290              295              300
Ile Cys Thr Lys Lys Ile Ser Leu
305              310

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<210> 2476

<211> 216

<212> PRT

<213> Unknown (p198-dir-0-8 conceptual translation of range 2-649)

<400>2476

```

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
 1              5              10              15
Asn Met Gln Ser Gln Val Pro Thr Ile Ser Tyr Ala Asp Cys Leu Thr
      20              25              30
Gln Leu Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu
      35              40              45
Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      50              55              60
Tyr Thr Ser Ile Met Ser Thr Lys Phe Cys Ala Leu Leu Val Leu Leu
      65              70              75              80
Leu Trp Met Leu Thr Ile Ser His Ala Leu Leu His Thr Leu Leu Met
      85              90              95
Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu His Phe Phe Cys
      100              105              110
Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr Tyr Val Asn
      115              120              125
Glu Leu Met Ile Phe Ile Met Gly Gly Ile Ile Ser Ile Ile Pro Phe
      130              135              140
Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser Ile Leu Lys
      145              150              155              160
Val Pro Ser Ser Gln Asp Ile His Lys Val Phe Ser Thr Cys Gly Ser
      165              170              175
His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
      180              185              190
Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Asn Glu Ile Ser Met Ala
      195              200              205
Met Met Tyr Thr Val Val Thr Pro
      210              215

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<210> 2477

<211> 236

<212> PRT

<213> Unknown (3810822-dir-0-8 conceptual translation of range 1-708)

<400>2477

```

Pro Met Tyr Leu Phe Leu Gly Asn Leu Ser Phe Ser Asp Leu Cys Phe
 1              5              10              15
Ser Ser Val Thr Met Pro Lys Leu Leu Gln Asn Met Gln Ser Gln Asp
      20              25              30
Thr Ser Ile Thr Tyr Val Gly Cys Leu Thr Gln Ser Val Leu Phe Leu
      35              40              45

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Ile Phe Phe Gly Gly Leu Glu Ile Phe Leu Leu Val Val Met Ala Tyr
  50          55          60
Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His Tyr Ser Ser Ile Met
  65          70          75          80
Ser Leu Lys Phe Cys Val Cys Ala Val Leu Ile Ser Trp Ile Asn Ser
          85          90          95
Pro Trp Tyr Ser Lys Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe
          100          105          110
Cys Glu Asp Asn Ile Ile Cys His Phe Phe Cys Asp Met Ser Ala Leu
          115          120          125
Leu Lys Leu Ala Cys Ser Asp Ile Tyr Ile Asn Glu Leu Val Ile Phe
          130          135          140
Ile Leu Gly Gly Pro Leu Val Val Ile Pro Phe Leu Leu Ile Val Val
  145          150          155          160
Ser Tyr Val Gln Ile Ile Phe Ser Ile Leu Lys Ala Ser Ser Thr Arg
          165          170          175
Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Thr Tyr Leu Thr Val Val
          180          185          190
Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Glu
          195          200          205
Lys Leu Tyr Ser Lys Glu Ala Ser Ile Thr Met Met Tyr Thr Val Val
          210          215          220
Thr Pro Met His Pro Phe Ile Tyr Thr Leu Arg Asn
  225          230          235

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<210> 2478

<211> 216

<212> PRT

<213> Unknown (OST044-dir-0-8 conceptual translation of range 2-649)

<400>2478

```

Leu Ala Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys Met Leu Met
  1          5          10          15
Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu Cys Ile Ser
          20          25          30
Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser Phe Leu Ile
          35          40          45
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
          50          55          60
Tyr Thr Val Ile Met Arg Glu Glu Leu Cys Val Phe Leu Val Ala Val
  65          70          75          80
Ser Trp Ile Leu Ser Cys Ala Ser Ser Leu Ser His Thr Leu Leu Leu
          85          90          95
Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His Val Phe Cys
          100          105          110
Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile Phe Leu Asn
          115          120          125
Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr Leu Pro Phe
          130          135          140
Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile Leu Arg
  145          150          155          160
Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr Cys Gly Ser
          165          170          175
His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe Gly Gln Tyr
          180          185          190
Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val Ile Val Ala
          195          200          205
Leu Met Tyr Thr Val Val Thr Pro
          210          215

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<210> 2479

<211> 216

<212> PRT

<213> Unknown (hg152-dir-0-8 conceptual translation of range 1-648)

<400>2479

```

Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys Met Leu Met
 1          5          10          15
Asp Met Arg Thr Lys Tyr Lys Ser Ile Leu Tyr Glu Glu Cys Ile Ser
          20          25          30
Gln Met Tyr Phe Phe Ile Phe Phe Thr Asp Leu Asp Ser Phe Leu Ile
          35          40          45
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
          50          55          60
Tyr Thr Val Val Met Arg Glu Glu Leu Cys Val Phe Leu Val Ala Val
          65          70          75          80
Ser Trp Ile Leu Ser Cys Asp Ser Ser Leu Ser His Thr Leu Leu Leu
          85          90          95
Thr Arg Leu Ser Phe Cys Ala Ala Asn Thr Ile Pro His Val Phe Cys
          100          105          110
Asp Leu Ala Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile Phe Leu Asn
          115          120          125
Glu Leu Val Met Phe Thr Val Gly Val Val Val Ile Thr Leu Pro Phe
          130          135          140
Met Cys Ile Leu Val Ser Tyr Gly Tyr Ile Gly Ala Thr Ile Leu Arg
          145          150          155          160
Val Pro Ser Thr Lys Gly Ile His Lys Ala Leu Ser Thr Cys Gly Ser
          165          170          175
His Leu Ser Val Val Ser Leu Tyr Tyr Gly Ser Ile Phe Gly Gln Tyr
          180          185          190
Leu Phe Pro Thr Val Ser Ser Ser Ile Asp Lys Asp Val Ile Val Ala
          195          200          205
Leu Met Tyr Thr Val Val Thr Pro
          210          215

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<210> 2480

<211> 112

<212> PRT

<213> Unknown (1142973-dir-0-5 conceptual translation of range 1-336)

<400>2480

```

His Pro Leu His Tyr Ile Thr Ile Met Ser Gln Ser Arg Cys Ala Met
 1          5          10          15
Leu Val Ala Val Ser Trp Val Ile Ala Ser Ala Cys Ala Leu Leu His
          20          25          30
Ser Leu Leu Leu Asp Gln Leu Ser Phe Cys Ala Asp His Thr Val Pro
          35          40          45
His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu Ser Cys Ser Asp
          50          55          60
Thr Ser Leu Asn Gln Leu Val Ile Phe Thr Ala Gly Leu Ala Ala Ile
          65          70          75          80
Met Leu Pro Phe Leu Cys Ile Leu Ile Ser Tyr Gly Arg Ile Gly Phe
          85          90          95
Thr Ile Leu Gln Val Pro Thr Thr Lys Gly Ile Cys Lys Ala Leu Ser
          100          105          110

```

<210> 2481

<211> 216

<212> PRT

<213> Unknown (hg32-dir-0-8 conceptual translation of range 1-648)

<400>2481


```

Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Val Pro Lys Met Leu Met
 1          5          10          15
Asn Met Gln Thr Gln His Leu Ala Val Phe Tyr Lys Gly Cys Ile Ser
      20          25          30
Gln Thr Tyr Phe Phe Ile Phe Phe Ala Asp Leu Asp Ser Phe Leu Ile
      35          40          45
Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
      50          55          60
Tyr Ala Thr Ile Met Thr Gln Ser Gln Cys Val Met Leu Val Ala Gly
      65          70          75          80
Ser Trp Val Ile Ala Cys Ala Cys Ala Leu Leu Asp Thr Leu Leu Leu
      85          90          95
Ala Gln Leu Ser Phe Cys Ala Asp His Ile Ile Pro His Tyr Phe Cys
      100          105          110
Asp Leu Gly Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr Ser Leu Asn
      115          120          125
Gln Leu Ala Ile Phe Thr Ala Ala Leu Thr Ala Ile Met Leu Pro Phe
      130          135          140
Leu Cys Ile Leu Val Ser Tyr Gly His Ile Gly Val Thr Ile Leu Gln
      145          150          155          160
Ile Pro Ser Thr Lys Gly Ile Cys Lys Ala Leu Ser Thr Cys Gly Ser
      165          170          175
His Leu Ser Val Val Thr Ile Tyr Tyr Arg Thr Ile Ile Gly Leu Tyr
      180          185          190
Phe Leu Pro Pro Ser Ser Asn Thr Asn Asp Lys Asn Ile Ile Ala Ser
      195          200          205
Val Ile Tyr Thr Ala Val Thr Pro
      210          215

```

<210> 2482

<211> 223

<212> PRT

<213> Unknown (3983375-dir-0-8 conceptual translation of range 1-669)

<400>2482

```

Ser His Leu Ala Phe Thr Asp Ile Ser Phe Ser Ser Val Thr Ala Pro
 1          5          10          15
Lys Met Leu Met Asn Met Leu Thr His Ser Gln Ser Ile Ser His Ala
      20          25          30
Gly Cys Val Ser Gln Ile Tyr Phe Phe Leu Leu Phe Gly Cys Ile Asp
      35          40          45
Asn Phe Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      50          55          60
His Pro Leu His Tyr Thr Thr Ile Met Ser Gln Ser Leu Cys Val Leu
      65          70          75          80
Leu Val Met Val Ser Trp Ala Phe Ser Ser Ser Asn Gly Leu Val His
      85          90          95
Thr Leu Leu Phe Ala Arg Leu Ser Leu Phe Arg Asp Asn Thr Val His
      100          105          110
His Phe Phe Cys Asp Leu Ser Ala Leu Leu Lys Leu Ser Ser Ser Asp
      115          120          125
Thr Thr Ile Asn Glu Leu Val Ile Leu Thr Leu Ala Val Val Val Ile
      130          135          140
Thr Val Pro Phe Ile Cys Ile Leu Val Ser Tyr Gly His Met Gly Ala
      145          150          155          160
Thr Ile Leu Arg Thr Pro Ser Ile Lys Gly Ile Cys Lys Ala Leu Ser
      165          170          175
Thr Cys Gly Ser His Leu Cys Val Val Ser Leu Tyr Tyr Gly Ala Ile
      180          185          190
Ile Gly Leu Tyr Phe Phe Pro Ser Ser Asn Asn Thr Asn Asp Lys Asp
      195          200          205

```

Val Ile Val Ala Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn
 210 215 220

<210> 2483

<211> 176

<212> PRT

<213> Unknown (3273636-dir-0-7 conceptual translation of range 4-531)

<400>2483

Gln Ala Leu Ala Tyr Asp Arg Phe Leu Ala Ile Cys Gln Pro Leu His
 1 5 10 15
 Tyr Arg Thr Ile Met Arg Asp Gly Phe Cys Val Leu Leu Val Val Gly
 20 25 30
 Ser Trp Phe Phe Ser Cys Val His Ala Leu Leu His Thr Leu Leu Leu
 35 40 45
 Ser Arg Leu Ser Phe Cys Ala Asp Asn Ala Ile Pro His Phe Phe Cys
 50 55 60
 Asp Phe Thr Ala Val Leu Lys Met Thr Cys Ser Asp Thr Ser Ile Asn
 65 70 75 80
 Glu Leu Val Ile Phe Ile Glu Gly Gly Leu Leu Thr Ser Leu Pro Leu
 85 90 95
 Ser Ala Ile Leu Gly Ser Tyr Val Arg Ile Gly Ala Ser Ile Leu Arg
 100 105 110
 Val Pro Ser Met Lys Arg Ile Cys Lys Ala Leu Ser Thr Cys Gly Ser
 115 120 125
 His Leu Phe Val Val Phe Leu Tyr Tyr Gly Thr Ile Ala Met Thr Tyr
 130 135 140
 Phe Phe Pro Ser Ser Tyr Asn Ser Lys Val Lys Gly Ile Ile Ala Ser
 145 150 155 160
 Val Ile Tyr Thr Val Val Ala Pro Met Leu Asn Pro Phe Ile Cys Ser
 165 170 175

<210> 2484

<211> 222

<212> PRT

<213> Unknown (4877296-dir-0-8 conceptual translation of range 2-667)

<400>2484

Ser His Leu Ala Leu Thr Asp Ile Ser Phe Ser Ser Val Thr Leu Pro
 1 5 10 15
 Lys Met Leu Met Asn Met Gln Thr Arg Cys Gln Ala Ile Thr Tyr Ala
 20 25 30
 Gly Cys Ile Ser Gln Val Tyr Cys Phe Ile Phe Phe Gly Cys Leu Asp
 35 40 45
 Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
 50 55 60
 His Pro Leu His Tyr Thr Ala Ile Met Arg Asp Glu Leu Cys Val Ile
 65 70 75 80
 Leu Val Ala Gly Arg Trp Leu Ala Ala Cys Ala Gln Ala Leu Leu His
 85 90 95
 Thr Leu Leu Val Asp Gln Leu Thr Leu Cys Ala Gly Thr Val Ile Pro
 100 105 110
 His Phe Phe Cys Asp Leu Ala Val Val Leu Lys Ser Ser Cys Ser Asp
 115 120 125
 Thr Ser Leu Asn Glu Leu Leu Ile Leu Thr Glu Gly Gly Leu Ile Phe
 130 135 140
 Thr Leu Pro Leu Gly Gly Ile Leu Gly Ser Tyr Ile Arg Met Ala Ala
 145 150 155 160
 Ile Ile Leu Lys Val Pro Ser Phe Thr Arg Ile Phe Lys Ala Leu Ser
 165 170 175
 Thr Cys Gly Ser His Leu Phe Val Val Phe Leu Tyr Tyr Gly Thr Ile

	180		185		190
Ala Gly Val Tyr Tyr Phe Pro Ser Ser Gly Asn Ser Lys Val Lys Asp					
195		200		205	
Ile Val Ala Ser Leu Met Tyr Met Val Val Thr Pro Met Leu					
210		215		220	

<210> 2485

<211> 173

<212> PRT

<213> Unknown (3273660-dir-0-7 conceptual translation of range 1-519)

<400>2485

Gln Ala Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Gln Leu Leu His					
1	5		10		15
Tyr Ser Thr Ile Met Arg Gln Glu Leu Cys Val Ser Leu Val Ser Gly					
20		25		30	
Ser Trp Phe Leu Cys Cys Ile Tyr Ala Leu Leu His Thr Leu Leu Leu					
35		40		45	
Val Gln Leu Ser Phe Ser Val Asp Asn Thr Ile Pro His Ser Asn Leu					
50		55		60	
Ile Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr Ser Leu Asn Glu Leu					
65		70		75	80
Val Ile Phe Pro Val Arg Gly Thr Leu Leu Ile Leu Ser Leu Phe Ser					
	85		90		95
Ile Leu Gly Ser Tyr Ile His Ile Gly Pro Thr Leu Leu Ser Val Ser					
100		105		110	
Ser Thr Arg Asp Ser Lys Val Cys Ser Thr Cys Gly Phe His His Phe					
115		120		125	
Ser Val Ser Leu Tyr His Arg Lys Leu Ala Asn Val Ser Phe Phe Ser					
130		135		140	
Leu Ser Trp Asp Ser Asn Gly Lys Asp Val Thr Thr Ser Val Val Tyr					
145		150		155	160
Ala Val Val Thr Pro Met Val Asn Pro Phe Ile Cys Ser					
	165		170		

<210> 2486

<211> 135

<212> PRT

<213> Unknown (3273658-dir-0-6 conceptual translation of range 1-405)

<400>2486

Ile Tyr Ala Leu Leu His Thr Leu Leu Leu Val Gln Leu Ser Phe Ser					
1	5		10		15
Val Asp Asn Thr Ile Pro His Ser Asn Leu Ile Ala Leu Leu Lys Leu					
20		25		30	
Ser Cys Ser Asp Thr Ser Leu Asn Glu Leu Val Ile Phe Pro Val Arg					
35		40		45	
Gly Thr Leu Leu Ile Pro Ser Leu Leu Ser Ile Leu Gly Ser Tyr Ile					
50		55		60	
His Ile Gly Pro Thr Leu Leu Ser Val Ser Ser Thr Arg Asp Ser Lys					
65		70		75	80
Val Cys Ser Thr Cys Gly Phe His His Phe Ser Val Ser Leu Tyr His					
	85		90		95
Arg Lys Arg Ala Asn Val Ser Phe Phe Ser Ser Ser Trp Asp Ser Asn					
100		105		110	
Gly Lys Asp Val Thr Thr Ser Val Val Tyr Ala Val Val Thr Pro Met					
115		120		125	
Leu Asn Pro Phe Ile Cys Ser					
130		135			

<210> 2487

<211> 176

<212> PRT

<213> Unknown (3273646-dir-0-7 conceptual translation of range 1-528)

<400>2487

Gln	Ala	Leu	Ala	Tyr	Asp	Arg	Phe	Leu	Ala	Val	Cys	His	Pro	Leu	His
1				5				10						15	
Tyr	Ala	Ile	Phe	Met	Arg	Glu	Arg	Leu	Cys	Ile	Phe	Leu	Leu	Ala	Gly
			20					25					30		
Ser	Trp	Leu	Leu	Ser	Gly	Ala	Ser	Ala	Leu	Thr	His	Thr	Leu	Leu	Val
		35					40					45			
Val	Gln	Leu	Ser	Phe	Cys	Ala	Asp	Asn	Ile	Ile	Leu	His	Phe	Phe	Cys
	50					55					60				
Asp	Leu	Val	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Thr	Ser	Leu	Asn
65					70				75					80	
Glu	Leu	Val	Ile	Phe	Thr	Val	Gly	Ser	Val	Gly	Leu	Val	Phe	Pro	Leu
				85				90						95	
Ser	Gly	Ile	Leu	Val	Ser	Tyr	Gly	Arg	Ile	Gly	Leu	Ser	Ile	Leu	Arg
		100					105						110		
Val	Pro	Ser	Thr	Lys	Gly	Val	Cys	Lys	Ala	Leu	Ser	Thr	Cys	Gly	Ser
	115					120						125			
His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Ile	Met	Ala	Val	Tyr
	130					135					140				
Phe	Ser	Ser	Ser	Ser	Gly	Gln	Ser	His	Glu	Lys	Asp	Ile	Ile	Ala	Ser
145					150					155				160	
Met	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Val	Asn	Pro	Val	Ile	Cys	Ser
				165					170					175	

<210> 2488

<211> 313

<212> PRT

<213> Unknown (205815-dir-0-11 conceptual translation of range 1-939)

<400>2488

Met	Ser	Ser	Thr	Asn	Gln	Ser	Ser	Val	Thr	Glu	Phe	Leu	Leu	Leu	Gly
1				5				10						15	
Leu	Ser	Arg	Gln	Pro	Gln	Gln	Gln	Gln	Leu	Leu	Phe	Leu	Leu	Phe	Leu
		20						25					30		
Ile	Met	Tyr	Leu	Ala	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala
	35						40					45			
Ile	Gly	Thr	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
	50					55					60				
Asn	Leu	Ser	Phe	Val	Asp	Val	Cys	Phe	Ser	Ser	Thr	Thr	Val	Pro	Lys
65					70				75					80	
Val	Leu	Ala	Asn	His	Ile	Leu	Gly	Ser	Gln	Ala	Ile	Ser	Phe	Ser	Gly
			85					90						95	
Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Leu	Ala	Val	Phe	Gly	Asn	Met	Asp	Asn
		100						105					110		
Phe	Leu	Leu	Ala	Val	Met	Ser	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His
	115						120					125			
Pro	Leu	His	Tyr	Thr	Thr	Lys	Met	Thr	Arg	Gln	Leu	Cys	Val	Leu	Leu
	130					135					140				
Val	Val	Gly	Ser	Trp	Val	Val	Ala	Asn	Met	Asn	Cys	Leu	Leu	His	Ile
145					150					155				160	
Leu	Leu	Met	Ala	Arg	Leu	Ser	Phe	Cys	Ala	Asp	Asn	Met	Ile	Pro	His
			165					170						175	
Phe	Phe	Cys	Asp	Gly	Thr	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Thr
		180						185					190		
His	Leu	Asn	Glu	Leu	Met	Ile	Leu	Thr	Glu	Gly	Ala	Val	Val	Met	Val
	195					200						205			
Thr	Pro	Phe	Val	Cys	Ile	Leu	Ile	Ser	Tyr	Ile	His	Ile	Thr	Cys	Ala

210		215		220
Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr				
225		230		235
Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile				240
	245		250	255
Ala Val Tyr Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met				
	260		265	270
Ala Ala Ala Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe				
	275		280	285
Ile Tyr Ser Leu Arg Asn Ser Asp Met Lys Ala Ala Leu Arg Lys Val				
	290		295	300
Leu Ala Met Arg Phe Pro Ser Lys Gln				
305		310		

<210> 2489

<211> 216

<212> PRT

<213> Unknown (hg91-dir-0-8 conceptual translation of range 1-648)

<400>2489

Phe Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala				
1	5	10	15	
Asn His Ile Leu Gly Ser Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr				
	20	25	30	
Gln Leu Tyr Phe Leu Ala Val Cys Gly Asn Met Asp Asn Phe Leu Leu				
	35	40	45	
Gly Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His				
	50	55	60	
Tyr Thr Thr Lys Met Thr Arg Gln Leu Cys Val Leu Leu Val Val Gly				
	65	70	75	80
Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His Ile Leu Leu Met				
	85	90	95	
Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His Phe Phe Cys				
	100	105	110	
Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn				
	115	120	125	
Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val Thr Pro Phe				
	130	135	140	
Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala Val Leu Arg				
	145	150	155	160
Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr Cys Gly Ser				
	165	170	175	
His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Ala Val Tyr				
	180	185	190	
Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met Ala Ala Ala				
	195	200	205	
Val Met Tyr Pro Val Val Thr Pro				
210		215		

<210> 2490

<211> 157

<212> PRT

<213> Unknown (902718-dir-0-6 conceptual translation of range 2-472)

<400>2490

Ile Cys His Pro Leu Gln Tyr Thr Thr Lys Met Thr His Gln Leu Cys				
1	5	10	15	
Ala Leu Leu Val Val Gly Ser Trp Val Val Ala Asn Leu Asn Cys Leu				
	20	25	30	
Leu His Ile Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ile				
	35	40	45	

```

Ile Pro His Phe Phe Cys Asp Ala Thr Pro Leu Leu Lys Leu Ser Cys
 50          55          60
Ser Asp Thr His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val
65          70          75          80
Ile Ile Val Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Val
          85          90          95
Thr Cys Ala Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ala
          100          105          110
Phe Ser Thr Arg Gly Ser His Pro Ala Val Val Cys Leu Phe Tyr Gly
          115          120          125
Thr Ile Ile Ala Glu Tyr Phe Ser Ser Ser Ser Pro His Ser Ala Gly
          130          135          140
Arg Asp Met Ala Gly Ala Met Met Tyr Thr Val Val Thr
145          150          155

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<210> 2491

<211> 221

<212> PRT

<213> Unknown (3769625-dir-0-8 conceptual translation of range 1-663)

<400>2491

```

Ser Asn Leu Ser Phe Val Asp Val Cys Phe Ser Ser Thr Thr Ala Pro
 1          5          10          15
Ser Val Leu Ala Asn His Ile Leu Gly Ser Gln Lys Ile Ser Phe Ser
          20          25          30
Gly Cys Leu Thr Gln Leu Tyr Phe Leu Cys Ile Phe Gly Asp Met Asp
          35          40          45
Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
          50          55          60
His Pro Leu Arg Tyr Thr Thr Lys Met Thr His Gln Val Cys Ala Leu
65          70          75          80
Leu Val Met Gly Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His
          85          90          95
Ile Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Ser Ile Ile Pro
          100          105          110
His Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp
          115          120          125
Thr His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met
          130          135          140
Val Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Trp
145          150          155          160
Ala Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ala Phe Ser
          165          170          175
Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Leu Tyr Gly Thr Val
          180          185          190
Ile Thr Val Tyr Phe Asn Pro Ser Thr Ser Tyr Ser Ala Gly Arg Asp
          195          200          205
Thr Ala Ala Ala Val Met Tyr Thr Val Val Thr Pro Met
210          215          220

```

<210> 2492

<211> 221

<212> PRT

<213> Unknown (3769644-dir-0-8 conceptual translation of range 1-663)

<400>2492

```

Thr Asn Leu Ser Phe Val Asp Val Cys Phe Ser Ser Ser Thr Val Pro
 1          5          10          15
Lys Val Leu Ala Asn His Ile Leu Gly Ser Gln Glu Ile Ser Phe Ser
          20          25          30
Gly Cys Leu Thr Gln Met Tyr Phe Leu Ser Val Phe Ala Asp Met Asp

```

35	40	45
Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys		
50	55	60
His Pro Leu His Tyr Thr Glu Lys Met Thr Arg Gln Leu Cys Ala Leu		
65	70	75
Leu Val Val Glu Ser Trp Val Ala Ala Asn Leu Asn Ala Leu Leu His		
85	90	95
Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Gly Asp Asn Ile Ile Pro		
100	105	110
His Phe Phe Cys Asp Ala Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp		
115	120	125
Thr His Leu Asn Glu Leu Met Ile Leu Thr Val Ala Gly Leu Ile Leu		
130	135	140
Leu Ala Pro Phe Val Cys Ile Leu Met Ser Tyr Ile Leu Ile Ala Cys		
145	150	155
Ala Val Val Arg Val Ser Ser Thr Gly Gly Arg Trp Lys Ala Phe Ser		
165	170	175
Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe Tyr Gly Thr Ile		
180	185	190
Ile Ala Val Tyr Phe Asn Pro Ala Ser Ser His Ser Ala Gly Arg Asp		
195	200	205
Met Ala Ser Ala Met Met Tyr Thr Val Val Thr Pro Met		
210	215	220

<210> 2493

<211> 327

<212> PRT

<213> Unknown (2808536-dir-0-11 conceptual translation of range 16-996)

<220>

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400>2493

Val Cys Phe Xaa Ile His Cys Leu Leu Cys Ser Trp Val Gln Thr Tyr	
1	15
Glu Arg Asp Lys Pro Val Ser Val Ser Glu Phe Leu Leu Gly Leu	
20	30
Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu Ser	
35	45
Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile	
50	60
Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn	
65	80
Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu	
85	95
Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu	
100	110
Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu	
115	125
Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu	
130	140
His Tyr Thr Ala Lys Met Ile His Gln Leu Cys Ala Leu Leu Val Thr	
145	160
Gly Ser Trp Val Val Ala Asn Ser Asn Ala Leu Leu His Thr Leu Leu	
165	175
Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His Ile Phe	
180	190
Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu	
195	205

Ser Glu Val Met Ile Leu Thr Glu Ala Ala Leu Val Thr Ile Thr Pro
 210 215 220
 Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr Cys Val Val Leu
 225 230 235 240
 Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly
 245 250 255
 Ser His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr Ile Met Ser Pro
 260 265 270
 Tyr Phe Arg Thr Ser Ser Ser His Ser Ala Gln Arg Asp Ile Ala Ala
 275 280 285
 Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn Pro Leu Ile Tyr
 290 295 300
 Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val Lys Val Val Ala
 305 310 315 320
 Val Lys Phe Phe Ser Val Gln
 325

<210> 2494

<211> 312

<212> PRT

<213> Unknown (2370144-dir-0-11 conceptual translation of range 1-936)

<400>2494

Met Ser Gly Thr Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu
 20 25 30
 Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ser
 35 40 45
 Val Ser Ile Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Ala Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn
 100 105 110
 Phe Leu Leu Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His
 115 120 125
 Pro Leu His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu
 130 135 140
 Val Ala Gly Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His
 165 170 175
 Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asn Thr
 180 185 190
 His Leu Asn Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile
 195 200 205
 Thr Pro Phe Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr
 210 215 220
 Val Leu Lys Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile
 245 250 255
 Ala Val Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr
 260 265 270
 Met Ala Thr Val Leu Tyr Thr Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Tyr Leu Lys Gly Ala Leu Lys Lys Val
 290 295 300

Ile Gly Arg Val Val Phe Ser Val
305 310

<210> 2495

<211> 216

<212> PRT

<213> Unknown (2921659-dir-0-8 conceptual translation of range 2-649)

<400>2495

Phe	Val	Asp	Ile	Cys	Phe	Ser	Phe	Thr	Thr	Val	Pro	Lys	Met	Leu	Ala
1			5					10						15	
Asn	His	Ile	Leu	Glu	Thr	Gln	Thr	Ile	Ser	Phe	Cys	Gly	Cys	Leu	Thr
		20					25					30			
Gln	Met	Tyr	Phe	Val	Phe	Met	Phe	Val	Asp	Met	Asp	Asn	Phe	Leu	Leu
	35					40					45				
Ala	Val	Met	Ala	Tyr	Asp	His	Phe	Val	Ala	Val	Cys	His	Pro	Leu	His
	50				55						60				
Tyr	Thr	Ala	Lys	Val	Thr	His	Gln	Leu	Cys	Ala	Leu	Leu	Val	Ala	Gly
65					70				75					80	
Leu	Trp	Val	Val	Ala	Asn	Leu	Asn	Val	Leu	Leu	His	Thr	Leu	Leu	Met
			85					90						95	
Ala	Pro	Leu	Ser	Phe	Cys	Ala	Asp	Asn	Ala	Ile	Thr	His	Phe	Phe	Cys
		100					105						110		
Asp	Val	Thr	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Thr	His	Leu	Asn
	115					120						125			
Glu	Val	Ile	Ile	Leu	Ser	Glu	Gly	Ala	Leu	Val	Met	Ile	Thr	Pro	Phe
	130					135					140				
Leu	Cys	Ile	Leu	Ala	Ser	Tyr	Met	His	Ile	Thr	Cys	Thr	Val	Leu	Lys
145					150					155				160	
Val	Pro	Ser	Thr	Lys	Gly	Arg	Trp	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser
			165					170						175	
His	Leu	Ala	Val	Val	Leu	Leu	Phe	Tyr	Ser	Thr	Ile	Ile	Ala	Val	Tyr
		180					185						190		
Phe	Asn	Pro	Leu	Ser	Ser	His	Ser	Ala	Glu	Lys	Asp	Thr	Met	Ala	Thr
	195					200						205			
Val	Leu	Tyr	Thr	Val	Val	Thr	Pro								
	210					215									

<210> 2496

<211> 216

<212> PRT

<213> Unknown (2921657-dir-0-8 conceptual translation of range 2-649)

<400>2496

Phe	Val	Asp	Ile	Cys	Phe	Ser	Ser	Thr	Thr	Val	Pro	Lys	Met	Leu	Ala
1			5					10						15	
Asn	His	Ile	Leu	Glu	Thr	Gln	Thr	Ile	Ser	Phe	Cys	Gly	Cys	Leu	Thr
		20					25					30			
Gln	Met	Tyr	Phe	Val	Phe	Met	Phe	Val	Asp	Met	Asp	Tyr	Phe	Leu	Leu
	35					40					45				
Ala	Val	Met	Ala	Tyr	Asp	His	Phe	Val	Ala	Val	Cys	His	Pro	Leu	His
	50				55						60				
Tyr	Thr	Ala	Lys	Met	Thr	His	Gln	Leu	Cys	Ala	Leu	Leu	Val	Ala	Gly
65					70				75					80	
Leu	Trp	Val	Val	Ala	Asn	Leu	Asn	Val	Leu	Leu	His	Thr	Leu	Leu	Met
			85					90						95	
Ala	Pro	Leu	Ser	Phe	Cys	Ala	Asp	Asn	Ala	Ile	Thr	His	Phe	Phe	Cys
		100					105						110		
Asp	Val	Thr	Pro	Leu	Leu	Glu	Leu	Ser	Cys	Ser	Asp	Thr	His	Leu	Asn
	115					120						125			
Glu	Val	Ile	Ile	Leu	Ser	Glu	Gly	Ala	Leu	Val	Met	Ile	Thr	Pro	Phe

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      130              135              140
Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys
145              150              155              160
Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
      165              170              175
His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr
      180              185              190
Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr
      195              200              205
Val Leu Tyr Thr Val Val Thr Pro
      210              215

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<210> 2497

<211> 216

<212> PRT

<213> Unknown (2921653-dir-0-8 conceptual translation of range 2-649)

<400>2497

```

Phe Val Asp Ile Cys Phe Ser Ser Thr Thr Val Pro Lys Met Leu Ala
1      5      10      15
Asn His Ile Leu Glu Thr Gln Thr Ile Ser Leu Cys Gly Cys Leu Thr
      20      25      30
Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn Phe Leu Leu
      35      40      45
Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His
      50      55      60
Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
65      70      75      80
Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
      85      90      95
Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys
      100      105      110
Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
      115      120      125
Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
      130      135      140
Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys
145      150      155      160
Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
      165      170      175
His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr
      180      185      190
Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Met Pro Thr
      195      200      205
Val Leu Tyr Thr Val Val Thr Pro
      210      215

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<210> 2498

<211> 216

<212> PRT

<213> Unknown (2921655-dir-0-8 conceptual translation of range 2-649)

<400>2498

```

Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys Met Leu Ala
1      5      10      15
Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr
      20      25      30
Gln Met Tyr Phe Val Phe Thr Phe Val Asp Met Asp Asn Phe Leu Leu
      35      40      45
Ala Val Met Ala Tyr Asp His Phe Val Ala Glu Cys His Pro Leu His
50      55      60

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Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
65          70          75          80
Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
          85          90          95
Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys
          100        105        110
Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
          115        120        125
Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
130          135          140
Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys
145          150        155        160
Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
          165        170        175
His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr
          180        185        190
Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr
          195        200        205
Val Leu Tyr Thr Val Val Thr Pro
210          215

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<210> 2499

<211> 216

<212> PRT

<213> Unknown (2921651-dir-0-8 conceptual translation of range 2-649)

<400>2499

```

Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys Met Leu Ala
1          5          10          15
Asp His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr
          20          25          30
Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn Phe Leu Leu
35          40          45
Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His
50          55          60
Tyr Thr Ala Arg Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
65          70          75          80
Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
          85          90          95
Ala Pro Leu Ser Phe Tyr Ala Asp Asn Ala Ile Thr His Phe Phe Cys
          100        105        110
Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
          115        120        125
Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
130          135          140
Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys
145          150        155        160
Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
          165        170        175
His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr
          180        185        190
Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr Ile Ala Thr
          195        200        205
Val Leu Tyr Thr Val Val Thr Pro
210          215

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<210> 2500

<211> 216

<212> PRT

<213> Unknown (2921692-dir-0-8 conceptual translation of range 2-649)

<400>2500

```

Phe Val Asp Ile Cys Phe Ser Cys Thr Thr Val Pro Lys Met Leu Ala
 1           5           10           15
Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly Cys Leu Thr
           20           25           30
Gln Met Tyr Phe Val Phe Met Phe Val Asp Thr Asp Asn Phe Leu Leu
           35           40           45
Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His Pro Leu His
           50           55           60
Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Ala Gly
65           70           75           80
Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr Leu Leu Met
           85           90           95
Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His Phe Phe Cys
           100          105          110
Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
           115          120          125
Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe
           130          135          140
Leu Cys Asn Leu Ala Ser Tyr Met His Ile Thr Cys Thr Gly Leu Lys
145          150          155          160
Gly Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser
           165          170          175
His Leu Ala Val Gly Leu Leu Phe Tyr Ser Thr Ile Thr Ala Val Tyr
           180          185          190
Phe Asn Pro Leu Ser Ser His Ser Ala Ala Lys Asp Thr Met Ala Thr
           195          200          205
Val Leu Tyr Thr Val Val Thr Pro
           210          215

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<210> 2501

<211> 224

<212> PRT

<213> Unknown (4877342-dir-0-8 conceptual translation of range 2-673)

<220>

<221> VARIANT

<222> (1)...(224)

<223> Xaa = Any Amino Acid

<400>2501

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Cys Asn Leu Ser Phe Gly Asp Ile Cys Phe Ser Ser Thr Thr Val Pro
 1           5           10           15
Lys Met Leu Ala Asn His Ile Leu Arg Lys Gln Thr Ile Pro Phe Ser
           20           25           30
Arg Cys Leu Ala Gln Met Tyr Phe Val Phe Thr Phe Met Asp Met Asp
           35           40           45
Asn Phe Leu Leu Ala Met Met Ala Tyr Asp His Phe Val Ala Val Cys
           50           55           60
His Pro Leu His Tyr Tyr Ala Lys Met Thr His Gln Leu Cys Ala Leu
65           70           75           80
Leu Val Thr Gly Ser Trp Val Ile Ala Asn Leu Asp Met Leu Leu His
           85           90           95
Thr Leu Leu Met Ala Xaa Leu Ser Phe Cys Ala Asp Asn Ala Ile Pro
           100          105          110
His Phe Phe Cys Asp Val Thr Thr Leu Leu Lys Leu Ser Cys Ser Asp
           115          120          125
Thr His Leu Ser Glu Val Met Ile Leu Thr Glu Ala Arg Pro Val Met
           130          135          140
Ser Thr Pro Phe Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Asn Cys
145          150          155          160

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Ala Val Leu Arg Val Gln Ser Thr Lys Gly Arg Trp Lys Thr Phe Ser
 165 170 175
 Thr Cys Gly Ser His Leu Ala Met Val Phe Leu Phe Tyr Gly Thr Met
 180 185 190
 Ile Phe Leu Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Ile Asp
 195 200 205
 Ile Ala Ala Ala Ala Met Arg Cys Leu Tyr Met Val Thr Pro Met Leu
 210 215 220

<210> 2502

<211> 216

<212> PRT

<213> Unknown (p105-dir-0-8 conceptual translation of range 2-649)

<400>2502

Leu Val Asp Phe Cys Phe Thr Ser Ala Thr Val Pro Lys Met Leu Leu
 1 5 10 15
 Asn Ile His Arg Gln Ile Gln Ser Ile Ser His Glu Gly Cys Leu Thr
 20 25 30
 Gln Ile Tyr Phe Cys Ile Leu Leu Ala Asn Met Asp Asn Phe Leu Leu
 35 40 45
 Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Gln
 50 55 60
 Tyr Thr Thr Ile Met Ser Leu Gln Leu Cys Cys Leu Met Leu Ala Gly
 65 70 75 80
 Ser Trp Leu Ile Ala Asn Phe His Ser Leu Leu His Thr Leu Leu Met
 85 90 95
 Ala Arg Leu Asp Phe Cys Ala Lys Asn Val Met Pro Tyr Phe Phe Cys
 100 105 110
 Asp Leu Val Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Asn
 115 120 125
 Gln Leu Met Ile Leu Leu Val Gly Gly Leu Ile Val Leu Ile Pro Phe
 130 135 140
 Leu Cys Ile Leu Ile Ser Tyr Thr His Ile Val Ser Val Val Leu Lys
 145 150 155 160
 Val Pro Ser Ala Leu Gly Lys Gln Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Ile Leu Phe Tyr Gly Thr Ile Thr Gly Val Tyr
 180 185 190
 Leu Asn Pro Ser Ser Ser His Ser Ala Glu Lys Asp Ser Val Ala Ser
 195 200 205
 Val Met Tyr Met Val Val Thr Pro
 210 215

<210> 2503

<211> 216

<212> PRT

<213> Unknown (p110-dir-0-8 conceptual translation of range 2-649)

<400>2503

Phe Val Asp Leu Cys Gln Ala Ser Thr Thr Met Pro Lys Met Leu Ile
 1 5 10 15
 Asn Ile Leu Thr His Ser Lys Ala Ile Pro Tyr Ala Gly Cys Leu Ile
 20 25 30
 Gln Met Tyr Ser Phe His Leu Phe Gly Thr Met Asp Ser Phe Leu Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg
 50 55 60
 Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Ile Leu Leu Val Gly Gly
 65 70 75 80
 Pro Trp Gly Thr Thr Asn Leu Gln Ser Val Val His Thr Ser Leu Met

85								90					95			
Ala	Lys	Leu	Thr	Phe	Cys	Ala	Asp	Asn	Lys	Ile	Pro	His	Phe	Phe	Cys	
100								105					110			
Asp	Leu	Met	Pro	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Thr	His	Ile	Asn	
115								120					125			
Glu	Leu	Val	Val	Leu	Val	Phe	Gly	Ile	Phe	Met	Gly	Ile	Ser	Pro	Leu	
130								135					140			
Val	Cys	Ile	Leu	Leu	Ser	Tyr	Ile	Cys	Ile	Phe	Cys	Ala	Val	Leu	Gln	
145								150					155			
Val	Pro	Ser	Ala	Glu	Gly	Lys	Arg	Lys	Ala	Phe	Ser	Thr	Arg	Gly	Ser	
165								170					175			
His	Leu	Thr	Val	Val	Leu	Leu	Phe	Tyr	Gly	Thr	Ile	Phe	Ala	Val	Tyr	
180								185					190			
Leu	Gln	Pro	Ser	Gly	Pro	Thr	Ser	Pro	Glu	Lys	Asp	Lys	Ala	Ala	Ala	
195								200					205			
Val	Met	Cys	Ala	Val	Val	Ile	Pro									
210								215								

<210> 2504

<211> 216

<212> PRT

<213> Unknown (p94-dir-0-8 conceptual translation of range 2-649)

<400>2504

Phe 1	Val	Asp	Leu	Cys 5	Gln	Ala	Ser	Thr	Thr 10	Met	Pro	Lys	Met	Leu 15	Ile
Asn	Ile	Leu	Thr	His	Ser	Lys	Ala	Ile 25	Pro	Tyr	Ala	Gly	Cys 30	Leu	Ile
Gln	Met	Tyr	Ser	Phe	His	Leu	Phe 40	Gly	Thr	Met	Asp	Ser	Phe	Leu	Leu
Ala	Val	Met	Ala	Tyr	Asp	Arg	Phe 55	Val	Ala	Ile	Phe 60	His	Pro	Leu	Arg
Tyr 65	Ala	Thr	Ile	Met	Ser	Pro	Arg 70	Leu	Cys	Ile 75	Leu	Leu	Val	Gly 80	Gly
Pro	Trp	Gly	Thr	Thr 85	Asn	Leu	Gln	Ser	Val 90	Val	His	Thr	Ser	Leu 95	Met
Ala	Lys	Leu	Thr 100	Phe	Cys	Ala	Asp 105	Asn	Lys	Ile	Pro	His	Phe 110	Phe	Cys
Asp	Leu	Met	Pro	Leu	Leu	Lys	Leu 120	Ser	Cys	Ser	Asp	Thr 125	His	Ile	Asn
Glu 130	Leu	Val	Val	Leu	Val	Phe 135	Gly	Ile	Phe	Met	Gly 140	Ile	Ser	Pro	Leu
Val 145	Cys	Ile	Leu	Leu	Ser	Tyr 150	Ile	Cys	Ile	Phe 155	Cys	Ala	Val	Leu	Gln 160
Val	Pro	Ser	Ala	Glu 165	Gly	Lys	Arg	Lys	Ala 170	Phe	Ser	Thr	Cys	Gly 175	Ser
His	Leu	Thr	Val	Val	Leu	Val	Phe 180	Tyr	Gly 185	Thr	Ile	Phe 190	Ala	Val	Tyr
Val	Gln	Pro 195	Ser	Gly	Pro	Thr	Ser 200	Pro	Glu	Lys	Asp	Lys 205	Ala	Ala	Ala
Val	Met	Cys	Ala	Val	Val	Ile 215	Pro								

<210> 2505

<211> 169

<212> PRT

<213> Unknown (4877330-dir-0-7 conceptual translation of range 3-509)

<400>2505

Asn Leu Ser Leu Val Asp Val Phe Leu Ser Ser Thr Thr Val Pro Lys
1 5 10 15

```

Met Leu Val Asn Leu Trp Thr Gln Pro Ser His Pro Ser Val Cys Leu
      20      25      30
Ala Gln Met His Ala Phe His Leu Phe Gly Thr Ile Asp Ser Phe Leu
      35      40      45
Leu Ala Val Met Ala Ile Asp Arg Phe Met Ala Ile Val His Arg Leu
      50      55      60
Cys Tyr Leu Ala Ile Met Ser Pro Arg Val Trp Gly Leu Leu Val Gly
      65      70      75      80
Glu Pro Trp Gln Ile Thr Asn Leu Gln Ser Leu Val His Thr Cys Leu
      85      90      95
Met Ala Gln Leu Thr Phe Cys Ala Gly Ser Glu Ile Pro His Phe Phe
      100     105     110
Cys Asp Leu Ile Pro Leu Pro Lys Leu Ser Ser Ser Asp Thr His Thr
      115     120     125
Asn Glu Pro Val Ile Phe Pro Phe Gly Ile Ile Leu Gly Ile Ser Ser
      130     135     140
Leu Ala Cys Ile Leu Phe Ser Tyr Thr Ser Ile Phe Gln Ala Val Phe
      145     150     155     160
Lys Ile Leu Ser Ala Gln Val Lys Trp
      165

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<210> 2506

<211> 315

<212> PRT

<213> Unknown (3184261-dir-59-13 conceptual translation of range 6034-6978)

<400>2506

```

Met Glu Pro Glu Lys Gln Thr Glu Ile Ser Glu Phe Phe Leu Gln Gly
  1      5      10      15
Leu Ser Glu Lys Pro Glu His Gln Thr Leu Leu Phe Thr Met Phe Leu
      20      25      30
Ser Thr Tyr Leu Val Thr Ile Ile Gly Asn Ala Leu Ile Ile Leu Ala
      35      40      45
Ile Ile Thr Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Phe
      50      55      60
Asn Leu Ser Leu Val Asp Thr Leu Leu Ser Ser Thr Thr Val Pro Lys
      65      70      75      80
Met Leu Ala Asn Ile Gln Ala Gln Ser Arg Ala Ile Pro Phe Val Gly
      85      90      95
Cys Leu Thr Gln Met Tyr Ala Phe His Leu Phe Gly Thr Met Asp Ser
      100     105     110
Phe Leu Leu Ala Val Met Ala Ile Asp Arg Phe Val Ala Ile Val His
      115     120     125
Pro Gln Arg Tyr Leu Val Leu Met Cys Ser Pro Val Cys Gly Leu Leu
      130     135     140
Leu Gly Ala Ser Trp Met Ile Thr Asn Leu Gln Ser Leu Ile His Thr
      145     150     155     160
Cys Leu Met Ala Gln Leu Thr Phe Cys Ala Gly Ser Glu Ile Ser His
      165     170     175
Phe Phe Cys Asp Leu Met Pro Leu Leu Lys Leu Ser Gly Ser Asp Thr
      180     185     190
His Thr Asn Glu Leu Val Ile Phe Ala Phe Gly Ile Val Val Gly Thr
      195     200     205
Ser Pro Phe Ser Cys Ile Leu Leu Ser Tyr Ile Arg Ile Phe Trp Thr
      210     215     220
Val Phe Lys Ile Pro Ser Thr Arg Gly Lys Trp Lys Ala Phe Ser Thr
      225     230     235     240
Cys Gly Leu His Leu Thr Val Val Ser Leu Ser Tyr Gly Thr Ile Phe
      245     250     255
Ala Val Tyr Leu Gln Pro Thr Ser Pro Ser Ser Ser Gln Lys Asp Lys
      260     265     270

```

Ala Ala Ala Leu Met Cys Gly Val Phe Ile Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Ile Arg Asn Lys Asp Met Lys Ala Ala Leu Gly Lys Leu
 290 295 300
 Ile Gly Lys Val Ala Val Pro Cys Pro Arg Pro
 305 310 315

<210> 2507

<211> 216

<212> PRT

<213> Unknown (p97-dir-0-8 conceptual translation of range 2-649)

<400>2507

Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Ala
 1 5 10 15
 Asn His Val Ser Gly Asn Lys Ala Ile Pro Tyr Ala Gly Cys Arg Thr
 20 25 30
 Gln Val Phe Phe Phe Ile Trp Phe Pro Gly Val Asp Ser Ile Leu Leu
 35 40 45
 Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Pro Leu His
 50 55 60
 Tyr Ser Met Ile Met Thr Pro Lys Val Cys Ala Phe Leu Ile Val Val
 65 70 75 80
 Ser Trp Phe Gly Ala Tyr Ala Ile Ala Leu Ile His Thr Val Leu Leu
 85 90 95
 Thr His Leu Ser Phe Cys Gly His Ser Glu Ile Pro His Phe Phe Cys
 100 105 110
 Asp Leu Ser Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
 115 120 125
 Asn Leu Met Val Asn Thr Val Gly Ala Leu Thr Ile Ile Ile Pro Phe
 130 135 140
 Ile Gly Ile Leu Ile Ser Tyr Thr Gln Ile Phe Met Thr Val Leu Arg
 145 150 155 160
 Ile Pro Ser Thr Val Gly Lys Trp Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Ile Thr Val Val Ser Leu Phe Tyr Gly Thr Leu Ile Gly Val Tyr
 180 185 190
 Phe Ser Pro Thr Thr Thr His Thr Ala Gln Gln Asp Thr Ala Ala Ala
 195 200 205
 Ala Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2508

<211> 216

<212> PRT

<213> Unknown (p99-dir-0-8 conceptual translation of range 2-649)

<400>2508

Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Ala
 1 5 10 15
 Asn His Val Ser Gly Asn Lys Met Ile Pro Tyr Pro Gly Cys Leu Thr
 20 25 30
 Gln Val Phe Phe Phe Ile Trp Phe Ala Gly Ile Asp Ser Phe Leu Leu
 35 40 45
 Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Pro Leu His
 50 55 60
 Tyr Ser Thr Val Met Thr Leu Arg Val Cys Val Leu Leu Leu Met Val
 65 70 75 80
 Ser Trp Phe Ser Ala Phe Ile Asn Ala Leu Thr His Ala Ala Leu Leu
 85 90 95
 Thr Pro Leu Ser Phe Cys Gly His Asn Glu Ile Pro His Phe Phe Cys


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      100      105      110
Asp Leu Ser Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
      115      120      125
Asp Leu Met Val Tyr Thr Val Gly Ala Leu Pro Ile Ile Thr Pro Phe
      130      135      140
Ile Gly Ile Leu Ile Ser Tyr Thr Arg Ile Phe Met Ala Val Leu Arg
      145      150      155      160
Val Pro Ser Ala Gly Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
      165      170      175
His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Leu Ile Gly Val Tyr
      180      185      190
Phe Ser Pro Thr Ser Thr Arg Thr Ala Gln Glu Asp Thr Val Ala Ala
      195      200      205
Val Met Tyr Thr Val Val Thr Pro
      210      215

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<210> 2509

<211> 216

<212> PRT

<213> Unknown (p96-dir-0-8 conceptual translation of range 2-649)

<400>2509

```

Leu Val Asp Leu Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Asn
 1      5      10      15
Asn Tyr Ile Ser Gln Asn Arg Thr Ile Ser Tyr Ala Gly Cys Leu Thr
      20      25      30
Gln Val Phe Phe Phe Leu Trp Phe Ala Gly Met Asp Ser Val Leu Leu
      35      40      45
Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Ser Leu His
      50      55      60
Tyr Ser Thr Val Met Thr Pro Lys Ile Cys Ala Leu Leu Val Gly Val
      65      70      75      80
Ser Trp Phe Trp Ala Tyr Asn Asn Ala Leu Ile His Thr Val Leu Leu
      85      90      95
Thr Arg Leu Ser Phe Cys Gly His Asn Glu Ile Pro His Phe Phe Cys
      100      105      110
Asp Leu Ser Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
      115      120      125
Asp Leu Met Ile Tyr Thr Val Gly Ala Leu Thr Ile Ile Leu Pro Phe
      130      135      140
Ile Gly Ile Met Ile Ser Tyr Val His Ile Phe Met Ala Val Leu Lys
      145      150      155      160
Ile Ser Ser Val Ser Gly Lys Gln Lys Val Phe Ser Thr Cys Gly Ser
      165      170      175
His Leu Thr Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr
      180      185      190
Phe Ser Pro Thr Ser Thr His Thr Ala Gln Gln Asp Thr Ala Ala Thr
      195      200      205
Val Met Tyr Thr Val Val Thr Pro
      210      215

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<210> 2510

<211> 216

<212> PRT

<213> Unknown (p92-dir-0-8 conceptual translation of range 2-649)

<400>2510

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Leu Phe Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val
 1      5      10      15
Asn His Ile Ser Lys Asn Lys Val Ile Pro Tyr Ser Met Cys Leu Thr
      20      25      30

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Gln Thr Phe Phe Phe Ser Trp Phe Ile Gly Thr Asp Gly Val Leu Leu
 35 40 45
 Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ala Pro Leu His
 50 55 60
 Cys Thr Met Ile Ile Thr Pro Arg Val Cys Val Phe Leu Val Ala Val
 65 70 75 80
 Ser Trp Ile Trp Thr Cys Val Asn Ser Leu Ile His Thr Thr Ser Leu
 85 90 95
 Asn Arg Leu Ser Phe Cys Gly His Asn Glu Ile His His Phe Phe Cys
 100 105 110
 Asp Leu Ser Ala Leu Ile Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
 115 120 125
 Asp Leu Leu Ile Tyr Thr Val Gly Gly Leu Lys Ala Ile Val Pro Phe
 130 135 140
 Ile Gly Ile Leu Leu Ser Tyr Ile His Ile Phe Val Ala Val Leu Arg
 145 150 155 160
 Ile Pro Ser Ala Gly Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr
 180 185 190
 Phe Ser Pro Thr Ser Thr His Thr Ala Gln Lys Asp Thr Ala Val Ala
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2511

<211> 216

<212> PRT

<213> Unknown (p95-dir-0-8 conceptual translation of range 2-649)

<220>

<221> VARIANT

<222> (1)...(216)

<223> Xaa = Any Amino Acid

<400>2511

Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Thr Leu Val
 1 5 10 15
 Asn Tyr Val Ser Gly Asn Lys Ala Ile Leu Tyr Ile Ser Cys Leu Ala
 20 25 30
 Gln Val Phe Phe Phe Ser Trp Phe Ala Gly Leu Asp Ser Ile Leu Leu
 35 40 45
 Ala Ser Met Ala Tyr Asp Arg Xaa Ile Ala Ile Cys Asp Pro Leu His
 50 55 60
 Tyr Thr Thr Val Met Thr Pro Arg Val Cys Val Leu Leu Val Ala Met
 65 70 75 80
 Cys Leu Phe Gly Gly Cys Ala Asn Ser Leu Thr His Asn Ile Leu Leu
 85 90 95
 Thr Gln Leu Ser Phe Cys Gly His Thr Glu Ile Pro Leu Phe Phe Cys
 100 105 110
 Asp Leu Asn Val Val Ile Arg Leu Ala Cys Ser Asp Thr Phe Ile Asn
 115 120 125
 Asp Trp Met Ile Tyr Thr Met Gly Gly Leu Thr Ala Ile Ile Pro Phe
 130 135 140
 Ser Gly Ile Leu Ile Ser Tyr Ile His Ile Phe Val Ala Met Leu Arg
 145 150 155 160
 Ile Leu Ser Ala Gln Gly Lys Trp Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ile Ala Val Tyr Leu Leu Asn Gly Thr Ile Ile Gly Val Tyr
 180 185 190
 Leu Asn Pro Thr Ser Ser His Thr Ala Gln Gln Asp Thr Ala Ser Ala

195 200 205
 Val Met Tyr Thr Met Val Thr Pro
 210 215
 <210> 2512
 <211> 216
 <212> PRT
 <213> Unknown (p125-dir-0-8 conceptual translation of range 2-649)

<400>2512
 Phe Val Asp Leu Cys Phe Thr Thr Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15
 Asn His Ile Ser Gly Asn Lys Thr Ile Pro Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Phe Phe Phe Ile Trp Phe Ala Ser Ile Asp Ser Phe Leu Leu
 35 40 45
 Val Ala Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Leu Arg
 50 55 60
 Tyr Ala Ser Leu Met Ile Pro Arg Leu Cys Ala Leu Leu Val Ala Thr
 65 70 75 80
 Ser Trp Ser Phe Ala Cys Ile Asn Ala Leu Thr His Thr Val Leu Leu
 85 90 95
 Thr Gln Leu Ser Phe Cys Ser His Asn Glu Ile Pro His Phe Phe Cys
 100 105 110
 Asp Leu Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Ile Asn
 115 120 125
 Asp Val Leu Val Tyr Thr Val Gly Ala Leu Pro Ile Leu Met Pro Phe
 130 135 140
 Val Gly Ile Leu Val Ser Tyr Thr Arg Ile Phe Ala Ala Val Leu Arg
 145 150 155 160
 Ile Pro Ser Ala Arg Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Val Ile Gly Val Tyr
 180 185 190
 Leu Ser Pro Met Ser Tyr His Thr Val Glu Lys Asp Thr Ala Ala Ala
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2513
 <211> 216
 <212> PRT
 <213> Unknown (p123-dir-0-8 conceptual translation of range 2-649)

<400>2513
 Phe Val Asp Leu Cys Leu Thr Thr Thr Thr Val Pro Lys Met Leu Leu
 1 5 10 15
 Asn Ile Gln Thr Gln Lys Lys Thr Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30
 Gln Met Tyr Phe Phe Leu Leu Leu Leu Asp Leu Asp Asn Met Ile Leu
 35 40 45
 Ala Val Met Ala Phe Asp Arg Tyr Met Ala Ile Cys His Pro Leu His
 50 55 60
 Tyr Thr Ser Val Met Leu Pro Ser Leu Cys Gly Leu Leu Met Ala Val
 65 70 75 80
 Leu Trp Val Val Ala Asn Leu Phe Ser Leu Leu Phe Thr Leu Leu Met
 85 90 95
 Ala Gln Leu Ser Phe Cys Gly Asn Asn Thr Ile Pro His Phe Phe Cys
 100 105 110
 Asp Leu Ser Val Leu Leu Lys Leu Ser Cys Ser Asp Thr His Ile Val
 115 120 125

Glu Asn Leu Leu Leu Ile Val Ser Gly Leu Leu Gly Val Thr Pro Leu
 130 135 140
 Ile Cys Ile Leu Val Ser Tyr Ser Arg Ile Val Ala Thr Val Met Arg
 145 150 155 160
 Ile Pro Ser Ala Lys Gly Lys Arg Lys Thr Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Ala Leu Phe Tyr Cys Ala Gly Phe Gly Val Phe
 180 185 190
 Phe Thr Pro Pro Ser Ser His Ser Gly Gly Lys Asp Thr Ala Ala Ser
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2514

<211> 222

<212> PRT

<213> Unknown (3983377-dir-0-8 conceptual translation of range 1-666)

<400>2514

Ala Asn Leu Ser Ser Val Asp Ile Ser Ala Pro Ser Val Ile Val Pro
 1 5 10 15
 Lys Ala Leu Val Asn His Met Leu Gly Ser Lys Ser Ile Ser Tyr Thr
 20 25 30
 Gly Cys Met Thr Gln Ile Tyr Phe Phe Ile Thr Phe Asn Asn Met Asp
 35 40 45
 Gly Phe Leu Leu Ser Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 50 55 60
 His Pro Leu His Tyr Thr Met Met Met Arg Pro Arg Leu Cys Val Leu
 65 70 75 80
 Leu Val Ala Ile Ser Trp Ala Ile Thr Asn Leu His Ala Leu Leu His
 85 90 95
 Thr Leu Leu Met Val Arg Leu Thr Phe Cys Ser His Asn Ala Val His
 100 105 110
 His Phe Phe Cys Asp Pro Tyr Pro Ile Leu Lys Leu Ser Cys Ser Asp
 115 120 125
 Thr Phe Ile Asn Asp Leu Met Val Phe Thr Ile Gly Gly Leu Val Phe
 130 135 140
 Met Thr Pro Phe Thr Cys Ile Ile Val Ser Tyr Ala Tyr Ile Phe Ser
 145 150 155 160
 Lys Val Leu Lys Leu Lys Ser Ala His Gly Ile Arg Lys Ala Leu Ser
 165 170 175
 Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Ala Ile
 180 185 190
 Leu Gly Ile Tyr Met His Pro Ser Thr Tyr Thr Val Gln Asp Thr
 195 200 205
 Val Ala Thr Val Ile Phe Thr Val Val Thr Pro Met Val Asn
 210 215 220

<210> 2515

<211> 156

<212> PRT

<213> Unknown (902714-dir-0-6 conceptual translation of range 2-469)

<400>2515

Ile Cys His Pro Leu His Tyr Thr Val Met Met Arg Pro Arg Leu Cys
 1 5 10 15
 Val Leu Leu Val Ala Val Ser Trp Val Ile Thr Asn Leu His Ala Leu
 20 25 30
 Leu His Thr Leu Leu Met Val Gln Leu Thr Phe Cys Ser His Asn Ala
 35 40 45
 Val His His Phe Phe Cys Asp Pro Tyr Pro Ile Leu Lys Leu Ser Cys

50 55 60
 Ser Asp Thr Phe Ile Asn Asp Ile Thr Ala Phe Thr Val Gly Gly Leu
 65 70 75 80
 Thr Ser Ile Thr Pro Phe Thr Cys Ile Thr Val Ser Tyr Ala Tyr Ile
 85 90 95
 Leu Ser Ser Val Leu Lys Phe Pro Ser Ile Gln Gly Ile Arg Lys Ala
 100 105 110
 Leu Ser Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly
 115 120 125
 Ala Ile Leu Gly Val Tyr Met His Pro Ser Ser Thr Tyr Ser Leu Gln
 130 135 140
 Asp Thr Val Ala Thr Ala Phe Phe Thr Val Val Thr
 145 150 155

<210> 2516

<211> 216

<212> PRT

<213> Unknown (OST034-dir-0-8 conceptual translation of range 2-649)

<400>2516

Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val
 1 5 10 15
 Asn Ile Gln Thr Lys Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr
 20 25 30
 Gln Met Tyr Phe Ser Ile Val Phe Val Val Ile Asp Asn Leu Leu Leu
 35 40 45
 Gly Thr Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro Leu Asn
 50 55 60
 Tyr Thr Ile Leu Met Arg Pro Arg Phe Gly Ile Leu Leu Thr Val Ile
 65 70 75 80
 Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu
 85 90 95
 Ile Gln Leu Leu Phe Cys Asn His Asn Thr Leu Pro His Phe Phe Cys
 100 105 110
 Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Leu Ile Asn
 115 120 125
 Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe
 130 135 140
 Thr Leu Ser Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Arg
 145 150 155 160
 Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Leu Leu Phe Tyr Gly Thr Ile Val Gly Val Tyr
 180 185 190
 Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala
 195 200 205
 Val Leu Phe Thr Val Val Thr Pro
 210 215

<210> 2517

<211> 323

<212> PRT

<213> Unknown (p156-dir-0-12 conceptual translation of range 34-1003)

<400>2517

Ser Glu Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu
 1 5 10 15
 Leu Trp Gly Leu Ser Asp Gln Pro Gln Gln His Ile Phe Phe Leu
 20 25 30
 Leu Phe Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile
 35 40 45

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Val Leu Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Phe
 50                      55                      60
Phe Leu Ala Ser Leu Ser Cys Ala Asp Ile Phe Phe Thr Ser Thr Thr
 65                      70                      75                      80
Val Pro Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser
                      85                      90                      95
Tyr Ala Gly Cys Leu Ala Gln Leu Tyr Phe Phe Gly Thr Ala Leu Leu
                      100                    105                    110
Leu Leu Thr Phe Gly Asp Met Asp Ile Phe Leu Leu Ala Thr Met Ala
                      115                    120                    125
Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His Tyr Met Met Ile
                      130                    135                    140
Met Ser Leu His Arg Cys Ala Leu Leu Val Thr Ala Cys Trp Thr Leu
 145                      150                    155                    160
Thr Ser Leu Val Ala Met Thr His Thr Phe Leu Ile Phe Arg Leu Ser
                      165                    170                    175
Phe Cys Ser Lys Ile Leu Pro Asp Phe Phe Cys Asp Leu Gly Pro Leu
                      180                    185                    190
Met Lys Val Ser Cys Ser Asp Ala Gln Val Asn Glu Leu Val Leu Leu
                      195                    200                    205
Phe Leu Gly Gly Ala Val Ile Leu Ile Pro Phe Met Leu Ile Leu Val
 210                      215                    220
Ser Tyr Ile Arg Ile Val Ser Ala Ile Leu Arg Ala Pro Ser Ala Gln
 225                      230                    235                    240
Gly Arg Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Val Val
                      245                    250                    255
Ala Leu Phe Phe Gly Thr Val Ile Arg Ala Tyr Leu Cys Pro Ser Ser
                      260                    265                    270
Ser Ser Ser Asn Ser Val Lys Glu Asp Thr Val Ala Ala Val Met Tyr
 275                      280                    285
Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn
 290                      295                    300
Lys Asp Met Lys Ala Ala Val Val Arg Leu Leu Lys Gly Arg Val Ser
 305                      310                    315                    320
Leu Ser Gln

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<210> 2518

<211> 320

<212> PRT

<213> Unknown (p38-dir-0-11 conceptual translation of range 34-993)

<400>2518

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Ser Asp Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu
 1                      5                      10                    15
Leu Ser Gly Leu Ser Asp Gln Pro Gln Gln His Ile Leu Phe Leu
                      20                    25                    30
Leu Phe Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile
                      35                    40                    45
Val Leu Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Phe
 50                      55                      60
Phe Leu Ala Ser Leu Ser Cys Ala Asp Ile Phe Phe Thr Ser Thr Thr
 65                      70                      75                      80
Val Pro Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser
                      85                      90                      95
Tyr Ala Gly Cys Leu Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly Asp
                      100                    105                    110
Met Asp Ile Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Met Ala
                      115                    120                    125
Ile Cys His Pro Leu His Tyr Met Met Ile Met Ser Leu His Arg Cys
 130                      135                    140

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Ala Leu Leu Val Thr Ala Cys Trp Thr Leu Thr Ser Leu Val Ala Met
 145 150 155 160
 Thr His Thr Phe Leu Ile Phe Arg Leu Ser Phe Cys Ser Lys Ile Ile
 165 170 175
 Pro Asp Phe Phe Cys Asp Leu Gly Pro Leu Met Lys Val Ser Cys Ser
 180 185 190
 Asp Thr Gln Val Ser Glu Leu Val Leu Phe Leu Gly Gly Ala Val
 195 200 205
 Ile Leu Ile Pro Phe Met Leu Ile Leu Val Ser Tyr Ile Arg Ile Val
 210 215 220
 Ser Ala Ile Leu Arg Ala Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Gly Ser His Leu Val Val Val Ala Leu Phe Phe Gly Thr
 245 250 255
 Val Ile Arg Ala Tyr Leu Cys Pro Ser Ser Ser Ser Ser Asn Ser Val
 260 265 270
 Asp Glu Asp Thr Ala Ala Ala Val Met Tyr Thr Val Val Thr Pro Leu
 275 280 285
 Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Ala Ala
 290 295 300
 Val Val Arg Leu Leu Lys Gly Arg Val Ser Phe Ser Gln Gly Gln Gly
 305 310 315 320

<210> 2519

<211> 317

<212> PRT

<213> Unknown (p27-dir-0-11 conceptual translation of range 34-984)

<220>

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400>2519

Ser Glu Leu Leu Glu Gly Gly Asn Gln Thr Ser Thr Phe Glu Phe Leu
 1 5 10 15
 Leu Trp Gly Leu Ser Asp Gln Pro Gln Gln Gln His Ile Phe Phe Leu
 20 25 30
 Leu Phe Leu Trp Met Tyr Val Val Thr Val Ala Gly Asn Leu Leu Ile
 35 40 45
 Val Leu Ala Ile Gly Thr Asp Thr His Leu His Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Ala Ser Leu Ser Cys Ala Asp Ile Phe Ser Thr Ser Thr Thr
 65 70 75 80
 Val Pro Lys Ala Leu Val Asn Ile Gln Thr Gln Ser Arg Ser Ile Ser
 85 90 95
 Tyr Ala Gly Cys Leu Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly Asp
 100 105 110
 Met Asp Ile Phe Leu Pro Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Leu Leu His Tyr Met Met Ile Met Ser Leu His Arg Cys
 130 135 140
 Ala Phe Leu Val Thr Ala Cys Trp Thr Leu Thr Ser Leu Leu Ala Met
 145 150 155 160
 Thr Arg Thr Phe Leu Ile Phe Arg Leu Ser Leu Cys Ser Xaa Ile Leu
 165 170 175
 Pro Gly Phe Phe Cys Asp Leu Gly Pro Leu Met Lys Val Ser Cys Ser
 180 185 190
 Asp Ala Gln Val Asn Glu Leu Val Leu Leu Phe Leu Gly Gly Ala Val
 195 200 205
 Ile Leu Ile Pro Phe Met Leu Ile Leu Val Ser Tyr Ile Arg Ile Val

210	215	220
Ser Ala Ile Leu Arg Ala	Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe	
225	230	235
Ser Thr Cys Asp Ser His	Leu Val Val Val Ala Leu Phe Phe Gly Thr	240
	245	250
Val Ile Arg Ala Tyr Leu	Cys Pro Ser Ser Ser Ser Ser Asn Ser Val	255
	260	265
Lys Glu Asp Thr Ala Ala	Ala Val Met Tyr Thr Val Val Thr Pro Leu	270
	275	280
Leu Asn Pro Phe Ile Tyr	Ser Met Arg Asn Lys Asp Met Lys Ala Ala	285
	290	300
Val Val Arg Leu Leu Lys	Gly Arg Val Ser Phe Ser Gln	
305	310	315

<210> 2520

<211> 242

<212> PRT

<213> Unknown (p80-dir-0-9 conceptual translation of range 5-731)

<400>2520

Thr Asp Ile Phe Phe Thr	Ser Thr Thr Val Pro Lys Ala Leu Val Asn	
1	5	10
Ile Gln Thr Gln Ser Thr	Ser Ile Ser Tyr Ala Gly Cys Leu Ala Gln	15
	20	25
Leu Tyr Phe Phe Leu Thr	Phe Gly Asp Met Asp Ile Phe Leu Leu Ala	30
	35	40
Val Met Ala Tyr Asp Arg	Tyr Val Ala Ile Cys His Pro Leu His Tyr	45
	50	55
Met Met Ile Met Ser Leu	Arg Arg Cys Ala Val Leu Val Ala Ala Cys	60
	65	70
Trp Thr Leu Thr Ser Leu	Val Ala Met Thr His Thr Phe Leu Ile Ser	75
	85	90
Gln Leu Ser Phe Cys Ser	Lys Ile Ile Pro Asp Phe Phe Cys Asp Leu	80
	100	105
Gly Pro Leu Met Lys Val	Ser Cys Phe Asp Thr Gln Val Asn Glu Leu	95
	115	120
Val Leu Leu Phe Leu Gly	Gly Thr Val Ile Leu Ile Pro Phe Met Leu	100
	130	135
Val Leu Val Ser Tyr Ile	Gln Ile Val Ser Ala Ile Leu Arg Ala Pro	110
	145	150
Ser Ala Gln Gly Arg Arg	Lys Ala Phe Ser Thr Cys Gly Ser His Leu	120
	165	170
Val Val Val Ala Leu Phe	Phe Gly Thr Val Ile Arg Ala Tyr Leu Cys	130
	180	185
Pro Ser Ser Ser Ser Ser	Ser Val Glu Glu Asp Thr Ala Ala Ala	140
	195	200
Val Met Tyr Thr Val Val	Thr Pro Leu Leu Asn Pro Phe Ile Tyr Ser	150
	210	215
Leu Arg Asn Lys Asp Met	Lys Ala Ala Val Val Arg Leu Leu Lys Gly	160
	225	230
Arg Val		235
		240

<210> 2521

<211> 225

<212> PRT

<213> Unknown (3983403-dir-0-8 conceptual translation of range 1-675)

<400>2521

Ala Thr Leu Ser Cys Val	Asp Ile Leu Phe Thr Ser Thr Thr Val Pro
1	5
	10
	15

Lys Ala Leu Val Asn Ile His Thr Gln Ser Arg Thr Ile Ser Tyr Ala
 20 25 30
 Gly Cys Leu Val Gln Leu Tyr Phe Phe Leu Thr Phe Gly Asp Met Asp
 35 40 45
 Ile Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 50 55 60
 His Pro Leu His Tyr Arg Met Ile Met Ser Phe Gln Arg Cys Ser Leu
 65 70 75 80
 Leu Val Thr Val Cys Trp Thr Leu Thr Thr Val Val Ala Met Thr His
 85 90 95
 Thr Phe Leu Ile Phe Arg Leu Ser Phe Cys Ser Gln Lys Val Ile Pro
 100 105 110
 Asp Phe Phe Cys Asp Leu Gly Pro Leu Met Lys Ile Ala Cys Ser Glu
 115 120 125
 Thr Arg Ile Asn Glu Leu Val Leu Leu Phe Leu Gly Gly Ala Val Ile
 130 135 140
 Leu Ile Pro Phe Leu Leu Ile Leu Met Ser Tyr Ile Arg Ile Val Ser
 145 150 155 160
 Ala Ile Leu Arg Val Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe Ser
 165 170 175
 Thr Cys Gly Ser His Leu Ser Val Val Ala Leu Phe Phe Gly Thr Val
 180 185 190
 Ile Arg Ala Tyr Leu Cys Pro Ser Ser Ser Ser Ser Asn Ser Val Val
 195 200 205
 Glu Asp Thr Ala Ala Ala Val Met Tyr Thr Val Val Thr Pro Val Leu
 210 215 220
 Asn
 225

<210> 2522

<211> 217

<212> PRT

<213> Unknown (p144-dir-0-8 conceptual translation of range 5-654)

<400>2522

Asp Asp Ile Leu Leu Val Ser Thr Ile Val Pro Lys Ala Leu Val Asn
 1 5 10 15
 Ile His Thr Gln Ser Arg Thr Ile Ser Tyr Ala Gly Cys Leu Val Gln
 20 25 30
 Leu Tyr Phe Phe Leu Thr Phe Gly Asp Met Asp Ile Phe Leu Leu Ala
 35 40 45
 Thr Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His Tyr
 50 55 60
 Arg Met Ile Met Ser Phe Gln Arg Cys Ser Leu Val Thr Val Cys
 65 70 75 80
 Trp Ile Leu Thr Thr Val Val Ala Met Thr His Thr Phe Leu Ile Phe
 85 90 95
 Trp Phe Ser Phe Tyr Ser Lys Lys Val Ile Pro Gly Phe Phe Cys Asp
 100 105 110
 Leu Glu Pro Leu Ile Lys Ile Pro Cys Ser Glu Thr Arg Ile Asn Glu
 115 120 125
 Leu Val Leu Leu Phe Leu Gly Ser Ala Val Val Phe Ile Leu Leu Leu
 130 135 140
 Leu Ile Leu Val Ser Tyr Ile Gln Ile Val Ser Ala Ile Phe Arg Val
 145 150 155 160
 Pro Ser Ala Gln Gly Arg His Lys Ala Phe Ser Thr Cys Gly Ser His
 165 170 175
 Leu Ser Val Val Ala Leu Phe Phe Gly Thr Val Ile Arg Ala Tyr Leu
 180 185 190
 Cys Pro Ser Ser Ser Ser Ser Asn Ser Val Val Glu Asp Thr Ala Ala
 195 200 205

Ala Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 2523

<211> 215

<212> PRT

<213> Unknown (p111-dir-0-8 conceptual translation of range 2-646)

<220>

<221> VARIANT

<222> (1)...(215)

<223> Xaa = Any Amino Acid

<400>2523

Val	Val	Asp	Val	Cys	Phe	Ser	Ser	Thr	Thr	Val	Pro	Lys	Met	Leu	Ala
1				5					10					15	
Asp	Met	Gln	Thr	Gly	Ser	His	Thr	Ile	Ser	Gln	Ala	Asp	Cys	Leu	Ser
		20						25					30		
Gln	Val	Tyr	Phe	Ser	Ile	Leu	Phe	Gly	Asp	Leu	Asp	Asp	Phe	Leu	Leu
		35					40					45			
Ala	Val	Met	Ser	Phe	Asp	Xaa	Tyr	Met	Ala	Ile	Cys	Arg	Pro	Leu	Cys
		50				55					60				
Tyr	Ala	Thr	Ala	Met	Ser	Ser	Gln	Cys	Cys	Val	Leu	Leu	Val	Ala	Thr
		65			70				75					80	
Cys	Trp	Val	Ile	Ala	Gln	Leu	Asn	Ser	Leu	Leu	His	Thr	Val	Leu	Leu
			85						90					95	
Ala	Gln	Leu	Thr	Phe	Cys	Ala	Asp	His	Thr	Ile	Pro	His	Phe	Phe	Cys
		100						105					110		
Asp	Leu	Ala	Leu	Leu	Leu	Pro	Leu	Ser	Cys	Ser	Asp	Thr	Ser	Ile	Asn
		115					120					125			
Glu	Leu	Val	Leu	Met	Ser	Met	Gly	Gly	Ala	Gly	Ile	Leu	Ile	Pro	Leu
		130				135					140				
Met	Cys	Ile	Leu	Gly	Ser	Tyr	Ala	Gln	Ile	Ile	Ser	Ala	Ile	Leu	Arg
		145			150					155				160	
Met	Pro	Ser	Ala	Gly	Ser	Lys	Arg	Ile	Ala	Phe	Ser	Thr	Ser	Ser	Ser
			165					170						175	
His	Leu	Ala	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Val	Ile	Ser	Glu	Tyr
		180						185					190		
Leu	Cys	Pro	Ser	Pro	Ser	Gly	Ser	Ser	Asp	Glu	Ser	Ser	Leu	Ala	Ala
		195					200					205			
Val	Leu	Tyr	Ala	Val	Val	Thr									
		210				215									

<210> 2524

<211> 216

<212> PRT

<213> Unknown (2921629-dir-0-8 conceptual translation of range 2-649)

<400>2524

Phe	Val	Asp	Met	Gly	Leu	Thr	Ser	Ser	Thr	Val	Thr	Lys	Met	Leu	Val
1				5					10					15	
Asn	Ile	Gln	Thr	Arg	His	His	Thr	Ile	Thr	Tyr	Thr	Gly	Cys	Leu	Thr
		20						25					30		
Gln	Met	Tyr	Phe	Phe	Leu	Met	Phe	Gly	Asp	Leu	Asp	Ser	Phe	Phe	Leu
		35					40					45			
Ala	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu	Cys
		50				55					60				
Tyr	Ser	Thr	Val	Met	Arg	Pro	Gln	Val	Cys	Ala	Leu	Met	Leu	Ala	Leu
		65			70				75					80	
Cys	Trp	Val	Leu	Thr	Asn	Ile	Val	Ala	Leu	Thr	His	Thr	Phe	Leu	Met
			85					90						95	

Ala Arg Leu Ser Phe Cys Val Thr Gly Glu Ile Ala His Phe Phe Cys
 100 105 110
 Asp Ile Thr Pro Val Leu Lys Leu Ser Cys Ser Asp Thr His Ile Asn
 115 120 125
 Glu Met Met Val Phe Val Leu Gly Gly Thr Val Leu Ile Val Pro Phe
 130 135 140
 Leu Cys Ile Val Thr Ser Tyr Ile His Ile Val Pro Ala Ile Leu Arg
 145 150 155 160
 Val Arg Thr Arg Gly Gly Val Gly Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Ala Tyr
 180 185 190
 Leu Cys Pro Pro Ser Ile Ala Ser Glu Glu Lys Asp Ile Ala Ala Ala
 195 200 205
 Ala Met Tyr Thr Ile Val Thr Pro
 210 215

<210> 2525

<211> 342

<212> PRT

<213> Unknown (1256388-dir-2-13 conceptual translation of range 379-1402)

<220>

<221> VARIANT

<222> (1)...(342)

<223> Xaa = Any Amino Acid

<400>2525

Phe Xaa Leu Ser Phe Leu Asn Tyr Arg Cys Ser Ile Arg Met Glu Asn
 1 5 10 15
 Gln Ser Ser Val Ser Glu Phe Phe Leu Arg Gly Ile Ser Gly Phe Pro
 20 25 30
 Glu Gln Gln Gln Leu Leu Tyr Gly Leu Phe Leu Cys Met Tyr Leu Val
 35 40 45
 Thr Leu Thr Gly Asn Val Leu Ile Ile Leu Ala Ile Gly Ser Asp Pro
 50 55 60
 His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser Phe Ala
 65 70 75 80
 Asp Met Gly Leu Ile Ser Ser Thr Val Thr Lys Met Leu Phe Asn Val
 85 90 95
 Gln Thr Gln Cys His Thr Ile Ser Tyr Thr Gly Cys Leu Thr Gln Met
 100 105 110
 Tyr Leu Phe Met Met Phe Gly Asp Leu Asp Ser Phe Phe Leu Ala Val
 115 120 125
 Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His Tyr Ser
 130 135 140
 Thr Ile Met Asn Ala Arg Ile Cys Val Leu Met Leu Ile Leu Cys Trp
 145 150 155 160
 Ile Leu Thr Asn Val Val Ala Leu Thr His Thr Leu Leu Met Ala Arg
 165 170 175
 Leu Ser Phe Cys Val Val Gly Glu Ile Ala His Phe Phe Cys Asp Val
 180 185 190
 Thr Ser Val Met Lys Leu Ser Cys Ser Asp Thr His Val Asn Glu Leu
 195 200 205
 Val Leu Ser Gly Phe Gly Gly Thr Val Leu Met Val Pro Phe Val Ser
 210 215 220
 Ile Val Ile Ser Tyr Val His Ile Val Phe Ala Val Leu Arg Ile Gln
 225 230 235 240
 Ser Ser Gly Gly Ser Ser Lys Ala Phe Ser Thr Cys Ser Ser His Leu
 245 250 255
 Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Val Tyr Leu Phe

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<210> 2526
<211> 216
<212> PRT
<213> Unknown (p101-dir-0-8 conceptual translation of range 2-649)
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<210> 2527
<211> 176
<212> PRT
<213> Unknown (3273640-dir-0-7 conceptual translation of range 4-531)
```

1535

```

Asp Leu Thr Pro Leu Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn
65          70          75          80
Lys Ile Phe Val Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe
      85          90          95
Ile Cys Ile Leu Ala Ser Tyr Val Arg Ile Ile Val Ala Ile Met Lys
      100        105        110
Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser
      115        120        125
His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
      130        135        140
Leu Cys Pro Ser Ser Val Arg Thr Ala Val Lys Glu Lys Ala Ser Ala
145          150        155        160
Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Cys Ser
      165        170        175

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<210> 2528

<211> 175

<212> PRT

<213> Unknown (3273644-dir-0-7 conceptual translation of range 4-528)

<400>2528

```

Ala Leu Glu Tyr Asp Arg Phe Leu Ala Ile Cys His Pro Leu His Tyr
1          5          10          15
Thr Thr Ile Met Ser Pro Gln Leu Cys Gly Leu Leu Ala Gly Gly Leu
      20          25          30
Trp Met Leu Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met Ala
      35          40          45
Arg Leu Val Phe Cys Gly Asn Asn Lys Ile Pro His Tyr Phe Cys Asp
      50          55          60
Leu Thr Pro Leu Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn Lys
65          70          75          80
Ile Phe Val Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe Ile
      85          90          95
Cys Ile Leu Ala Ser Tyr Val Arg Ile Ile Val Ala Ile Met Lys Val
      100        105        110
Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser His
      115        120        125
Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr Leu
      130        135        140
Cys Pro Ser Ser Val Arg Thr Ala Val Lys Glu Lys Ala Ser Ala Val
145          150        155        160
Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe Ile Cys Ser
      165        170        175

```

<210> 2529

<211> 158

<212> PRT

<213> Unknown (3273656-dir-0-6 conceptual translation of range 4-477)

<400>2529

```

Ala Leu Glu Tyr Asp Arg Phe Leu Ala Ile Cys His Pro Leu His Tyr
1          5          10          15
Thr Thr Thr Met Ser Pro Gln Leu Cys Gly Leu Leu Ala Gly Gly Leu
      20          25          30
Trp Met Leu Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met Ala
      35          40          45
Arg Leu Val Phe Cys Gly Asn Asn Lys Ile Pro His Tyr Phe Cys Asp
      50          55          60
Leu Thr Pro Leu Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn Lys
65          70          75          80
Ile Phe Val Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe Ile

```


Thr Thr Ile Gly Val Tyr Leu Cys Pro Ser Ser Val Arg Thr Ala Val
 130 135 140
 Lys Glu Lys Ala Ser Ala Val Met Tyr Thr Ala Val Thr
 145 150 155

<210> 2532

<211> 313

<212> PRT

<213> Unknown (p82-dir-0-11 conceptual translation of range 1-939)

<400>2532

Met Glu Pro Arg Asn Gln Thr Ser Ala Ser Gln Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Glu Lys Pro Glu Gln Glu Thr Leu Leu Phe Ser Leu Phe Phe
 20 25 30
 Cys Met Tyr Leu Val Met Val Val Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Leu Val Asp Phe Cys Leu Ala Thr Asn Thr Ile Pro Lys
 65 70 75 80
 Met Leu Val Ser Leu Gln Thr Gly Ser Lys Ala Ile Ser Tyr Pro Cys
 85 90 95
 Cys Leu Ile Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser
 100 105 110
 Val Ile Ile Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Ala Lys Ile Met Ser Leu Arg Leu Cys Arg Leu Leu
 130 135 140
 Val Gly Ala Leu Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile
 145 150 155 160
 Leu Leu Met Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His
 165 170 175
 Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr
 180 185 190
 Ser Val Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala
 195 200 205
 Thr Pro Phe Val Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Val Ala
 210 215 220
 Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile
 245 250 255
 Gly Val Tyr Leu Cys Pro Ser Ser Val Leu Thr Thr Val Lys Glu Lys
 260 265 270
 Ala Ser Ala Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Leu Lys Gly Ala Leu Arg Lys Leu
 290 295 300
 Val Asn Arg Lys Ile Thr Ser Ser Ser
 305 310

<210> 2533

<211> 157

<212> PRT

<213> Unknown (902331-dir-0-6 conceptual translation of range 2-472)

<400>2533

Ile Cys His Pro Leu His Tyr Thr Ala Arg Met Asn Leu Cys Leu Cys
 1 5 10 15
 Val Gln Leu Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His Ala Leu

```

      20      25      30
Leu His Thr Val Leu Ile Ala Gln Leu Ser Phe Cys Ala Ser Asn Ile
      35      40      45
Ile His His Phe Leu Cys Asp Leu Asn Pro Leu Leu Gln Leu Ser Cys
      50      55      60
Ser Asp Val Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly Asp Leu
      65      70      75      80
Leu Ala Leu Thr Pro Leu Val Cys Ile Leu Val Ser Tyr Gly Leu Ile
      85      90      95
Phe Ser Thr Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln Arg Ala
      100      105      110
Val Ser Thr Cys Ser Cys His Leu Ser Val Val Val Leu Phe Tyr Gly
      115      120      125
Thr Ala Ile Ala Val Tyr Phe Ser Pro Ser Ser Pro His Met Pro Glu
      130      135      140
Ser Asp Thr Leu Ser Thr Ile Met Tyr Ser Met Val Ala
      145      150      155

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<210> 2534

<211> 217

<212> PRT

<213> Unknown (p152-rev-0-8 conceptual translation of range 2-652)

<400>2534

```

Phe Leu Asp Ile Gly Phe Ile Ser Thr Ile Ile Pro Lys Met Leu Asp
 1      5      10      15
His Ile Ser Ser Gly Ile Lys Leu Ile Ser Tyr Gly Glu Cys Leu Thr
      20      25      30
Gln Leu Tyr Phe Ser Gly Leu Phe Ala Asp Leu Asp Asn Asn Phe Leu
      35      40      45
Leu Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile Ser His Pro Leu
      50      55      60
His Tyr Ala Leu Thr Met Asn Ser Gln Arg Cys Val Leu Leu Val Ala
      65      70      75      80
Val Ser Trp Val Ile Thr Ile Leu His Ala Leu Val His Thr Leu Leu
      85      90      95
Val Thr Arg Leu Ser Phe Cys Gly Pro Asn Ile Ile Pro His Phe Phe
      100      105      110
Cys Asp Leu Val Pro Leu Leu Lys Leu Ala Cys Ser Ser Thr Cys Val
      115      120      125
Asn Asp Leu Val Leu Ile Leu Val Ala Gly Thr Leu Leu Ile Ala Pro
      130      135      140
Phe Val Cys Ile Leu Met Ser Tyr Phe Tyr Ile Ala Leu Ala Ile Leu
      145      150      155      160
Arg Ile Asp Ser Pro Arg Gly Lys Gln Arg Ala Phe Ser Ser Cys Thr
      165      170      175
Ser His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Ala Ile Gly Val
      180      185      190
Tyr Leu Cys Pro Pro Ser Ser His Ser Asp Gly Lys Asp Arg Val Phe
      195      200      205
Ser Val Met Tyr Thr Val Val Thr Pro
      210      215

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<210> 2535

<211> 156

<212> PRT

<213> Unknown (902317-dir-0-6 conceptual translation of range 5-472)

<400>2535

```

Cys His Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val
 1      5      10      15

```


Lys Met Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu
 20 25 30
 His Thr Phe Leu Met Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile
 35 40 45
 Pro His Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr
 50 55 60
 Ser Thr Tyr Leu Asn Thr Leu Met Ile His Thr Glu Gly Ala Val Val
 65 70 75 80
 Ile Ser Gly Ala Leu Ala Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile
 85 90 95
 Leu Val Val Leu Arg Ile Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe
 100 105 110
 Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly Thr
 115 120 125
 Leu Ser Trp Val Tyr Phe Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys
 130 135 140
 Gly Arg Ile Ile Thr Val Val Tyr Thr Val Val Thr
 145 150 155

<210> 2536

<211> 215

<212> PRT

<213> Unknown (OST226-dir-0-8 conceptual translation of range 2-646)

<400>2536

Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Gln
 1 5 10 15
 Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr Thr Gly Cys Leu Ala
 20 25 30
 Gln Thr Tyr Ser Ser Leu Leu Arg Arg His Glu Asn Phe Ile Leu Ala
 35 40 45
 Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Phe His Tyr
 50 55 60
 Thr Met Ile Leu Thr Arg Met Leu Cys Val Lys Met Val Val Met Cys
 65 70 75 80
 His Ala Leu Ser His Leu His Ala Met Leu His Thr Phe Leu Met Gly
 85 90 95
 Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile Pro His Phe Phe Cys Asp
 100 105 110
 Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr Ser Thr Tyr Leu Asn Thr
 115 120 125
 Leu Met Ile His Thr Glu Gly Ala Val Val Ile Ser Gly Ala Leu Ala
 130 135 140
 Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile Leu Val Val Leu Arg Ile
 145 150 155 160
 Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe Ser Thr Arg Gly Ser His
 165 170 175
 Leu Thr Val Val Ala Ile Phe Tyr Gly Thr Leu Ser Trp Val Tyr Phe
 180 185 190
 Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys Gly Arg Ile Ile Thr Val
 195 200 205
 Val Tyr Thr Val Val Thr Pro
 210 215

<210> 2537

<211> 319

<212> PRT

<213> Unknown (4190944-dir-20-13 conceptual translation of range 2175-3131)

<220>

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400>2537

Gln Gln Met Asp Asn Ser Asn Trp Thr Ser Val Ser His Phe Val Leu
 1 5 10 15
 Leu Gly Ile Ser Thr His Pro Glu Glu Gln Ile Pro Leu Phe Leu Val
 20 25 30
 Phe Ser Leu Met Tyr Ala Ile Asn Ile Ser Gly Asn Leu Ala Ile Ile
 35 40 45
 Thr Leu Ile Leu Ser Ala Pro Arg Leu His Ile Pro Met Tyr Ile Phe
 50 55 60
 Leu Ser Asn Leu Ala Leu Thr Asp Ile Cys Phe Thr Ser Thr Thr Val
 65 70 75 80
 Pro Lys Met Leu Gln Ile Ile Phe Ser Pro Thr Lys Val Ile Ser Tyr
 85 90 95
 Thr Gly Cys Leu Ala Gln Thr Tyr Phe Phe Ile Cys Phe Ala Val Met
 100 105 110
 Glu Asn Phe Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile
 115 120 125
 Cys His Pro Phe His Tyr Thr Met Ile Leu Thr Arg Met Leu Cys Val
 130 135 140
 Lys Met Val Val Met Cys His Ala Leu Ser His Leu His Ala Met Leu
 145 150 155 160
 His Thr Phe Leu Ile Gly Gln Leu Ile Phe Cys Ala Asp Asn Arg Ile
 165 170 175
 Pro His Phe Phe Cys Asp Leu Tyr Ala Leu Met Lys Ile Ser Cys Thr
 180 185 190
 Ser Thr Tyr Leu Asn Thr Leu Met Ile His Thr Glu Gly Ala Val Val
 195 200 205
 Ile Ser Gly Ala Leu Ala Phe Ile Thr Ala Ser Tyr Ala Cys Ile Ile
 210 215 220
 Leu Val Val Leu Arg Ile Pro Ser Ala Lys Gly Arg Trp Lys Thr Phe
 225 230 235 240
 Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly Thr
 245 250 255
 Leu Ser Trp Val Tyr Phe Arg Pro Leu Ser Ser Tyr Ser Val Thr Lys
 260 265 270
 Gly Arg Ile Ile Thr Val Val Tyr Thr Val Val Thr Pro Met Leu Asn
 275 280 285
 Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Val Lys Gly Gly Phe Met
 290 295 300
 Lys Trp Met Ser Arg Met Gln Thr Phe Phe Phe Arg Xaa Asn Pro
 305 310 315

<210> 2538

<211> 326

<212> PRT

<213> Unknown (4190944-dir-490-12 conceptual translation of range 49118-50095)

<220>

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400>2538

Ile Cys Tyr Ser Val Ser Leu Ser Leu Gly Glu Pro Thr Thr Met Gly
 1 5 10 15
 Arg Asn Asn Leu Thr Arg Pro Ser Glu Phe Ile Leu Leu Gly Leu Ser
 20 25 30

Ser Arg Pro Glu Asp Gln Lys Pro Leu Phe Ala Val Phe Leu Pro Ile
 35 40 45
 Tyr Leu Ile Thr Val Ile Gly Asn Leu Leu Ile Ile Leu Ala Ile Arg
 50 55 60
 Ser Asp Thr Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Ile Leu
 65 70 75 80
 Ser Phe Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys Met Leu
 85 90 95
 Val Asn Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Gly Glu Cys Leu
 100 105 110
 Thr Gln Met Tyr Phe Phe Leu Ala Phe Gly Asn Thr Asp Ser Tyr Leu
 115 120 125
 Leu Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Phe
 130 135 140
 His Tyr Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu Leu Val
 145 150 155 160
 Leu Ser Phe Cys Ile Pro His Phe His Ser Leu Leu His Ile Leu Leu
 165 170 175
 Thr Asn Gln Leu Ile Phe Cys Ala Ser Asn Val Ile His His Phe Phe
 180 185 190
 Cys Asp Asp Gln Pro Val Leu Lys Leu Ser Cys Ser Ser His Phe Val
 195 200 205
 Lys Glu Ile Thr Val Met Thr Glu Gly Leu Ala Val Ile Met Thr Pro
 210 215 220
 Phe Ser Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Thr Val Leu
 225 230 235 240
 Lys Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly
 245 250 255
 Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile Ser Tyr Val
 260 265 270
 Tyr Phe Gln Pro Leu Ser Asn Tyr Thr Val Lys Asp Gln Ile Ala Thr
 275 280 285
 Ile Ile Tyr Thr Val Leu Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser
 290 295 300
 Leu Arg Asn Lys Asp Met Lys Gln Gly Leu Ala Lys Leu Met His Arg
 305 310 315 320
 Met Lys Cys Gln Xaa Lys
 325

<210> 2539

<211> 214

<212> PRT

<213> Unknown (hg23-dir-0-8 conceptual translation of range 4-645)

<400>2539

Val Asp Ile Cys Tyr Val Thr Val Ile Ile Pro Lys Met Leu Val Asn
 1 5 10 15
 Phe Leu Ser Glu Thr Lys Thr Ile Ser Tyr Ser Glu Cys Leu Thr Gln
 20 25 30
 Met Tyr Phe Phe Leu Ala Cys Gly Asn Thr Asp Ser Tyr Leu Leu Ala
 35 40 45
 Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Phe His Tyr
 50 55 60
 Ile Thr Ile Met Ser His Arg Cys Cys Val Leu Leu Leu Val Leu Ser
 65 70 75 80
 Phe Cys Ile Pro His Leu His Ser Leu Leu His Ile Leu Leu Thr Asn
 85 90 95
 Gln Val Ile Phe Cys Ala Ser Asn Val Ile His His Phe Phe Cys Asp
 100 105 110
 Asp Gln Pro Val Leu Lys Leu Ser Cys Ser Ser His Phe Val Lys Glu
 115 120 125

Ile Thr Val Met Thr Glu Gly Leu Ala Val Ile Met Thr Pro Phe Ser
 130 135 140
 Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Thr Val Leu Lys Ile
 145 150 155 160
 Pro Ser Ala Ala Gly Lys Arg Lys Ala Phe Ser Thr Cys Gly Ser His
 165 170 175
 Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile Ser Tyr Leu Tyr Phe
 180 185 190
 Gln Pro Leu Ser Asn Tyr Thr Val Lys Asp Gln Ile Ala Thr Ile Ile
 195 200 205
 Tyr Pro Val Leu Thr Pro
 210

<210> 2540

<211> 316

<212> PRT

<213> Unknown (4190944-dir-624-13 conceptual translation of range 62576-63523)

<400>2540

Met Gly Met Ser Asn Leu Thr Arg Leu Ser Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Arg Ser Glu Asp Gln Arg Pro Leu Phe Ala Leu Phe Leu
 20 25 30
 Ile Ile Tyr Leu Val Thr Leu Met Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Ile His Ser Asp Pro Arg Leu Gln Asn Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Ile Leu Ser Phe Ala Asp Ile Cys Tyr Thr Thr Val Ile Val Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Tyr Ala Glu
 85 90 95
 Cys Leu Ala Gln Met Tyr Phe Phe Leu Val Phe Gly Asn Ile Asp Ser
 100 105 110
 Tyr Leu Leu Ala Ala Met Ala Ile Asn Arg Cys Val Ala Ile Cys Asn
 115 120 125
 Pro Phe His Tyr Val Thr Val Met Asn Arg Arg Cys Cys Val Leu Leu
 130 135 140
 Leu Ala Phe Pro Ile Thr Phe Ser Tyr Phe His Ser Leu Leu His Val
 145 150 155 160
 Leu Leu Val Asn Arg Leu Thr Phe Cys Thr Ser Asn Val Ile His His
 165 170 175
 Phe Phe Cys Asp Val Asn Pro Val Leu Lys Leu Ser Cys Ser Ser Thr
 180 185 190
 Phe Val Asn Glu Ile Val Ala Met Thr Glu Gly Leu Ala Ser Val Met
 195 200 205
 Ala Pro Phe Val Cys Ile Ile Ile Ser Tyr Leu Arg Ile Leu Ile Ala
 210 215 220
 Val Leu Lys Ile Pro Ser Ala Ala Gly Lys His Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ser Ile Ser
 245 250 255
 Tyr Val Tyr Leu Gln Pro Leu Ser Ser Tyr Thr Val Lys Asp Arg Ile
 260 265 270
 Ala Thr Ile Asn Tyr Thr Val Leu Thr Ser Val Leu Asn Pro Phe Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu Gln Lys Leu Ile
 290 295 300
 Asn Lys Ile Lys Ser Gln Met Ser Arg Phe Ser Thr
 305 310 315

<210> 2541
 <211> 327
 <212> PRT
 <213> Unknown (4190944-dir-1371-13 conceptual translation of range 137254-138234)

<220>
 <221> VARIANT
 <222> (1)...(327)
 <223> Xaa = Any Amino Acid

<400>2541

Arg	Lys	Ser	Arg	Asp	Met	Glu	Ile	Lys	Asn	Tyr	Ser	Ser	Ser	Thr	Ser
1				5					10					15	
Gly	Phe	Ile	Leu	Gly	Leu	Ser	Ser	Asn	Pro	Gln	Leu	Gln	Lys	Pro	
		20					25					30			
Leu	Phe	Ala	Ile	Phe	Leu	Ile	Met	Tyr	Leu	Leu	Ala	Ala	Val	Gly	Asn
		35					40					45			
Val	Leu	Ile	Ile	Pro	Ala	Ile	Tyr	Ser	Asp	Pro	Arg	Leu	His	Thr	Pro
		50					55				60				
Met	Tyr	Phe	Phe	Leu	Ser	Asn	Leu	Ser	Phe	Met	Asp	Ile	Cys	Phe	Thr
65					70				75					80	
Thr	Val	Ile	Val	Pro	Lys	Met	Leu	Val	Asn	Phe	Leu	Ser	Glu	Thr	Lys
				85					90					95	
Val	Ile	Ser	Tyr	Val	Gly	Cys	Leu	Ala	Gln	Met	Tyr	Phe	Phe	Met	Ala
			100					105					110		
Phe	Gly	Asn	Thr	Asp	Ser	Tyr	Leu	Leu	Ala	Ser	Met	Ala	Ile	Asp	Arg
		115					120					125			
Leu	Val	Ala	Ile	Cys	Asn	Pro	Leu	His	Tyr	Asp	Val	Val	Met	Lys	Pro
						135					140				
Arg	His	Cys	Leu	Leu	Met	Leu	Leu	Gly	Ser	Cys	Ser	Ile	Ser	His	Leu
145					150					155					160
His	Ser	Leu	Phe	Arg	Val	Leu	Leu	Met	Ser	Arg	Leu	Ser	Phe	Cys	Ala
				165					170					175	
Ser	His	Ile	Ile	Lys	His	Phe	Phe	Cys	Asp	Thr	Gln	Pro	Val	Leu	Lys
			180					185					190		
Leu	Ser	Cys	Ser	Asp	Thr	Ser	Ser	Ser	Gln	Met	Val	Val	Met	Thr	Glu
		195					200					205			
Thr	Leu	Ala	Val	Ile	Val	Thr	Pro	Phe	Leu	Cys	Ile	Ile	Phe	Ser	Tyr
		210				215					220				
Leu	Arg	Ile	Met	Val	Thr	Val	Leu	Arg	Ile	Pro	Ser	Ala	Ala	Gly	Lys
225						230				235					240
Trp	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Thr	Ala	Val	Ala	Leu
			245						250					255	
Phe	Tyr	Gly	Ser	Ile	Ile	Tyr	Val	Tyr	Phe	Arg	Pro	Leu	Ser	Met	Tyr
			260					265					270		
Ser	Val	Val	Arg	Asp	Arg	Val	Ala	Thr	Val	Met	Tyr	Thr	Val	Val	Thr
		275					280					285			
Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Met	Lys
		290				295					300				
Arg	Gly	Leu	Lys	Lys	Leu	Gln	Asp	Arg	Ile	Tyr	Arg	Xaa	Lys	Glu	Gln
305					310					315					320
Asn	Val	Gly	Val	Ser	Xaa	Leu									
						325									

<210> 2542
 <211> 216
 <212> PRT
 <213> Unknown (hgl6-dir-0-8 conceptual translation of range 1-648)

<400>2542

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Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro Lys Met Leu Val
 1          5          10          15
Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Val Gly Cys Leu Ala
      20          25          30
Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp Ser Tyr Leu Leu
      35          40          45
Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
      50          55          60
Tyr Asp Val Val Met Lys Pro Arg His Cys Leu Leu Met Leu Leu Gly
65          70          75          80
Ser Tyr Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
      85          90          95
Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys His Phe Phe Cys
      100          105          110
Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
      115          120          125
Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
      130          135          140
Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val Thr Val Leu Arg
145          150          155          160
Ile Pro Ser Ala Ala Arg Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
      165          170          175
His Leu Thr Ala Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr
      180          185          190
Phe Arg Pro Leu Ser Met Tyr Ser Val Val Arg Asp Arg Val Ala Thr
      195          200          205
Val Met Tyr Thr Val Val Thr Pro
      210          215

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<210> 2543

<211> 323

<212> PRT

<213> Unknown (4190944-dir-1112-13 conceptual translation of range 111405-112373)

<220>

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400>2543

```

Arg Asp Met Glu Thr Lys Asn Tyr Ser Ser Ser Thr Ser Gly Phe Ile
 1          5          10          15
Leu Leu Gly Leu Ser Ser Asn Pro Lys Leu Gln Lys Pro Leu Phe Ala
      20          25          30
Ile Phe Leu Ile Met Tyr Leu Leu Thr Ala Val Gly Asn Val Leu Ile
      35          40          45
Ile Leu Ala Ile Tyr Ser Asp Pro Arg Leu His Thr Pro Met Tyr Phe
      50          55          60
Phe Leu Ser Asn Leu Ser Phe Met Asp Ile Cys Phe Thr Thr Val Ile
65          70          75          80
Val Pro Lys Met Leu Val Asn Phe Leu Ser Glu Thr Lys Ile Ile Ser
      85          90          95
Tyr Val Gly Cys Leu Ile Gln Met Tyr Phe Phe Met Ala Phe Gly Asn
      100          105          110
Thr Asp Ser Tyr Leu Leu Ala Ser Met Ala Ile Asp Arg Leu Val Ala
      115          120          125
Ile Cys Asn Pro Leu His Tyr Asp Val Val Met Lys Pro Trp His Cys
      130          135          140
Leu Leu Met Leu Leu Gly Ser Cys Ser Ile Ser His Leu His Ser Leu
145          150          155          160

```

Phe Arg Val Leu Leu Met Ser Arg Leu Ser Phe Cys Ala Ser His Ile
 165 170 175
 Ile Lys His Phe Phe Cys Asp Thr Gln Pro Val Leu Lys Leu Ser Cys
 180 185 190
 Ser Asp Thr Ser Ser Ser Gln Met Val Val Met Thr Glu Thr Leu Ala
 195 200 205
 Val Ile Val Thr Pro Phe Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile
 210 215 220
 Ile Val Thr Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Val Leu Phe Tyr Gly
 245 250 255
 Ser Val Ile Tyr Val Tyr Phe Arg Pro Leu Ser Met Tyr Ser Val Met
 260 265 270
 Lys Gly Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu
 275 280 285
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Arg Gly Leu
 290 295 300
 Lys Lys Leu Arg His Arg Ile Tyr Ser Xaa Lys Glu Gln Asn Val Gly
 305 310 315 320
 Met Ser Lys

<210> 2544

<211> 216

<212> PRT

<213> Unknown (OST046-dir-0-8 conceptual translation of range 2-649)

<400>2544

Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro Lys Met Leu Val
 1 5 10 15
 Asn Phe Leu Ser Glu Thr Lys Ile Ile Ser Tyr Val Gly Cys Leu Val
 20 25 30
 Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp Ser Tyr Leu Leu
 35 40 45
 Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
 50 55 60
 Tyr Asp Val Val Met Lys Pro Trp His Cys Leu Leu Met Leu Leu Gly
 65 70 75 80
 Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
 85 90 95
 Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys His Phe Phe Cys
 100 105 110
 Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
 115 120 125
 Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
 130 135 140
 Leu Cys Thr Ile Phe Ser Tyr Leu Gln Ile Ile Val Thr Val Leu Arg
 145 150 155 160
 Ile Pro Ser Ala Ala Arg Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val Ile Tyr Val Tyr
 180 185 190
 Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Gly Arg Val Ala Thr
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2545

<211> 216

<212> PRT

<213> Unknown (p100-dir-0-8 conceptual translation of range 2-649)

<400>2545

```

Leu Val Asp Leu Cys Phe Thr Thr Val Ile Val Pro Gln Met Leu Val
 1              5              10              15
Ser Met Leu Met Gln Asn Lys Ala Ile Ser Phe Ala Gln Cys Ile Ala
      20              25              30
Gln Met Tyr Phe Phe Val Ala Phe Gly Ile Thr Asp Ser Phe Leu Leu
      35              40              45
Ala Ala Met Pro Ile Asp Arg Tyr Met Ala Ile Cys Asn Pro Leu His
      50              55              60
Tyr Thr Thr Thr Met Ser Pro Arg Arg Cys Val Leu Leu Val Ala Met
65              70              75              80
Ser Trp Val Val Ser His Phe His Ser Leu Val His Thr Leu Leu Met
      85              90              95
Ala Arg Leu Ser Phe Cys Gly Pro Asn Ala Ile His His Phe Phe Cys
      100             105             110
Asp Val Gln Pro Leu Leu Thr Leu Ser Cys Ser Asp Thr Ser Ile Asn
      115             120             125
Glu Val Leu Ala Phe Thr Glu Gly Ser Leu Val Ile Met Ser Pro Phe
      130             135             140
Leu Phe Ile Val Ile Ser Tyr Val Trp Ile Thr Arg Ala Val Leu Arg
145             150             155             160
Val Pro Ser Gly Arg Gly Arg Tyr Lys Ala Phe Ser Thr Cys Ser Ser
      165             170             175
His Ile Thr Val Val Val Leu Phe Tyr Gly Thr Ile Val Ser Val Tyr
      180             185             190
Ile Arg Pro Ser Ser Thr Tyr Ser Val Thr Lys Asp Arg Val Val Thr
      195             200             205
Val Ile Tyr Thr Val Val Thr Pro
      210             215

```

<210> 2546

<211> 328

<212> PRT

<213> Unknown (4190944-rev-159-13 conceptual translation of range 16099-17082)

<220>

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400>2546

```

Phe Gln Ala Gly Xaa Leu Ser Leu Met Met Ser Phe Ala Pro Asn Ala
 1              5              10              15
Ser His Ser Pro Val Phe Leu Leu Leu Gly Phe Ser Arg Ala Asn Ile
      20              25              30
Ser Tyr Thr Leu Leu Phe Phe Leu Phe Leu Ala Ile Tyr Leu Thr Thr
      35              40              45
Ile Leu Gly Asn Val Thr Leu Val Leu Leu Ile Ser Trp Asp Ser Arg
      50              55              60
Leu His Ser Pro Met Tyr Tyr Leu Leu Arg Gly Leu Ser Val Ile Asp
65              70              75              80
Met Gly Leu Ser Thr Val Thr Leu Pro Gln Leu Leu Ala His Leu Val
      85              90              95
Ser His Tyr Pro Thr Ile Pro Ala Ala Arg Cys Leu Ala Gln Phe Phe
      100             105             110
Phe Phe Tyr Ala Phe Gly Val Thr Asp Thr Leu Val Ile Ala Val Met
      115             120             125
Ala Leu Asp Arg Tyr Val Ala Ile Cys Asp Pro Leu His Tyr Ala Leu

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130	135	140
Val Met Asn His Gln Arg Cys Ala Cys Leu Leu Ala Leu Ser Trp Val		
145	150	155
Val Ser Ile Leu His Thr Met Leu Arg Val Gly Leu Val Leu Pro Leu		160
	165	170
Cys Trp Thr Gly Asp Ala Gly Gly Asn Val Asn Leu Pro His Phe Phe		175
	180	185
Cys Asp His Arg Pro Leu Leu Arg Ala Ser Cys Ser Asp Ile His Ser		190
	195	200
Asn Glu Leu Ala Ile Phe Phe Glu Gly Gly Phe Leu Met Leu Gly Pro		205
	210	215
Cys Ala Leu Ile Val Leu Ser Tyr Val Arg Ile Gly Ala Ala Ile Leu		220
225	230	235
Arg Leu Pro Ser Ala Ala Gly Arg Arg Arg Ala Val Ser Thr Cys Gly		240
	245	250
Ser His Leu Thr Met Val Gly Phe Leu Tyr Gly Thr Ile Ile Cys Val		255
	260	265
Tyr Phe Gln Pro Pro Phe Gln Asn Ser Gln Tyr Gln Asp Met Val Ala		270
	275	280
Ser Val Met Tyr Thr Ala Ile Thr Pro Leu Ala Asn Pro Phe Val Tyr		285
	290	295
Ser Leu His Asn Lys Asp Val Lys Gly Ala Leu Cys Arg Leu Leu Glu		300
305	310	315
Trp Val Lys Val Asp Pro Xaa Leu		320
	325	

<210> 2547

<211> 216

<212> PRT

<213> Unknown (hg99-dir-0-8 conceptual translation of range 1-648)

<400>2547

Phe Ala Asp Leu Cys Phe Ala Ser Val Thr Val Pro Lys Met Leu Asp		
1	5	10
Asn Leu Leu Ala His Asp His Ser Ile Ser Leu Ala Gly Cys Leu Thr		15
	20	25
Gln Met Tyr Phe Phe Phe Ala Leu Gly Val Thr Asp Ser Cys Leu Leu		30
	35	40
Ala Asp Met Ala Tyr Asp Cys Tyr Val Asp Ile Arg His Pro Leu Pro		45
	50	55
Tyr Asp Thr Arg Met Ser Arg Ala Met Cys Ala Ala Leu Val Gly Met		60
65	70	75
Ala Trp Val Val Ser His Val His Ser Leu Leu Tyr Ile Leu Leu Met		80
	85	90
Ala Arg Leu Ser Phe Cys Ala Ser His Gln Val Pro His Phe Phe Cys		95
	100	105
Asp His Gln Pro Leu Leu Arg Leu Ser Cys Ser Asp Asn His His Ile		110
	115	120
Gln Leu Leu Ile Phe Thr Glu Gly Ala Ala Val Val Val Thr Pro Phe		125
	130	135
Leu Leu Ile Leu Ala Ser Tyr Gly Ala Ile Ala Ala Ala Val Leu Gln		140
145	150	155
Leu Pro Ser Ala Ser Gly Arg Leu Arg Ala Val Ser Thr Cys Gly Ser		160
	165	170
His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Val Ile Ala Val Tyr		175
	180	185
Phe Gln Ala Thr Ser Arg Arg Glu Ala Glu Trp Gly Arg Val Ala Thr		190
	195	200
Val Met Tyr Thr Val Val Thr Pro		205
	210	215

<210> 2548

<211> 319

<212> PRT

<213> Unknown (p16-dir-0-11 conceptual translation of range 1-960)

<400>2548

```

Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1           5           10           15
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys
          20           25           30
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala
          35           40           45
Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu
          50           55           60
Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro
65           70           75           80
Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln
          85           90           95
Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu
          100          105          110
Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys
          115          120          125
Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser
          130          135          140
Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His
145          150          155          160
Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg
          165          170          175
Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp
          180          185          190
Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val
          195          200          205
Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val
          210          215          220
Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly
225          230          235          240
Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser
          245          250          255
Val Leu Ser Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr
          260          265          270
Asp Arg Leu Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn
          275          280          285
Pro Phe Ile Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys
          290          295          300
Arg Gly Leu Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala
305          310          315

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<210> 2549

<211> 158

<212> PRT

<213> Unknown (2564509-dir-0-6 conceptual translation of range 1-474)

<400>2549

```

Ile Cys Ser Pro Leu His Tyr Gly Met Val Met Ser Arg Arg Met Cys
 1           5           10           15
Phe Cys Leu Val Ala Ile Ser Trp Leu Val Ile Ala Val His Ser Val
          20           25           30
Leu His Ser Val Leu Thr Ser Arg Leu Ser Phe Cys Gly Ser Asn Gln
          35           40           45
Ile His His Phe Phe Cys Asp Met Thr Pro Leu Leu Lys Leu Ser Cys
          50           55           60

```

Ser Asp Thr Ser Val Asn Glu Leu Val Ile Phe Ile Glu Gly Pro Phe
 65 70 75 80
 Ser Val Ala Val Pro Leu Gly Ile Val Leu Val Ser Tyr Val Arg Ile
 85 90 95
 Ile Ser Ala Ile Leu Lys Ile Arg Ser Pro Glu Gly Arg His Arg Ala
 100 105 110
 Phe Ser Thr Cys Ser Ser His Leu Met Val Val Ile Leu Tyr Phe Gly
 115 120 125
 Thr Ile Ile Phe Met Tyr Phe Arg Pro Thr Ser Ser Tyr Ser Leu Asp
 130 135 140
 Tyr Asp Arg Val Val Ser Val Met Tyr Thr Val Val Ala Pro
 145 150 155

<210> 2550

<211> 156

<212> PRT

<213> Unknown (2564511-dir-0-6 conceptual translation of range 1-468)

<400>2550

Asn Pro Leu His Tyr Thr Thr Val Met Ser Lys Lys Val Cys Leu Leu
 1 5 10 15
 Leu Val Gly Met Leu Trp Leu Trp Ala Val Leu Tyr Ser Leu Met His
 20 25 30
 Ile Val Leu Ile Ser Arg Leu Ser Phe Cys Gly Ser Asn Gln Ile Asn
 35 40 45
 His Phe Val Cys Asp Thr Val Pro Leu Phe Lys Leu Ser Cys Ser Asp
 50 55 60
 Thr Ser Thr Asn Gln Leu Val Ile Phe Thr Val Gly Ser Leu Ile Val
 65 70 75 80
 Met Val Pro Phe Leu Ile Val Leu Ile Ser Tyr Ala Arg Ile Val Phe
 85 90 95
 Ala Ile Leu Lys Ile Ser Ser Thr Asp Gly Arg Arg Lys Thr Phe Ser
 100 105 110
 Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Tyr Phe Gly Thr Ile
 115 120 125
 Met Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser Leu Thr Lys Asp
 130 135 140
 Arg Val Ala Ser Val Met Tyr Thr Val Leu Ala Pro
 145 150 155

<210> 2551

<211> 158

<212> PRT

<213> Unknown (2564513-dir-0-6 conceptual translation of range 1-474)

<400>2551

Ile Cys Asp Pro Leu Arg Tyr Thr Val Val Met Ser Lys Arg Ile Cys
 1 5 10 15
 Leu Gln Met Val Ala Gly Ser Trp Val Leu Val Ser Leu His Ser Leu
 20 25 30
 Leu His Thr Val Leu Thr Ala Arg Leu Ser Phe Cys Gly Arg Asn Leu
 35 40 45
 Ile Arg His Phe Phe Cys Glu Met Ser Pro Leu Phe Ala Leu Ser Cys
 50 55 60
 Ser Asp Thr Thr Thr Asn Glu Leu Val Ile Phe Thr Glu Gly Ser Phe
 65 70 75 80
 Ser Leu Ala Leu Pro Phe Leu Leu Ile Leu Phe Ser Tyr Leu Arg Ile
 85 90 95
 Leu Ser Thr Val Leu Arg Ile Arg Ser Val Asp Gly Lys Cys Arg Ala
 100 105 110
 Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ala Leu Phe Tyr Gly

115	120	125
Thr Leu Phe Ser Val Tyr	Phe Arg Pro Ser Ser Ser	His Ser Leu Asp
130	135	140
Asn Asp Arg Val Val Ser	Ile Met Tyr Thr Ala Il	Thr Pro
145	150	155

<210> 2552

<211> 315

<212> PRT

<213> Unknown (4808260-rev-1059-13 conceptual translation of range 106061-107005)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400>2552

Cys Leu Leu Ser Glu Val Met Leu Asn Thr Thr Ser Val Thr Glu Phe	
1 5 10 15	
Leu Leu Leu Gly Val Thr Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe	
20 25 30	
Val Val Phe Leu Thr Ile Tyr Phe Ile Ser Val Thr Gly Asn Gly Ala	
35 40 45	
Val Leu Met Ile Val Ile Ser Asp Pro Arg Leu His Ser Leu Met Tyr	
50 55 60	
Phe Phe Leu Gly Asn Leu Ser Tyr Leu Asp Ile Cys Tyr Ser Thr Val	
65 70 75 80	
Thr Leu Pro Lys Met Leu Gln Asn Phe Leu Ser Thr His Lys Ala Ile	
85 90 95	
Ser Phe Leu Gly Cys Ile Ser Gln Leu His Phe Phe His Phe Leu Gly	
100 105 110	
Ser Thr Glu Ser Met Leu Phe Ala Val Met Ala Phe Asp Leu Ser Val	
115 120 125	
Ala Ile Cys Lys Pro Leu Arg Tyr Thr Val Ile Met Asn Pro Gln Leu	
130 135 140	
Cys Thr Gln Met Ala Ile Thr Ile Trp Val Ile Gly Phe Phe His Ala	
145 150 155 160	
Leu Leu His Ser Val Met Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn	
165 170 175	
Arg Ile His His Phe Leu Cys Asp Ile Lys Pro Leu Leu Lys Leu Ala	
180 185 190	
Cys Gly Asn Thr Glu Leu Asn Gln Trp Leu Leu Ser Thr Val Thr Gly	
195 200 205	
Thr Ile Ala Met Gly Pro Phe Phe Leu Thr Leu Leu Ser Tyr Phe Tyr	
210 215 220	
Ile Ile Thr Tyr Leu Phe Phe Lys Thr Arg Ser Cys Ser Met Leu Cys	
225 230 235 240	
Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met Val Val Ile Leu Phe	
245 250 255	
Tyr Ala Pro Val Leu Phe Thr Tyr Ile His Pro Ala Leu Glu Ser Phe	
260 265 270	
Met Asp Gln Asp Arg Ile Val Ala Ile Met Tyr Thr Val Val Thr Pro	
275 280 285	
Val Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly	
290 295 300	
Ala Leu Gly Arg Val Ile Arg Arg Leu Xaa Phe	
305 310 315	

<210> 2553

<211> 162

<212> PRT

<213> Unknown (1617234-dir-0-6 conceptual translation of range 1-486)

<400>2553

```

Asn Ala Ile Cys Asn Pro Leu Leu Tyr Asn Thr Ile Met Asn Lys Arg
 1           5           10           15
Thr Cys Val Ile Leu Ile Val Gly Ser Trp Leu Ile Ala Ser Ile Asn
      20           25           30
Ser Leu Ile His Thr Ile Leu Thr Phe Met Leu Pro Phe Cys Gly Ser
      35           40           45
Asn Ala Ile Asp Ser Phe Phe Cys Asp Met Pro Pro Leu Leu Lys Leu
      50           55           60
Ala Cys Thr Asp Thr Leu Val Asn Gln Ile Val Ile Phe Val Thr Gly
65           70           75           80
Ser Cys Ile Ile Ala Gly Pro Phe Met Leu Thr Val Phe Ser Tyr Val
      85           90           95
Gln Ile Ile Ser Thr Ile Val Ser Ile Arg Ser Ser Ser Arg Lys Lys
      100          105          110
Lys Ala Phe Ser Thr Cys Thr Ser His Ile Thr Ala Val Val Ile Phe
      115          120          125
Tyr Val Pro Ser Ile Cys Ile Tyr Phe Arg Pro Lys Ser Asn Gln Ala
      130          135          140
Met Ile Gln Asp Lys Met Ala Thr Val Ile Cys Ala Val Ile Thr Pro
145          150          155          160
Leu Leu

```

<210> 2554

<211> 160

<212> PRT

<213> Unknown (4877310-dir-0-6 conceptual translation of range 2-481)

<400>2554

```

Ala Ala Ile Cys Lys Pro Leu His Tyr Asn Thr Ile Met Asn Lys Arg
 1           5           10           15
Leu Cys Val Cys Leu Ala Leu Gly Cys Trp Gly Val Gly Val Ile Asn
      20           25           30
Ser Thr Ile His Val Phe Phe Thr Phe Gln Leu Pro Phe Cys Arg Ser
      35           40           45
Arg His Ile Asn His Phe Phe Cys Glu Val Pro Pro Phe Phe Arg Leu
      50           55           60
Ser Cys Gln Asp Thr Trp Phe Asn Glu Leu Ala Met Tyr Ile Ser Ala
65           70           75           80
Cys Ile Ile Ala Ile Cys Ala Phe Phe Leu Thr Leu Ile Ser Tyr Ile
      85           90           95
Tyr Ile Ile Ser Ser Ile Ala Lys Ile Arg Ala Pro Gln Gly Arg Tyr
      100          105          110
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ala Val Tyr
      115          120          125
Tyr Gly Thr Ile Met Phe Ile Tyr Leu His Pro His Ser Ala Tyr Ser
      130          135          140
Pro Glu Met Gly Lys Ile Val Ser Ile Ile Tyr Thr Ser Val Thr Pro
145          150          155          160

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<210> 2555

<211> 160

<212> PRT

<213> Unknown (4877337-dir-0-6 conceptual translation of range 2-481)

<400>2555

```

Ile Cys Ser Pro Leu Leu Tyr Phe Thr Lys Met Ser Thr Arg Val Tyr

```

```

1           5           10           15
Val Gln Leu Leu Thr Val Ala Tyr Val Gly Gly Phe Leu Asn Ala Cys
      20           25           30
Ser Phe Thr Ile Cys Phe Tyr Tyr Leu Leu Cys Gly Pro Asn Arg
      35           40           45
Val Asn His Phe Phe Cys Asp Phe Ala Pro Leu Val Glu Phe Ser Cys
      50           55           60
Ser Asp Ile Ser Ile Pro Ala Val Val Pro Ser Phe Thr Ala Gly Ser
      65           70           75           80
Ile Ile Val Val Thr Val Ile Val Ile Ala Ile Ser Tyr Ile Tyr Ile
      85           90           95
Leu Ile Thr Ile Leu Lys Met Arg Ser Thr Glu Gly His His Lys Ala
      100          105          110
Phe Ser Thr Cys Thr Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly
      115          120          125
Thr Ile Thr Leu Ile Tyr Val Met Pro Lys Ser Ser Phe Ser Thr Asp
      130          135          140
Gln Asn Lys Val Val Cys Val Phe Tyr Thr Val Val Ile Pro Met Leu
      145          150          155          160

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<210> 2556

<211> 315

<212> PRT

<213> Unknown (4680263-dir-1-12 conceptual translation of range 259-1203)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400>2556

```

Glu Met Glu Pro Gly Asn Tyr Thr Val Val Thr Glu Phe Ile Leu Leu
1           5           10           15
Gly Leu Thr Asp Asp Ile Thr Val Ser Val Ile Leu Phe Val Met Phe
      20           25           30
Leu Ile Val Tyr Ser Val Thr Leu Met Gly Asn Leu Asn Ile Ile Val
      35           40           45
Leu Ile Arg Thr Ser Pro Gln Leu His Thr Pro Met Tyr Leu Phe Leu
      50           55           60
Ser His Leu Ala Phe Leu Asp Ile Gly Tyr Ser Ser Ser Val Thr Pro
      65           70           75           80
Ile Met Leu Arg Gly Phe Leu Arg Lys Gly Thr Phe Ile Pro Val Ala
      85           90           95
Gly Cys Val Ala Gln Leu Cys Ile Val Val Ala Phe Gly Thr Ser Glu
      100          105          110
Ser Phe Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
      115          120          125
Ser Pro Leu Leu Tyr Ser Thr Gln Met Ser Ser Thr Val Cys Ile Leu
      130          135          140
Leu Val Gly Thr Ser Tyr Leu Gly Gly Trp Val Asn Ala Trp Ile Phe
      145          150          155          160
Thr Gly Cys Ser Leu Asn Leu Ser Phe Cys Gly Pro Asn Lys Ile Asn
      165          170          175
His Phe Phe Cys Asp Tyr Ser Pro Leu Leu Lys Leu Ser Cys Ser His
      180          185          190
Asp Phe Ser Phe Glu Val Ile Pro Ala Ile Ser Ser Gly Ser Ile Ile
      195          200          205
Val Val Thr Val Phe Ile Ile Ala Leu Ser Tyr Val Tyr Ile Leu Val
      210          215          220
Ser Ile Leu Lys Met Arg Ser Thr Glu Gly Arg Gln Lys Ala Phe Ser
      225          230          235          240

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<210> 2557
<211> 312
<212> PRT
<213> Unknown (1246533-dir-0-11 conceptual translation of range 1-936)
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<210> 2558
<211> 313
<212> PRT
```

<213> Unknown (p28-dir-0-11 conceptual translation of range 1-939)

<400>2558

```

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Cys Phe Leu Leu Gly
 1           5           10           15
Phe Ser Glu Gln Leu Glu Glu Gln Lys Pro Leu Phe Gly Ser Phe Leu
      20           25           30
Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
      35           40           45
Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
      50           55           60
Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
      65           70           75           80
Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
      85           90           95
Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
      100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Ile Phe Leu
      130          135          140
Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
      145          150          155          160
Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His
      165          170          175
Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
      180          185          190
Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
      195          200          205
Ile Cys Val Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr
      210          215          220
Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
      225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
      245          250          255
Cys Val Asp Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr
      260          265          270
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
      290          295          300
Ile Trp Val Arg Lys Ile His Ser Pro
      305          310

```

<210> 2559

<211> 117

<212> PRT

<213> Unknown (2695895-dir-0-5 conceptual translation of range 2-351)

<220>

<221> VARIANT

<222> (1)...(117)

<223> Xaa = Any Amino Acid

<400>2559

```

Asp Leu Cys Tyr Ser Thr Val Ile Ala Pro Lys Ala Leu Ala Ile Phe
 1           5           10           15
Leu Ser Lys Asp Lys Lys Ile Ser Tyr Asn Gly His Ala Ala Xaa Phe
      20           25           30
Tyr Phe Leu Cys Cys Val Gly Thr Glu Gly Leu Leu Leu Ala Val Met
      35           40           45

```


Ala Tyr Asp His Phe Ser Ala Phe Cys Ser Pro Phe Leu Tyr Pro Val
 50 55 60
 Arg Met Ser Gln Gln Val Cys Val His Leu Val Ile Gly Ser Tyr Ile
 65 70 75 80
 Cys Gly Gly Ile Asn Ser Met Val Gln Thr Gly Phe Thr Phe Ser Leu
 85 90 95
 Asn Phe Cys Gly Glu Asn Xaa Leu Asp His Phe Phe Cys Asp Val Pro
 100 105 110
 Ala Leu Ile Lys Ile
 115

<210> 2560

<211> 216

<212> PRT

<213> Unknown (2921661-dir-0-8 conceptual translation of range 2-649)

<400>2560

Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Ala
 1 5 10 15
 Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly Cys Leu Leu
 20 25 30
 Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala Phe Leu Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60
 Tyr Ile Leu Ile Met Ser Pro Gly Leu Arg Ile Phe Leu Val Ser Ala
 65 70 75 80
 Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr Leu Leu Met
 85 90 95
 Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His Phe Leu Cys
 100 105 110
 Asp Ile Asn Pro Leu Leu Gly Leu Ser Cys Thr Asp Pro Phe Thr Asn
 115 120 125
 Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu Ile Cys Val
 130 135 140
 Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr Ile Leu Lys
 145 150 155 160
 Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe Cys Val Asp
 180 185 190
 Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr Val Ala Ser
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 2561

<211> 313

<212> PRT

<213> Unknown (p19-dir-0-11 conceptual translation of range 1-939)

<400>2561

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Phe Phe Leu Leu Gly
 1 5 10 15
 Phe Ser Glu Gln Leu Glu Glu Gln Lys Ala Leu Phe Gly Ser Phe Leu
 20 25 30
 Phe Met Tyr Leu Val Met Val Ala Gly Asn Leu Leu Ile Ile Leu Val
 35 40 45
 Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys

65					70					75				80
Met	Leu	Ala	Asn	Ile	Gln	Ile	Gln	Ser	Gln	Ala	Ile	Ser	Tyr	Ser Gly
				85					90					95
Cys	Leu	Leu	Gln	Leu	Tyr	Phe	Phe	Met	Leu	Phe	Val	Met	Leu	Glu Ala
			100					105					110	
Phe	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	His	Tyr	Val	Ala	Ile	Cys His
			115				120					125		
Pro	Leu	His	Tyr	Ile	Leu	Ile	Met	Ser	Pro	Gly	Leu	Cys	Val	Phe Leu
			130				135				140			
Val	Ser	Ala	Ser	Trp	Ile	Met	Asn	Ala	Leu	Tyr	Ser	Leu	Leu	His Thr
					150					155				160
Leu	Leu	Met	Asn	Ser	Leu	Ser	Phe	Cys	Ala	Asn	His	Glu	Ile	Pro His
			165					170						175
Phe	Phe	Cys	Asp	Ile	Asp	Pro	Leu	Leu	Ser	Leu	Ser	Cys	Ala	Asp Pro
			180					185					190	
Phe	Thr	Asn	Glu	Leu	Val	Ile	Phe	Ile	Thr	Gly	Gly	Leu	Thr	Gly Leu
			195				200					205		
Ile	Cys	Val	Leu	Cys	Leu	Ile	Ile	Ser	Tyr	Thr	Asn	Val	Phe	Ser Thr
			210				215				220			
Ile	Leu	Lys	Ile	Pro	Ser	Ala	Gln	Gly	Lys	Arg	Lys	Ala	Phe	Ser Thr
					230					235				240
Cys	Ser	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Phe	Cys	Gly	Thr	Ser Phe
			245					250						255
Cys	Val	Tyr	Phe	Ser	Pro	Pro	Ser	Thr	Arg	Ser	Ala	Gln	Lys	Asp Thr
			260					265				270		
Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro Phe
			275				280					285		
Ile	Tyr	Ser	Leu	Arg	Asn	Gln	Glu	Ile	Lys	Ser	Ser	Leu	Arg	Lys Leu
			290			295					300			
Ile	Trp	Val	Arg	Lys	Ile	His	Ser	Pro						
305					310									

<210> 2562

<211> 313

<212> PRT

<213> Unknown (p40-dir-0-11 conceptual translation of range 1-938)

<400>2562

Met	Glu	Gly	Lys	Asn	Leu	Thr	Ser	Ile	Ser	Glu	Phe	Phe	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Glu	Gln	Leu	Glu	Glu	Gln	Lys	Ala	Leu	Leu	Val	Ser	Phe	Leu
			20					25					30		
Phe	Met	Tyr	Leu	Val	Thr	Val	Ala	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Val
			35				40					45			
Ile	Ile	Thr	Asp	Thr	Gln	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala
			50			55					60				
Asn	Leu	Ser	Leu	Ala	Asp	Ala	Cys	Phe	Val	Ser	Thr	Thr	Val	Pro	Lys
65				70				75						80	
Met	Leu	Ala	Asn	Ile	Gln	Ile	Gln	Ser	Gln	Ala	Ile	Ser	Tyr	Ser Gly	
			85					90					95		
Cys	Leu	Leu	Gln	Leu	Tyr	Phe	Phe	Met	Leu	Phe	Val	Met	Leu	Glu Ala	
			100					105					110		
Phe	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	His	Tyr	Val	Ala	Ile	Cys His	
			115				120					125			
Pro	Leu	His	Tyr	Ile	Leu	Ile	Met	Ser	Pro	Gly	Leu	Cys	Val	Phe Leu	
			130				135				140				
Val	Ser	Ala	Ser	Trp	Ile	Met	Asp	Ala	Leu	His	Ser	Leu	Leu	His Thr	
					150					155				160	
Leu	Leu	Met	Asn	Ser	Leu	Ser	Phe	Tyr	Ala	Asn	His	Glu	Thr	Pro His	
			165					170						175	
Phe	Phe	Cys	Asp	Ile	Asp	Pro	Leu	Leu	Ser	Leu	Ser	Cys	Thr	Asp Pro	

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      180      185      190
Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
      195      200      205
Val Cys Val Leu Cys Leu Ile Ile Ser Tyr Thr Asn Ile Phe Ser Thr
      210      215      220
Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
225      230      235      240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
      245      250      255
Cys Val Tyr Phe Ile Pro Pro Ser Thr Arg Ser Ala Gln Lys Asp Thr
      260      265      270
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
      290      295      300
Ile Trp Val Arg Glu Ile His Ser Pro
305      310

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<210> 2563

<211> 161

<212> PRT

<213> Unknown (293757-dir-0-6 conceptual translation of range 2-484)

<400>2563

```

Arg Tyr Val Ala Ile Cys Lys Pro Leu Thr Tyr Lys Val Ile Met Ser
1      5      10      15
Pro Lys Ile Cys Cys Leu Leu Ile Phe Ser Ser Tyr Leu Met Gly Phe
      20      25      30
Ala Ser Ala Met Ala His Thr Gly Cys Met Ile Arg Leu Ser Phe Cys
      35      40      45
Asp Ser Asn Ile Ile Asn His Tyr Met Cys Asp Ile Phe Pro Leu Leu
      50      55      60
Pro Leu Ser Cys Ser Ser Thr Tyr Val Asn Glu Leu Met Ser Ser Val
65      70      75      80
Val Val Gly Ser Ala Ile Ile Leu Cys Cys Leu Ile Ile Leu Ile Ser
      85      90      95
Tyr Ala Met Ile Leu Phe Asn Ile Ile His Met Ser Ser Gly Lys Gly
      100      105      110
Trp Ser Lys Ala Leu Gly Thr Cys Gly Ser His Ile Ile Thr Val Ser
      115      120      125
Leu Phe Tyr Gly Ser Gly Leu Leu Ala Tyr Val Lys Pro Ser Ser Ala
      130      135      140
Lys Thr Val Gly Gln Gly Lys Phe Phe Ser Val Phe Tyr Thr Leu Leu
145      150      155      160
Val

```

<210> 2564

<211> 313

<212> PRT

<213> Unknown (p39-dir-0-11 conceptual translation of range 1-939)

<400>2564

```

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Phe Phe Leu Leu Gly
1      5      10      15
Phe Ser Glu Gln Leu Glu Glu Gln Lys Ala Leu Phe Gly Ser Phe Leu
      20      25      30
Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
      35      40      45
Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
50      55      60

```

Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
 85 90 95
 Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
 100 105 110
 Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Val Phe Leu
 130 135 140
 Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
 145 150 155 160
 Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His
 165 170 175
 Phe Phe Cys Asp Ile Asp Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
 180 185 190
 Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
 195 200 205
 Val Cys Val Leu Cys Leu Ile Ile Ser Tyr Thr Asn Ile Phe Ser Thr
 210 215 220
 Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
 245 250 255
 Cys Val Tyr Phe Ile Pro Pro Ser Thr Arg Ser Ala Gln Lys Asp Thr
 260 265 270
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
 290 295 300
 Ile Trp Val Arg Glu Ile His Ser Pro
 305 310

<210> 2565

<211> 315

<212> PRT

<213> Unknown (3738097-rev-723-12 conceptual translation of range 72448-73392)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400>2565

Met Leu Ala Arg Asn Asn Ser Leu Val Thr Glu Phe Ile Leu Ala Gly
 1 5 10 15
 Leu Thr Asp Arg Pro Glu Phe Trp Gln Pro Phe Phe Phe Leu Phe Leu
 20 25 30
 Val Ile Tyr Ile Val Thr Met Val Gly Asn Leu Gly Leu Ile Thr Leu
 35 40 45
 Phe Gly Leu Asn Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Phe
 50 55 60
 Asn Leu Ser Phe Ile Asp Leu Cys Tyr Ser Ser Val Phe Thr Pro Lys
 65 70 75 80
 Met Leu Met Asn Phe Val Ser Lys Lys Asn Ile Ile Ser Asn Val Gly
 85 90 95
 Cys Met Thr Arg Leu Phe Phe Phe Leu Phe Phe Val Ile Ser Glu Cys
 100 105 110
 Tyr Met Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125

Pro Leu Leu Tyr Lys Val Thr Met Ser His Gln Val Cys Ser Met Leu
 130 135 140
 Thr Phe Ala Ala Tyr Ile Met Gly Leu Ala Gly Ala Thr Ala His Thr
 145 150 155 160
 Gly Cys Met Phe Arg Leu Thr Phe Cys Ser Ala Asn Ile Ile Asn His
 165 170 175
 Tyr Leu Cys Asp Ile Leu Pro Leu Leu Gln Leu Ser Cys Thr Ser Thr
 180 185 190
 Tyr Val Asn Glu Val Val Val Leu Ile Val Val Gly Thr Asn Ile Thr
 195 200 205
 Val Pro Ser Cys Thr Ile Leu Ile Ser Tyr Val Phe Ile Val Thr Ser
 210 215 220
 Ile Leu His Ile Lys Ser Thr Gln Gly Arg Ser Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Val Ile Ala Leu Ser Leu Phe Phe Gly Ser Ala Ala
 245 250 255
 Phe Met Tyr Ile Lys Tyr Ser Ser Gly Ser Met Glu Gln Gly Lys Val
 260 265 270
 Phe Ser Val Phe Tyr Thr Asn Val Val Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Lys Ala Leu
 290 295 300
 Ile Lys Ile Gln Arg Arg Asn Ile Phe Xaa Leu
 305 310 315

<210> 2566

<211> 313

<212> PRT

<213> Unknown (p41-dir-0-11 conceptual translation of range 1-938)

<400>2566

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Phe Phe Leu Leu Gly
 1 5 10 15
 Phe Ser Glu Gln Leu Glu Glu Gln Lys Ala Leu Phe Gly Ser Phe Leu
 20 25 30
 Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
 35 40 45
 Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
 65 70 75 80
 Met Leu Ala Asn Ile Arg Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
 85 90 95
 Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
 100 105 110
 Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Val Phe Leu
 130 135 140
 Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
 145 150 155 160
 Leu Leu Met Asn Ser Leu Ser Phe Cys Thr Asn Arg Glu Ile Pro His
 165 170 175
 Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
 180 185 190
 Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Val Ala Gly Leu
 195 200 205
 Val Cys Val Leu Cys Leu Ile Ile Ser Tyr Met Asn Val Phe Ser Thr
 210 215 220
 Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Ser Ser Phe Ser Thr
 225 230 235 240

Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
 245 250 255
 Cys Val Tyr Val Ser Pro Pro Ser Thr Leu Ser Ala Gln Lys Asp Thr
 260 265 270
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Ile
 290 295 300
 Ile Trp Val Arg Lys Ile His Ser Pro
 305 310

<210> 2567

<211> 315

<212> PRT

<213> Unknown (2317703-dir-0-13 conceptual translation of range 211-1155)

<220>

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400>2567

Met Ala Thr Gly Asn Tyr Cys Val Phe Pro Glu Phe Ile Leu Thr Gly
 1 5 10 15
 Leu Ser Lys Lys Ser Glu Leu Gln Met Pro Leu Phe Val Leu Phe Leu
 20 25 30
 Gly Ile Tyr Ile Val Thr Val Val Gly Asn Leu Gly Met Ile Thr Leu
 35 40 45
 Ile Arg Leu Ser Ser Leu Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
 50 55 60
 Ser Leu Ser Phe Ile Asp Leu Cys His Ser Thr Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Val Ala Glu Lys Asn Ile Ile Ser Tyr Thr Gly
 85 90 95
 Cys Met Thr Gln Leu Phe Phe Phe Leu Ile Phe Ala Ile Ala Glu Cys
 100 105 110
 His Met Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Asn Ala Ile Met Ser Tyr Gln Ser Tyr Ile Ser Met
 130 135 140
 Ile Ser Gly Val Tyr Ile Ile Gly Val Val Cys Ala Ser Ala His Thr
 145 150 155 160
 Gly Phe Met Ile Arg Ser Gln Phe Cys Asn Leu Asp Val Ile Asn His
 165 170 175
 Tyr Phe Cys Asp Leu Leu Pro Leu Leu Glu Leu Ala His Ser Ser Thr
 180 185 190
 Tyr Val Asn Glu Leu Val Ile Leu Ile Cys Gly Thr Cys Asn Ile Val
 195 200 205
 Val Pro Thr Leu Thr Ile Leu Thr Ser Tyr Ile Phe Ile Ile Ala Thr
 210 215 220
 Ile Leu His Ile Arg Ser Thr Glu Gly Arg Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Ile Leu Ala Val Ala Val Phe Phe Gly Ser Ala Ala
 245 250 255
 Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys
 260 265 270
 Val Ser Ser Val Phe Tyr Thr Ile Val Val Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Ser Thr Ala Leu Lys Lys Ile
 290 295 300
 Leu Glu Arg Lys Ser Phe Val Xaa Thr Glu Val

305

310

315

<210> 2568

<211> 114

<212> PRT

<213> Unknown (888-dir-0-5 conceptual translation of range 2-343)

<400>2568

```

Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Ser Asn Thr Leu Cys
 1           5           10           15
Ile Arg Leu Leu Val Leu Ser Leu Leu Gly Gly Leu Leu His Ala Ile
           20           25           30
Ile His Ser Ser Phe Leu Phe Arg Leu Thr Phe Cys Asp Ser Ile Ile
           35           40           45
Val His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Thr Cys
           50           55           60
Thr Asp Pro Ser Ile Asn Tyr Leu Ile Val Phe Ile Phe Ala Gly Ser
65           70           75           80
Ile Gln Met Phe Thr Ile Leu Ile Val Leu Val Ser Tyr Thr Leu Val
           85           90           95
Leu Phe Thr Ile Leu Arg Lys Lys Ser Leu Gln Gly Ile Lys Lys Ala
           100          105          110
Phe Ser

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<210> 2569

<211> 159

<212> PRT

<213> Unknown (1514485-dir-0-6 conceptual translation of range 2-478)

<400>2569

```

Val Ala Ile Cys Asn Pro Leu Leu Tyr Thr Ile Ser Met Pro Lys Ser
 1           5           10           15
Leu Cys Met Lys Leu Val Ala Gly Ser Tyr Leu Gly Gly Val Leu Asn
           20           25           30
Ser Leu Thr Gln Thr Cys Cys Leu Leu Pro Leu Pro Phe Cys Gly Pro
           35           40           45
Asn Val Ile Asn His Tyr Phe Cys Asp Thr Asn Pro Leu Leu Lys Leu
           50           55           60
Thr Cys Ser Asp Gly Arg Leu Asn Glu Leu Leu Val Thr Phe Asn
65           70           75           80
Gly Thr Ile Ser Met Thr Val Leu Leu Ile Val Ile Ser Tyr Val
           85           90           95
Tyr Ile Leu Val Ser Ile Leu Ser Ile Arg Ser Ala Arg Gly Arg His
           100          105          110
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Leu Thr Val Thr Leu Phe
           115          120          125
Tyr Val Pro Ala Gly Leu Ser His Met Gln Pro Gly Ser Lys Tyr Ser
           130          135          140
Leu Asp Met Glu Lys Val Thr Ala Val Phe Tyr Thr Leu Leu Val
145          150          155

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<210> 2570

<211> 131

<212> PRT

<213> Unknown (1514487-dir-0-5 conceptual translation of range 2-394)

<400>2570

```

Val Ala Ile Cys Ser Pro Leu Leu Tyr Ser Thr Val Met Thr Lys Arg
 1           5           10           15
Val Cys Met Gln Leu Val Val Gly Ser Tyr Met Gly Gly Leu Leu Asn

```

	20		25		30										
Ser	Leu	Thr	His	Thr	Cys	Gly	Leu	Leu	Gly	Leu	Pro	Phe	Cys	Gly	Pro
	35						40					45			
Asn	Val	Ile	Asn	His	Tyr	Phe	Cys	Asp	Ile	Pro	Pro	Leu	Leu	Gln	Leu
	50					55					60				
Ala	Cys	Ser	Asp	Thr	His	Arg	Asn	Glu	Thr	Leu	Leu	Leu	Ala	Phe	Ser
65					70				75					80	
Ala	Val	Ile	Ala	Leu	Phe	Thr	Leu	Phe	Val	Ile	Thr	Ala	Ser	Tyr	Met
			85					90					95		
Leu	Ile	Leu	Ser	Val	Ile	Leu	Lys	Ile	Gln	Ser	Asp	Asp	Gly	Arg	Lys
	100						105					110			
Lys	Thr	Phe	His	Thr	Cys	Ala	Ser	His	Leu	Thr	Ala	Ile	Thr	Ile	Phe
	115						120					125			
Phe	Gly	Ser													
	130														

<210> 2571

<211> 114

<212> PRT

<213> Unknown (32508-dir-0-5 conceptual translation of range 2-343)

<400>2571

Ile	Val	Ser	Pro	Leu	Leu	Tyr	Thr	Val	Ala	Met	Ser	Asp	Arg	Lys	Cys
1				5				10					15		
Val	Glu	Leu	Val	Thr	Gly	Ser	Trp	Ile	Gly	Gly	Ile	Val	Asn	Thr	Leu
	20						25					30			
Ile	His	Thr	Ile	Ser	Leu	Arg	Arg	Leu	Ser	Phe	Cys	Arg	Leu	Asn	Ala
	35					40					45				
Val	Ser	His	Phe	Phe	Cys	Asp	Ile	Pro	Ser	Leu	Leu	Lys	Leu	Ser	Cys
	50				55					60					
Ser	Asp	Thr	Ser	Met	Asn	Glu	Leu	Leu	Leu	Leu	Thr	Phe	Ser	Gly	Val
65					70				75					80	
Ile	Ala	Met	Ala	Thr	Phe	Leu	Thr	Val	Ile	Ile	Ser	Tyr	Ile	Phe	Ile
			85					90					95		
Ala	Phe	Ala	Ser	Leu	Arg	Ile	His	Ser	Ala	Ser	Gly	Arg	Gln	Gln	Ala
		100					105						110		
Phe	Ser														

<210> 2572

<211> 315

<212> PRT

<213> Unknown (p42-dir-0-11 conceptual translation of range 1-945)

<400>2572

Met	Glu	Ser	Glu	Ala	Gly	Thr	Asn	Arg	Thr	Ala	Val	Ala	Glu	Phe	Ile
1				5					10					15	
Leu	Leu	Gly	Leu	Val	Gln	Thr	Glu	Glu	Met	Gln	Ser	Val	Val	Phe	Val
	20						25					30			
Leu	Leu	Leu	Phe	Ala	Tyr	Leu	Val	Thr	Gly	Gly	Asn	Pro	Ser	Ile	
	35					40					45				
Leu	Ala	Ala	Val	Leu	Val	Glu	Pro	Lys	Leu	His	Thr	Pro	Met	Tyr	Phe
	50				55					60					
Phe	Leu	Gly	Asn	Leu	Ser	Val	Leu	Asp	Val	Gly	Cys	Ile	Thr	Val	Thr
65					70				75					80	
Val	Pro	Ala	Met	Leu	Gly	Arg	Leu	Leu	Ser	His	Lys	Cys	Ile	Ile	Ser
			85					90					95		
Tyr	Asp	Ala	Cys	Leu	Ser	Gln	Leu	Phe	Phe	Phe	His	Leu	Leu	Ala	Gly
	100						105					110			
Met	Asp	Cys	Phe	Leu	Leu	Thr	Ala	Met	Ala	Tyr	Asp	Arg	Phe	Leu	Ala
	115						120					125			


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Ile Cys Arg Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
 130                      135                      140
Gly Met Leu Val Ala Val Ser Trp Thr Cys Ala Phe Thr Asn Ala Leu
145                      150                      155                      160
Thr His Thr Ile Ala Leu Thr Thr Leu Asn Phe Cys Gly Pro Ser Val
                      165                      170                      175
Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
                      180                      185                      190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Val Ala Ala Ala Phe
                      195                      200                      205
Met Ala Val Val Pro Leu Val Leu Ile Ser Val Ser Tyr Ala His Val
210                      215                      220
Val Ala Ala Val Leu Gln Ile His Ser Ala Glu Gly Arg Lys Lys Ala
225                      230                      235                      240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
                      245                      250                      255
Thr Gly Val Phe Ser Tyr Met Arg Leu Gly Ser Val Glu Ser Ser Asp
260                      265                      270
Lys Asp Lys Gly Val Gly Val Phe Met Thr Val Ile Asn Pro Met Leu
275                      280                      285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Thr Asp Val Gln Gly Ala Leu
290                      295                      300
Trp Gln Leu Leu Val Gly Lys Arg Ser Leu Thr
305                      310                      315

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<210> 2573

<211> 315

<212> PRT

<213> Unknown (p176-dir-0-11 conceptual translation of range 1-945)

<400>2573

```

Met Gln Pro Glu Ser Gly Ala Asn Gly Thr Val Ile Ala Glu Phe Ile
 1                      5                      10                      15
Leu Leu Gly Leu Leu Glu Ala Pro Gly Leu Gln Pro Val Val Phe Val
20                      25                      30
Leu Phe Leu Phe Ala Tyr Leu Val Thr Val Gly Gly Asn Leu Ser Ile
35                      40                      45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ser Pro Met Tyr Phe
50                      55                      60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Ser Val Thr
65                      70                      75                      80
Val Pro Ser Met Leu Ser Arg Leu Leu Ser Arg Lys Arg Ala Val Pro
85                      90                      95
Cys Gly Ala Cys Leu Thr Gln Leu Phe Phe Phe His Leu Phe Val Gly
100                      105                      110
Val Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Phe Leu Ala
115                      120                      125
Ile Cys Arg Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
130                      135                      140
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu
145                      150                      155                      160
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu
165                      170                      175
Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
180                      185                      190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Ala Val Gly Phe Ile
195                      200                      205
Met Ala Gly Thr Pro Met Ala Leu Ile Val Ile Ser Tyr Ile His Val
210                      215                      220
Ala Ala Ala Val Leu Arg Ile Arg Ser Val Glu Gly Arg Lys Lys Ala
225                      230                      235                      240

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Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Met Phe Tyr Gly
 245 250 255
 Ser Gly Ile Phe Asn Tyr Met Arg Leu Gly Ser Thr Lys Leu Ser Asp
 260 265 270
 Lys Asp Lys Ala Val Gly Ile Phe Asn Thr Val Ile Asn Pro Met Val
 275 280 285
 Asn Pro Ile Ile Tyr Arg Phe Arg Asn Pro Glu Val Gln Ser Ala Ile
 290 295 300
 Trp Arg Met Leu Thr Gly Arg Arg Ser Leu Ala
 305 310 315

<210> 2574

<211> 162

<212> PRT

<213> Unknown (1552397-dir-0-6 conceptual translation of range 1-486)

<400>2574

Val Ala Val Cys His Pro Leu Leu Tyr Val Phe His Met Ser Gln Lys
 1 5 10 15
 His Cys Thr Phe Phe Val Ser Ala Ala Trp Ile Ile Gly Phe Leu Asp
 20 25 30
 Pro Thr Ser Tyr Val Val Leu Ile Ser Lys Phe Ser Phe Cys Thr Ser
 35 40 45
 Asn Ile Ile Asp His Phe Phe Cys Asp Leu Ala Pro Leu Leu Lys Leu
 50 55 60
 Ser Cys Ser Asp Thr Phe Gln Ile Glu Val Leu Asn Tyr Val Glu Ser
 65 70 75 80
 Ala Leu Val Thr Leu Asn Ser Phe Val Leu Thr Val Ile Ser Tyr Ile
 85 90 95
 Phe Thr Ile Ser Ala Ile Leu Asn Ile Lys Ser Ala Glu Gly Arg His
 100 105 110
 Lys Ala Phe Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe
 115 120 125
 Tyr Ser Thr Ile Ile Ser Leu Tyr Ile Arg Pro Ile Ser Thr Tyr Ala
 130 135 140
 Pro Lys Gln Asp Gln Phe Phe Ala Leu Leu Tyr Ile Val Leu Ile Pro
 145 150 155 160
 Leu Leu

<210> 2575

<211> 161

<212> PRT

<213> Unknown (1552399-dir-0-6 conceptual translation of range 1-483)

<400>2575

Val Ala Ile Cys Tyr Pro Leu His Tyr Ala Leu Arg Met Ser Leu Lys
 1 5 10 15
 His Cys Ala Lys Ile Ile Val Gly Val Trp Val Ala Gly Phe Leu Ala
 20 25 30
 Pro Val Ile His Thr Val Leu Met Thr Asn Leu Ser Phe Cys Ser Ser
 35 40 45
 Asn His Ile Asn His Phe Leu Cys Asp Leu Thr Pro Val Leu Lys Ile
 50 55 60
 Ser Cys Ser Asp Thr Ser Leu Ile Glu Met Ile Thr Tyr Ile Asp Gly
 65 70 75 80
 Val Ile Val Ala Phe Ser Thr Phe Thr Ile Thr Ser Val Ser Tyr Val
 85 90 95
 Phe Ile Leu Phe Lys Ile Leu Lys Ile His Ser Ser Gln Gly Lys Lys
 100 105 110
 Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe

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<210> 2576
<211> 160
<212> PRT
<213> Unknown (4877302-dir-0-6 conceptual translation of range 2-481)
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<210> 2577
<211> 153
<212> PRT
<213> Unknown (2564501-dir-0-6 conceptual translation of range 1-459)
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1566

<210> 2578

<211> 152

<212> PRT

<213> Unknown (2564499-dir-0-6 conceptual translation of range 1-456)

<400>2578

```

Asn Pro Leu Arg Tyr Thr Thr Ile Met Ser Arg Lys Val Cys Ser Leu
 1              5              10              15
Leu Val Leu Ala Cys Trp Val Gly Gly Ala Val His Ser Thr Ala Gln
      20              25              30
Val Leu Leu Val Met Thr Leu Pro Phe Cys Gly Pro Asn Glu Val Gly
      35              40              45
His Phe Phe Cys Asp Ile Pro Pro Leu Phe Pro Leu Val Cys Thr Asp
      50              55              60
Thr Phe Leu Ser Gly Val Leu Ile Met Ser Asn Ser Gly Leu Ile Ser
      65              70              75              80
Leu Ala Cys Phe Leu Thr Leu Ile Ile Ser Tyr Thr Leu Ile Leu Leu
      85              90              95
Ala Val Arg Arg Cys Ser Ala Glu Gly Lys Ser Lys Ala Leu Ser Thr
      100             105             110
Cys Gly Thr His Leu Thr Val Val Thr Ile Ala Phe Gly Pro Ser Ile
      115             120             125
Phe Ile Tyr Met Lys Pro Met Asn Leu Gln Val Asp Lys Ile Val Ala
      130             135             140
Leu Phe Phe Val Ile Ile Thr Pro
145              150

```

<210> 2579

<211> 205

<212> PRT

<213> Unknown (hg449-dir-0-7 conceptual translation of range 1-616)

<220>

<221> VARIANT

<222> (1)...(205)

<223> Xaa = Any Amino Acid

<400>2579

```

Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr Asp
 1              5              10              15
Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala Gln
      20              25              30
Ile Phe Leu His Phe Cys Gly Ile Pro Trp Ile Phe Leu Leu Pro Leu
      35              40              45
Met Thr Asn Asp Gln Tyr Met Ala Asn Cys Lys Leu Tyr Tyr Tyr Thr
      50              55              60
Thr Ile Met Ser Cys Arg Val Cys His Leu Leu Val Ala Gly Phe Trp
      65              70              75              80
Leu Arg Gly Ile Ile His Ser Met Val Gln Ile Leu Val Ser Val Gln
      85              90              95
Leu Phe Phe Cys Gly Pro Asn Met Ile Asp His Ser Phe Cys Asp Leu
      100             105             110
Gln Val Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Val Glu Gly Val
      115             120             125
Ile Val Leu Ala Asn Ser Glu Leu Val Ser Val Phe Phe Leu Ile Leu
      130             135             140
Val Ser Ser Tyr Ile Ile Ile Leu Val Asn Leu Arg Asn His Ser Ala
      145             150             155             160
Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys Ala Ser Tyr Leu Val Phe
      165             170             175

```

Xaa Thr Cys Ile Phe Leu Tyr Val Xaa Leu Ser Ser Thr Phe Thr Lys
 180 185 190
 Asp Lys Leu Val Ala Val Phe Tyr Val Ile Ile Thr Pro
 195 200 205

<210> 2580

<211> 154

<212> PRT

<213> Unknown (902708-dir-0-6 conceptual translation of range 2-463)

<400>2580

Ile Cys Lys Pro Leu His Tyr Met Thr Ile Met Ser Arg Pro Val Cys
 1 5 10 15
 Ile Phe Leu Val Gly Ala Ala Val Ile Leu Gly Phe Ile His Gly Ala
 20 25 30
 Ile Gln Thr Leu Phe Met Ala Gln Leu Pro Phe Cys Gly Pro Asn Ile
 35 40 45
 Ile Asn His Phe Met Cys Asp Leu Ile Pro Leu Leu Glu Leu Ala Cys
 50 55 60
 Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser Gly Ser
 65 70 75 80
 Leu Cys Leu Leu Thr Phe Ser Met Leu Val Val Ser Tyr Val Val Ile
 85 90 95
 Pro Arg Ser Leu Arg Asn His Ser Ser Glu Gly Arg Arg Lys Ala Leu
 100 105 110
 Ser Thr Cys Ala Ser His Val Thr Val Val Val Leu Phe Leu Val Pro
 115 120 125
 Cys Ser Tyr Leu Tyr Leu Arg Pro Met Thr Ser Phe Pro Thr Asn Lys
 130 135 140
 Ala Val Thr Val Phe Cys Thr Leu Val Thr
 145 150

<210> 2581

<211> 114

<212> PRT

<213> Unknown (32513-dir-0-5 conceptual translation of range 2-343)

<400>2581

Ile Cys Tyr Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Arg Ile Cys
 1 5 10 15
 Val Ala Leu Ala Val Gly Thr Trp Leu Leu Gly Cys Ile His Ser Ser
 20 25 30
 Ile Leu Thr Ser Leu Thr Phe Thr Leu Pro Tyr Cys Gly Pro Asn Glu
 35 40 45
 Val Asp His Phe Phe Cys Asp Ile Pro Ala Leu Leu Pro Leu Ala Cys
 50 55 60
 Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Thr Ser Val Gly Leu
 65 70 75 80
 Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr Thr Arg Ile
 85 90 95
 Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg Arg Arg Ala
 100 105 110
 Phe Ser

<210> 2582

<211> 114

<212> PRT

<213> Unknown (32516-dir-0-5 conceptual translation of range 2-343)

<400>2582

```

Ile Cys His Pro Leu Asn Tyr Pro Val Ile Met Asn Arg Gly Val Phe
 1          5          10          15
Met Lys Leu Val Ile Phe Ser Trp Ile Ser Gly Ile Met Val Ala Thr
          20          25          30
Val Gln Thr Thr Trp Val Phe Ser Phe Pro Phe Cys Gly Pro Asn Glu
          35          40          45
Ile Asn His Leu Phe Cys Glu Thr Pro Pro Val Leu Glu Leu Val Cys
          50          55          60
Ala Asp Thr Phe Leu Phe Glu Ile Tyr Ala Phe Thr Gly Thr Ile Leu
65          70          75          80
Ile Val Met Val Pro Phe Leu Leu Ile Leu Leu Ser Tyr Ile Arg Val
          85          90          95
Leu Phe Ala Ile Leu Lys Met Pro Ser Thr Thr Gly Arg Gln Lys Ala
          100          105          110
Phe Ser

```

<210> 2583

<211> 195

<212> PRT

<213> Unknown (2252615-dir-0-7 conceptual translation of range 1-586)

<400>2583

```

Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr
 1          5          10          15
Ser Cys Val Arg Pro Gln Met Leu Val His Leu Trp Gly Pro His Lys
          20          25          30
Thr Ile Ser Phe Leu Gly Cys Ala Val Gln Leu Phe Ile Phe Leu Leu
          35          40          45
Leu Gly Thr Thr Glu Cys Val Leu Leu Thr Val Met Ala Phe Asp Arg
          50          55          60
Tyr Val Ala Val Cys Gln Pro Leu His Tyr Ala Thr Ile Met His Pro
65          70          75          80
Arg Leu Cys Arg Gln Leu Ala Ala Val Ala Trp Val Met Gly Leu Val
          85          90          95
Gln Ser Ile Val Gln Thr Pro Pro Thr Leu Arg Leu Pro Phe Cys Pro
          100          105          110
His Arg Gln Ile Asp Asp Phe Val Cys Gln Val Pro Ser Leu Ile Arg
          115          120          125
Leu Ser Cys Gly Asp Thr Thr Phe Asn Gly Ile Gln Leu Ala Val Ser
          130          135          140
Ser Val Val Phe Leu Val Val Pro Leu Ala Leu Ile Leu Ile Ser Tyr
145          150          155          160
Gly Ala Ile Ala Arg Ala Val Leu Arg Ile Ser Ser Ala Thr Ala Trp
          165          170          175
Arg Lys Ala Leu Gly Thr Cys Ser Ser His Leu Ala Val Val Thr Leu
          180          185          190
Phe Tyr Ser
          195

```

<210> 2584

<211> 106

<212> PRT

<213> Unknown (3328023-dir-0-5 conceptual translation of range 1-318)

<400>2584

```

Thr Thr Glu Cys Val Leu Leu Thr Val Met Ala Phe Asp Arg Tyr Val
 1          5          10          15
Ala Val Cys Gln Pro Leu His Tyr Ala Thr Ile Met His Pro Arg Leu
          20          25          30
Cys Arg Gln Leu Ala Ala Val Ala Trp Val Met Gly Leu Val Gln Ser

```

```

      35      40      45
Ile Val Gln Thr Pro Pro Thr Leu Arg Leu Pro Phe Cys Pro His Arg
  50      55      60
Arg Val Asp Asp Phe Val Cys Glu Val Pro Ala Leu Ile Arg Leu Ser
65      70      75      80
Cys Gly Asp Thr Thr Tyr Asn Glu Ile Gln Met Ala Val Ala Ser Val
      85      90      95
Phe Ile Leu Val Val Pro Leu Ser Leu Ile
      100      105

```

<210> 2585

<211> 194

<212> PRT

<213> Unknown (2828696-dir-0-7 conceptual translation of range 1-582)

<400>2585

```

Tyr Phe Phe Leu Ser Asp Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr
  1      5      10      15
Ser Cys Val Pro Gln Met Leu Val Asn Leu Trp Gly Pro Lys Lys Thr
      20      25      30
Ile Ser Phe Leu Gly Cys Ser Val Gln Leu Phe Ile Phe Leu Ser Leu
      35      40      45
Gly Thr Thr Glu Cys Ile Leu Leu Thr Val Met Ala Phe Asp Arg Tyr
50      55      60
Val Ala Val Cys Gln Pro Leu His Tyr Ala Thr Ile Ile His Pro Arg
65      70      75      80
Leu Cys Trp Gln Leu Ala Ser Val Ala Trp Val Met Ser Leu Val Gln
      85      90      95
Ser Ile Val Gln Lys Pro Ser Thr Leu His Leu Pro Phe Cys Pro His
      100      105      110
Gln Gln Ile Asp Asp Phe Leu Cys Glu Val Pro Ser Leu Ile Gly Leu
      115      120      125
Ser Cys Gly Asp Thr Ser Tyr Asn Glu Ile Gln Leu Ala Val Ser Ser
      130      135      140
Val Ile Phe Val Val Val Pro Leu Ser Leu Ile Leu Ala Tyr Tyr Gly
145      150      155      160
Ala Thr Ala Gln Ala Val Leu Arg Ile Asn Ser Ala Thr Ala Trp Arg
      165      170      175
Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Phe
      180      185      190
Tyr Ser

```

<210> 2586

<211> 318

<212> PRT

<213> Unknown (4160199-rev-489-12 conceptual translation of range 49035-49987)

<400>2586

```

Gln Glu Gln Ala Met Val Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu
  1      5      10      15
Leu Gly Phe Ser Glu His Pro Gly Leu Glu Arg Thr Leu Phe Val Val
      20      25      30
Val Phe Thr Ser Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile
      35      40      45
Leu Leu Ser Ala Leu Asp Pro Lys Leu His Ser Pro Met Tyr Phe Phe
50      55      60
Leu Ser Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val
65      70      75      80
Pro Gln Met Leu Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe

```

```
<210> 2587
<211> 320
<212> PRT
<213> Unknown (1041044-dir-3-13 conceptual translation of range 488-1447)
```

Gln 1	Glu	Gln	Ala	Met 5	Asp	Asn	Gln	Ser	Ser 10	Thr	Pro	Gly	Phe	Leu 15	Leu
Leu	Gly	Phe	Ser 20	Glu	His	Pro	Gly	Leu 25	Gly	Arg	Thr	Leu	Phe 30	Val	Asp
Val	Ile	Thr 35	Ser	Tyr	Leu	Leu	Thr 40	Leu	Val	Gly	Asn	Thr 45	Leu	Ile	Ile
Leu 50	Leu	Ser	Ala	Leu	Asp	Thr 55	Lys	Leu	His	Ser	Pro 60	Met	Tyr	Phe	Phe
Leu 65	Ser	Asn	Leu	Ser	Phe 70	Leu	Asp	Leu	Cys	Phe 75	Thr	Thr	Ser	Cys	Val
Pro	Gln	Met	Leu 85	Ala	Asn	Leu	Trp	Gly	Pro 90	Lys	Lys	Thr	Ile 95	Ser	Phe
Leu	Asp	Cys	Ser 100	Val	Gln	Ile	Phe	Ile 105	Phe	Leu	Ser	Leu	Gly 110	Thr	Thr
Glu	Cys	Ile 115	Leu	Met	Lys	Val	Met 120	Ala	Phe	Asp	Arg	Tyr 125	Val	Ala	Val
Cys	Gln	Pro	Leu	His	Tyr	Ala 135	Thr	Ile	Ile	His	Pro 140	Arg	Leu	Cys	Trp
Gln 145	Leu	Ala	Ser	Val	Ala 150	Trp	Val	Ile	Gly	Leu 155	Val	Gly	Ser	Val	Val
Gln	Thr	Pro	Ser 165	Thr	Leu	His	Leu	Pro 170	Phe	Cys	Pro	Asp	Arg 175	Gln	Val
Asp	Asp	Phe 180	Val	Cys	Glu	Val	Pro	Ala 185	Leu	Ile	Arg	Leu	Ser 190	Cys	Glu
Asp	Thr	Ser	Tyr	Asn	Glu	Ile	Gln	Val	Ala	Val	Ala	Ser	Val	Phe	Ile

195	200	205
Leu Val Val Pro Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr		
210	215	220
Trp Ala Val Leu Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe		
225	230	235
Gly Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser		
	245	250
Val Ile Ala Val Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg		
	260	265
Gly Lys Phe Phe Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn		
	275	280
Pro Leu Val Tyr Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg		
	290	295
Arg Leu Leu Gly Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala		
305	310	315
		320

<210> 2588

<211> 316

<212> PRT

<213> Unknown (3093312-dir-1364-13 conceptual translation of range 136584-137530)

<400>2588

Val Ala Met Ile Ile Ile Cys Asn Asp Ser His Ser Asp Phe Ile Leu		
1	5	10
Leu Gly Phe Ser Asn Lys Pro His Leu Glu Lys Ile Leu Phe Val Ile		
	20	25
Ile Phe Ile Phe Tyr Phe Leu Thr Leu Ala Gly Asn Met Val Ile Val		
	35	40
Leu Val Ser Leu Lys Asp Pro Lys Leu His Ile Pro Met Tyr Phe Phe		
	50	55
Leu Ser Asn Leu Ser Leu Val Asp Leu Cys Leu Thr Ser Ser Cys Val		
	65	70
Pro Gln Met Leu Ile Asn Phe Trp Gly Pro Glu Lys Thr Ile Ser Tyr		
	85	90
Ile Gly Cys Ala Ile Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr		
	100	105
Glu Tyr Val Leu Leu Val Val Met Ala Val Asp Cys Tyr Val Ala Val		
	115	120
Cys His Pro Leu Gln Asn Thr Met Ile Met His Pro Lys Leu Cys Leu		
	130	135
Gln Leu Ala Ile Leu Ala Trp Gly Thr Gly Leu Ala Gln Ser Leu Ile		
	145	150
Gln Ser Pro Ala Thr Leu Arg Leu Pro Phe Cys Ser Gln Arg Met Val		
	165	170
Asp Asp Val Val Cys Glu Val Pro Ala Leu Ile Gln Leu Ser Ser Thr		
	180	185
Asp Thr Thr Tyr Ser Glu Ile Gln Met Ser Ile Ala Ser Val Val Leu		
	195	200
Leu Val Met Pro Leu Ile Ile Leu Ser Ser Ser Gly Ala Ile Ala		
	210	215
Lys Ala Val Leu Arg Ile Lys Ser Thr Ala Gly Gln Lys Lys Ala Phe		
	225	230
Gly Thr Cys Ile Ser His Leu Leu Val Val Ser Leu Phe Tyr Gly Thr		
	245	250
Val Thr Gly Val Tyr Leu Gln Pro Lys Asn His Tyr Pro His Glu Trp		
	260	265
Gly Lys Phe Leu Thr Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn		
	275	280
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Ile		
	290	295
		300

Arg Leu Gly Arg Arg Thr Trp Asp Ser Gln Asn Asn
305 310 315

<210> 2589

<211> 348

<212> PRT

<213> Unknown (5262456-dir-612-12 conceptual translation of range 61285-62326)

<220>

<221> VARIANT

<222> (1)...(348)

<223> Xaa = Any Amino Acid

<400>2589

Leu	Ile	Phe	Cys	Pro	Met	Ala	Asn	Thr	Leu	Ser	Ser	Leu	Asn	Ser	Cys
1				5					10				15		
Asn	Val	Phe	Leu	Leu	Val	Leu	Asn	Arg	Val	Met	Gly	Met	Thr	Asn	Ser
		20						25					30		
Ser	Val	Lys	Gly	Asp	Phe	Ile	Leu	Val	Gly	Phe	Ser	His	Gln	Pro	His
		35					40					45			
Leu	Glu	Lys	Ile	Leu	Phe	Val	Ala	Val	Leu	Ile	Ser	Tyr	Leu	Leu	Thr
	50					55					60				
Leu	Val	Gly	Asn	Thr	Val	Ile	Ile	Leu	Ile	Cys	Ser	Val	Asp	Pro	Lys
65					70					75					80
Leu	Lys	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	His	Leu	Ser	Leu	Val	Asp
				85					90					95	
Ile	Cys	Phe	Thr	Thr	Ser	Ile	Val	Pro	Gln	Leu	Leu	Trp	Asn	Leu	Lys
			100					105					110		
Gly	Pro	Asp	Lys	Thr	Ile	Thr	Phe	Leu	Gly	Cys	Val	Ile	Gln	Leu	Tyr
		115					120					125			
Ile	Ser	Leu	Ala	Leu	Gly	Ser	Thr	Glu	Cys	Val	Leu	Leu	Ala	Val	Met
	130					135					140				
Ala	Phe	Asp	Arg	Tyr	Ala	Ala	Val	Cys	Lys	Pro	Leu	His	Tyr	Thr	Ala
145					150					155					160
Val	Met	Asn	Pro	Gln	Leu	Cys	Gln	Ala	Leu	Ala	Gly	Val	Ala	Trp	Leu
				165					170					175	
Ser	Gly	Val	Gly	Asn	Thr	Leu	Ile	Gln	Gly	Thr	Val	Thr	Leu	Trp	Leu
			180					185					190		
Pro	Arg	Cys	Gly	His	Arg	Leu	Leu	Gln	His	Phe	Phe	Cys	Glu	Val	Pro
		195				200						205			
Ser	Met	Ile	Lys	Leu	Ala	Cys	Val	Asp	Ile	His	Asp	Asn	Glu	Val	Gln
	210					215					220				
Leu	Phe	Val	Ala	Ser	Leu	Val	Leu	Leu	Leu	Leu	Pro	Leu	Val	Leu	Ile
225					230					235					240
Leu	Leu	Ser	Tyr	Gly	His	Ile	Ala	Lys	Val	Val	Ile	Arg	Ile	Lys	Ser
			245						250					255	
Val	Gln	Ala	Trp	Cys	Lys	Gly	Leu	Gly	Thr	Cys	Gly	Ser	His	Leu	Ile
			260					265					270		
Val	Val	Ser	Leu	Phe	Cys	Gly	Thr	Ile	Thr	Ala	Val	Tyr	Ile	Gln	Ser
		275					280					285			
Asn	Ser	Ser	Tyr	Ala	His	Ala	His	Gly	Lys	Phe	Ile	Ser	Leu	Phe	Tyr
	290					295					300				
Thr	Val	Val	Thr	Pro	Thr	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Asn
305					310					315					320
Asn	Asp	Val	Lys	Gly	Ala	Leu	Arg	Leu	Phe	Asn	Arg	Asp	Leu	Gly	Thr
			325						330					335	
Xaa	Lys	Met	Lys	Gln	Ser	Thr	Gln	Arg	Ser	Thr	Phe				
			340					345							

<210> 2590

<211> 312

<212> PRT

<213> Unknown (200153-dir-0-11 conceptual translation of range 1-936)

<400>2590

```

Met Glu Val Asp Ser Asn Ser Ser Ser Gly Thr Phe Ile Leu Met Gly
 1           5           10           15
Val Ser Asp His Pro His Leu Glu Ile Ile Phe Phe Ala Val Ile Leu
          20           25           30
Ala Ser Tyr Leu Leu Thr Leu Val Gly Asn Leu Thr Ile Ile Leu Leu
          35           40           45
Ser Arg Leu Asp Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50           55           60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Thr Thr Ser Ser Val Pro Gln
          65           70           75           80
Met Leu Lys Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Gly Gly
          85           90           95
Cys Val Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
          100          105          110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
          115          120          125
Pro Leu His Tyr Met Thr Val Met Asn Pro Arg Leu Cys Trp Gly Leu
          130          135          140
Ala Ala Ile Ser Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
          145          150          155          160
Thr Phe Thr Leu Gln Leu Pro Phe Cys Gly His Arg Lys Val Asp Asn
          165          170          175
Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr
          180          185          190
Ser Leu Asn Glu Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Val
          195          200          205
Val Pro Val Ser Val Ile Leu Val Ser Tyr Cys Phe Ile Ala Gln Ala
          210          215          220
Val Met Lys Ile Arg Ser Val Glu Gly Arg Arg Lys Ala Phe Asn Thr
          225          230          235          240
Cys Val Ser His Leu Val Val Val Phe Leu Phe Tyr Gly Ser Ala Ile
          245          250          255
Tyr Gly Tyr Leu Leu Pro Ala Lys Ser Ser Asn Gln Ser Gln Gly Lys
          260          265          270
Phe Ile Ser Leu Phe Tyr Ser Val Val Thr Pro Met Val Asn Pro Leu
          275          280          285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly Arg Leu
          290          295          300
Leu Gly Lys Gly Arg Gly Ala Ser
          305          310

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<210> 2591

<211> 157

<212> PRT

<213> Unknown (902728-dir-0-6 conceptual translation of range 2-472)

<400>2591

```

Val Cys Arg Pro Leu His Tyr Met Thr Val Met Asn Pro Arg Leu Cys
 1           5           10           15
Trp Val Leu Ala Ala Ile Ser Trp Leu Gly Gly Leu Gly Asn Ser Val
          20           25           30
Ile Gln Ser Thr Phe Thr Leu Gln Leu Pro Phe Cys Gly His Arg Lys
          35           40           45
Val Asp Asn Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys
          50           55           60
Gly Asp Thr Ser Leu Asn Glu Ala Val Leu Asn Gly Val Cys Thr Phe

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65					70					75				80
Phe	Thr	Ala	Val	Pro	Leu	Ser	Ile	Ile	Leu	Val	Ser	Tyr	Cys	Phe Ile
				85					90					95
Ala	Gln	Ala	Val	Met	Lys	Ile	Arg	Ser	Val	Glu	Gly	Arg	Arg	Lys Ala
			100					105					110	
Phe	Asn	Thr	Cys	Val	Ser	His	Leu	Val	Val	Val	Phe	Leu	Phe	Tyr Gly
		115					120					125		
Ser	Ala	Ile	Tyr	Gly	Tyr	Leu	Leu	Pro	Ala	Lys	Ser	Ser	Asn	Gln Asp
		130					135					140		
Gln	Gly	Lys	Phe	Ile	Ser	Leu	Phe	Tyr	Ser	Val	Val	Thr		
145					150					155				

<210> 2592

<211> 312

<212> PRT

<213> Unknown (p146-dir-0-11 conceptual translation of range 1-936)

<400>2592

Met	Asp	Gly	Val	Asn	Asp	Ser	Ser	Leu	Gln	Gly	Phe	Val	Leu	Met	Ser
1				5					10					15	
Ile	Ser	Asp	His	Pro	Gln	Leu	Glu	Met	Ile	Phe	Phe	Ile	Ala	Ile	Leu
		20						25					30		
Phe	Ser	Tyr	Leu	Leu	Thr	Leu	Leu	Gly	Asn	Ser	Thr	Ile	Ile	Leu	Leu
		35					40					45			
Ser	Arg	Leu	Glu	Ala	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
		50					55				60				
Asn	Leu	Ser	Ser	Leu	Asp	Leu	Ala	Phe	Ala	Thr	Ser	Ser	Val	Pro	Gln
65					70					75				80	
Met	Leu	Ile	Asn	Leu	Trp	Gly	Pro	Gly	Lys	Thr	Ile	Ser	Tyr	Gly	Gly
			85						90					95	
Cys	Ile	Thr	Gln	Leu	Tyr	Val	Phe	Leu	Trp	Leu	Gly	Ala	Thr	Glu	Cys
			100					105					110		
Ile	Leu	Leu	Val	Val	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Val	Cys	Arg
		115					120					125			
Pro	Leu	Arg	Tyr	Thr	Ala	Ile	Met	Asn	Pro	Gln	Leu	Cys	Trp	Leu	Leu
		130					135					140			
Ala	Val	Ile	Ala	Trp	Leu	Gly	Gly	Leu	Gly	Asn	Ser	Val	Ile	Gln	Ser
145					150					155				160	
Thr	Phe	Thr	Leu	Gln	Leu	Pro	Leu	Cys	Gly	His	Arg	Arg	Val	Glu	Gly
			165						170					175	
Phe	Leu	Cys	Glu	Val	Pro	Ala	Met	Ile	Lys	Leu	Ala	Cys	Gly	Asp	Thr
			180					185					190		
Ser	Leu	Asn	Gln	Ala	Val	Leu	Asn	Gly	Val	Cys	Thr	Phe	Phe	Thr	Ala
		195					200					205			
Val	Pro	Leu	Ser	Ile	Ile	Val	Ile	Ser	Tyr	Cys	Leu	Ile	Ala	Gln	Ala
		210					215					220			
Val	Leu	Lys	Ile	His	Ser	Ala	Glu	Gly	Arg	Arg	Lys	Ala	Phe	Asn	Thr
225					230					235				240	
Cys	Leu	Ser	His	Leu	Val	Val	Phe	Leu	Phe	Tyr	Gly	Ser	Ala	Ser	
			245						250				255		
Tyr	Gly	Tyr	Leu	Leu	Pro	Ala	Lys	Asn	Ser	Lys	Gln	Asp	Gln	Gly	Lys
			260					265					270		
Phe	Ile	Ser	Leu	Phe	Tyr	Ser	Leu	Val	Thr	Pro	Met	Val	Asn	Pro	Leu
		275					280					285			
Ile	Tyr	Thr	Leu	Arg	Asn	Met	Glu	Val	Lys	Gly	Ala	Leu	Arg	Arg	Leu
		290					295					300			
Leu	Gly	Lys	Gly	Arg	Glu	Val	Gly								
305					310										

<210> 2593

<211> 216

<212> PRT

<213> Unknown (2921701-dir-0-8 conceptual translation of range 2-648)

<400>2593

```

Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val
 1           5           10           15
Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala
 20           25           30
Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu
 35           40           45
Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg Pro Leu His
 50           55           60
Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala
 65           70           75           80
Ser Arg Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser Thr Leu Thr
 85           90           95
Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys
 100          105          110
Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn
 115          120          125
Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu Ile Pro Leu
 130          135          140
Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg
 145          150          155          160
Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser
 165          170          175
His Leu Ile Val Val Ser Leu Phe Lys Gly Thr Ala Val Ser Val Tyr
 180          185          190
Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser
 195          200          205
Leu Phe Tyr Gly Ile Ile Ala Pro
 210          215

```

<210> 2594

<211> 216

<212> PRT

<213> Unknown (2921699-dir-0-8 conceptual translation of range 2-649)

<400>2594

```

Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val
 1           5           10           15
Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala
 20           25           30
Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu
 35           40           45
Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg Pro Leu His
 50           55           60
Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala
 65           70           75           80
Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser Thr Leu Thr
 85           90           95
Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys
 100          105          110
Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn
 115          120          125
Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu Ile Pro Leu
 130          135          140
Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg
 145          150          155          160
Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser
 165          170          175

```

His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val Ser Val Tyr
 180 185 190
 Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser
 195 200 205
 Leu Phe Tyr Gly Ile Ile Ala Pro
 210 215

<210> 2595

<211> 215

<212> PRT

<213> Unknown (2921706-dir-0-8 conceptual translation of range 2-646)

<220>

<221> VARIANT

<222> (1)...(215)

<223> Xaa = Any Amino Acid

<400>2595

Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln Met Leu Val
 1 5 10 15
 Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly Cys Val Ala
 20 25 30
 Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr Leu Leu Leu
 35 40 45
 Ala Val Thr Ser Leu Ile Gly Cys Ser Tyr Cys Arg Pro Leu His Tyr
 50 55 60
 Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu Ala Ala Ala Ser
 65 70 75 80
 Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser Thr Leu Thr Leu
 85 90 95
 Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His Phe Leu Cys Glu
 100 105 110
 Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr Thr Ala Asn Glu
 115 120 125
 Ala Glu Leu Phe Leu Asp Ser Glu Leu Phe His Leu Ile Pro Leu Thr
 130 135 140
 Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala Val Leu Arg Ile
 145 150 155 160
 Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser His
 165 170 175
 Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val Ser Val Tyr Leu
 180 185 190
 Xaa Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys Met Val Ser Leu
 195 200 205
 Phe Tyr Gly Ile Ile Ala Pro
 210 215

<210> 2596

<211> 112

<212> PRT

<213> Unknown (1142995-dir-0-5 conceptual translation of range 1-336)

<400>2596

Arg Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln
 1 5 10 15
 Leu Ala Ala Val Ser Trp Ile Ile Gly Phe Gly Asn Ser Val Trp Leu
 20 25 30
 Ser Ile Leu Thr Leu Gln Leu Pro Arg Cys Gly His Tyr Val Ile Asp
 35 40 45
 His Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp
 50 55 60

Val Thr Ala Asn Glu Ala Glu Leu Phe Phe Val Ser Val Phe Phe His
 65 70 75 80
 Leu Thr Pro Leu Ser Leu Ile Leu Thr Ser Tyr Ala Phe Ile Ala Arg
 85 90 95
 Ala Ile Leu Lys Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly
 100 105 110

<210> 2597

<211> 314

<212> PRT

<213> Unknown (3080457-rev-750-12 conceptual translation of range 75137-76079)

<400>2597

Asn Met Asn Trp Val Asn Lys Ser Val Pro Gln Glu Phe Ile Leu Leu
 1 5 10 15
 Val Phe Ser Asp Gln Pro Trp Leu Glu Ile Pro Pro Phe Val Met Phe
 20 25 30
 Leu Phe Ser Tyr Ile Leu Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu
 35 40 45
 Val Ser His Val Asp Phe Lys Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro
 65 70 75 80
 Gln Met Leu Val Asn Ile Cys Asn Thr Arg Lys Val Ile Ser Tyr Gly
 85 90 95
 Gly Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ser Thr Glu
 100 105 110
 Cys Leu Leu Leu Ala Val Met Cys Phe Asp Arg Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Ser Ile Ile Met His Gln Arg Leu Cys Phe Gln
 130 135 140
 Leu Ala Ala Ala Ser Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln
 145 150 155 160
 Ser Thr Trp Thr Leu Lys Met Pro Leu Cys Gly His Lys Glu Val Asp
 165 170 175
 His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp
 180 185 190
 Thr Thr Ala Asn Glu Ala Glu Leu Phe Phe Ile Ser Val Leu Phe Leu
 195 200 205
 Leu Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln
 210 215 220
 Ala Val Leu Arg Ile Gln Ser Ala Glu Gly Gln Arg Lys Ala Phe Gly
 225 230 235 240
 Thr Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala
 245 250 255
 Ile Ser Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly
 260 265 270
 Lys Met Val Ser Leu Phe Cys Gly Ile Ile Ala Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Ala Phe Lys Arg
 290 295 300
 Leu Leu Gln Arg Val Phe Leu Ile Lys Lys
 305 310

<210> 2598

<211> 343

<212> PRT

<213> Unknown (506841-dir-0-12 conceptual translation of range 60-1090)

<220>

<221> VARIANT

<222> (1)...(343)

<223> Xaa = Any Amino Acid

<400>2598

Cys Ile Ile Tyr Met Ser Val Ala Asn Glu Ser Ile Ser Arg Glu Phe
 1 5 10 15
 Ile Leu Leu Gly Phe Ser Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe
 20 25 30
 Val Val Phe Leu Val Ser Tyr Ile Leu Thr Ile Phe Gly Asn Met Met
 35 40 45
 Ile Ile Leu Val Ser Arg Leu Asp Ser Lys Leu His Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Thr Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser
 65 70 75 80
 Thr Val Pro Gln Met Leu Ile Asn Ile Cys Ser Thr Arg Lys Val Ile
 85 90 95
 Ser Tyr Gly Gly Cys Val Val Gln Leu Phe Ile Phe Leu Ser Leu Gly
 100 105 110
 Ser Thr Glu Cys Phe Leu Leu Gly Val Met Ser Leu Asp Arg Phe Leu
 115 120 125
 Ala Ile Cys Arg Pro Leu His Tyr Ser Val Ile Met His Gln Arg Arg
 130 135 140
 Cys Leu His Leu Ala Ala Cys Trp Ile Ser Gly Phe Ser Asn Ser
 145 150 155 160
 Val Leu Gln Ser Thr Trp Thr Leu Gln Met Pro Leu Cys Gly His Lys
 165 170 175
 Glu Val Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser
 180 185 190
 Cys Val Asp Thr Thr Ala Asn Glu Ala Glu Leu Phe Phe Ile Ser Val
 195 200 205
 Leu Phe Leu Leu Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe
 210 215 220
 Ile Val Gln Ala Val Leu Lys Ile Arg Ser Ala Glu Cys Arg Arg Lys
 225 230 235 240
 Ala Phe Gly Thr Cys Gly Ser His Leu Ile Val Val Val Leu Phe Tyr
 245 250 255
 Gly Thr Ala Ile Tyr Met Tyr Leu Gln Pro Pro Ser Pro Ser Lys
 260 265 270
 Asp Arg Gly Lys Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Pro Met
 275 280 285
 Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Glu Glu Val Lys Gly Ala
 290 295 300
 Phe Lys Arg Leu Met Lys Arg Ile Ile Leu Ile Gly Lys Xaa Gly Val
 305 310 315 320
 Pro Glu Xaa Xaa Pro Tyr Xaa Tyr Lys Tyr Ile Phe Ile Ala Cys Lys
 325 330 335
 Leu Tyr Cys Phe Leu Leu Cys
 340

<210> 2599

<211> 348

<212> PRT

<213> Unknown (3093312-rev-75-13 conceptual translation of range 7680-8721)

<220>

<221> VARIANT

<222> (1)...(348)

<223> Xaa = Any Amino Acid

<400>2599

Leu Ile Ala Phe Leu Ser Tyr Ile Phe Leu Gly Val Arg Asn Lys Xaa
 1 5 10 15
 Val Ile Met Asn Trp Glu Asn Glu Ser Ser Pro Lys Glu Phe Ile Leu
 20 25 30
 Leu Gly Phe Ser Asp Arg Ala Trp Leu Gln Met Pro Leu Phe Val Val
 35 40 45
 Leu Leu Ile Ser Tyr Thr Ile Thr Ile Phe Gly Asn Val Ser Ile Met
 50 55 60
 Met Val Cys Ile Leu Asp Pro Lys Leu His Thr Pro Met Tyr Phe Phe
 65 70 75 80
 Leu Thr Asn Leu Ser Ile Leu Asp Leu Cys Tyr Thr Thr Thr Thr Val
 85 90 95
 Pro His Met Leu Val Asn Ile Gly Cys Asn Lys Lys Thr Ile Ser Tyr
 100 105 110
 Ala Gly Cys Val Ala His Leu Ile Ile Phe Leu Ala Leu Gly Ala Thr
 115 120 125
 Glu Cys Leu Leu Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val
 130 135 140
 Cys Arg Pro Leu His Tyr Val Val Ile Met Asn Tyr Trp Phe Cys Leu
 145 150 155 160
 Arg Met Ala Ala Phe Ser Trp Leu Ile Gly Phe Gly Asn Ser Val Leu
 165 170 175
 Gln Ser Ser Leu Thr Leu Asn Met Pro Arg Cys Gly His Gln Glu Val
 180 185 190
 Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala
 195 200 205
 Asp Thr Lys Pro Ile Glu Ala Glu Leu Phe Phe Phe Ser Val Leu Ile
 210 215 220
 Leu Leu Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Gly Phe Ile Ala
 225 230 235 240
 Gln Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe
 245 250 255
 Gly Thr Cys Gly Ser His Met Ile Val Val Ser Leu Phe Tyr Gly Thr
 260 265 270
 Ala Ile Tyr Met Tyr Leu Gln Pro Ser Ser Thr Ser Lys Asp Trp
 275 280 285
 Gly Lys Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Ser Met Leu Asn
 290 295 300
 Ser Leu Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Glu Ala Phe Lys
 305 310 315 320
 Arg Leu Met Pro Arg Ile Phe Phe Cys Lys Lys Xaa Arg Ser Thr Pro
 325 330 335
 Ser Val Met Arg Ile Phe Leu Val Phe Pro Tyr Leu
 340 345

<210> 2600

<211> 272

<212> PRT

<213> Unknown (5262456-rev-0-10 conceptual translation of range 184-1000)

<400>2600

Met Trp Ile Asn Asn Gln Ser Ser Leu Asp Asp Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Pro Trp Leu Glu Thr Pro Leu Val Ile Phe Leu Val
 20 25 30
 Ala Tyr Ile Phe Ser Leu Phe Gly Asn Ile Ser Ile Ile Leu Val Ser
 35 40 45
 His Leu Asp Pro Gln Leu Asp Ser Pro Met Tyr Phe Phe Val Ser Asn
 50 55 60
 Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln Met
 65 70 75 80

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Leu Val Asn Leu Arg Gly Pro Glu Lys Thr Ile Ser Tyr Gly Gly Cys
      85                      90                      95
Val Ala Gln Leu Tyr Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys Ile
      100                    105                    110
Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Lys Pro
      115                    120                    125
Leu His Tyr Pro Val Ile Met Asn His Arg Arg Cys Ile His Met Ala
      130                    135                    140
Ala Gly Thr Trp Ile Ser Gly Phe Ala Asn Ser Leu Val Gln Ser Thr
      145                    150                    155                    160
Leu Thr Val Val Ala Pro Arg Cys Gly Gln Arg Val Leu Asp His Phe
      165                    170                    175
Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ile Asp Ile Arg
      180                    185                    190
Val Asn Glu Met Glu Leu Asn Val Leu Gly Ala Leu Leu Leu Met
      195                    200                    205
Pro Leu Thr Leu Ile Leu Gly Thr Tyr Val Phe Ile Ala Gln Ala Val
      210                    215                    220
Met Arg Ile Cys Ser Ala Glu Ser Arg Trp Lys Ala Phe Asn Thr Cys
      225                    230                    235                    240
Ala Ser His Leu Leu Val Val Ser Leu Phe Tyr Phe Thr Ala Ile Ser
      245                    250                    255
Met Tyr Val Gln Pro Pro Ser Ser Tyr Ser His Asp Arg Gly Lys Ile
      260                    265                    270

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<210> 2601

<211> 350

<212> PRT

<213> Unknown (3093312-dir-1027-12 conceptual translation of range 102817-103865)

<220>

<221> VARIANT

<222> (1)...(350)

<223> Xaa = Any Amino Acid

<400>2601

```

Phe Leu Ser Gly Asn Arg Lys Xaa Met Met Met Glu Lys Xaa Asn Ala
  1                      5                      10                      15
Ser Ser Glu Gly Tyr Phe Ile Leu Val Gly Phe Ser Asn Trp Pro Tyr
      20                    25                    30
Leu Glu Val Val Leu Phe Val Val Ile Leu Ile Phe Cys Leu Met Thr
      35                    40                    45
Leu Ile Gly Asn Leu Phe Ile Ile Ile Leu Thr Tyr Leu Asp Ser His
      50                    55                    60
Leu His Thr Pro Leu Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu Asp
      65                    70                    75                    80
Leu Cys Tyr Thr Thr Ser Ser Ile Pro Gln Leu Leu Val Ser Leu Trp
      85                    90                    95
Gly Val Glu Lys Thr Ile Ser Tyr Ala Gly Cys Met Val Gln Leu Tyr
      100                   105                   110
Phe Phe Leu Thr Leu Gly Thr Thr Glu Cys Val Leu Leu Val Val Met
      115                   120                   125
Ser Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro Leu His Tyr Thr Val
      130                   135                   140
Leu Met His Ser Arg Phe Cys His Leu Leu Ala Val Ala Ser Trp Val
      145                   150                   155                   160
Ser Gly Phe Thr Asn Pro Ala Leu His Ser Ser Phe Thr Phe Trp Val
      165                   170                   175
Pro Leu Cys Gly His Arg Gln Ile Asp His Phe Phe Cys Glu Val Pro
      180                   185                   190

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Ala Leu Leu Xaa Leu Ser Phe Val Asn Thr Arg Glu Asn Lys Leu Thr
 195 200 205
 Leu Met Ile Thr Ser Ser Ile Phe Val Leu Leu Leu Thr Leu Ile
 210 215 220
 Phe Thr Ser Tyr Gly Ala Ile Ala Gln Ala Val Leu Arg Met Gln Ser
 225 230 235 240
 Thr Thr Gly Leu Gln Lys Val Phe Gly Thr Cys Gly Ala His His Met
 245 250 255
 Val Val Ser Leu Phe Phe Ile Pro Ala Met Cys Met Tyr Leu Gln Pro
 260 265 270
 Pro Ser Gly Asn Ser Gln Asp Gln Gly Lys Phe Ile Ala Leu Phe Tyr
 275 280 285
 Thr Val Val Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
 290 295 300
 Lys Asp Val Arg Gly Val Val Lys Arg Leu Arg Gly Trp Glu Xaa Ala
 305 310 315 320
 Cys Val Cys Val Ile Leu Thr Ile Xaa Trp Ser Leu Ser Ser Gln Xaa
 325 330 335
 Phe Ile His Leu Phe Ile Tyr Gln Pro Phe Phe Tyr Ser Leu
 340 345 350

<210> 2602

<211> 205

<212> PRT

<213> Unknown (5262456-dir-273-9 conceptual translation of range 27452-28066)

<400>2602

Gln Lys Ile Ala Lys Met Ile Asn Asp Ser Tyr Phe Gly Trp Leu Met
 1 5 10 15
 Leu Leu Gly Phe Pro Gly Lys Pro Gln Leu Glu Met Ile Ile Ser Gly
 20 25 30
 Val Val Phe Phe Phe Tyr Ala Ile Ser Leu Met Gly Asn Met Val Leu
 35 40 45
 Ile Leu Leu Pro Leu Leu Asp Lys His Leu Gln Thr Pro Ile Tyr Phe
 50 55 60
 Phe Leu Arg Asn Leu Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile
 65 70 75 80
 Val Pro Gln Met Leu Val Asn Ala Trp Gly Lys Asp Lys Lys Ile Thr
 85 90 95
 Phe Gly Gly Cys Ala Phe Gln Leu Phe Thr Asn Val Thr Leu Cys Thr
 100 105 110
 Val Glu Cys Met Leu Leu Ala Val Met Ser Tyr Asp Pro Phe Asn Ala
 115 120 125
 Val Cys Lys Pro Leu Asp Tyr Met Thr Ile Met Asn Pro Gln Leu Cys
 130 135 140
 Gln Gly Leu Val Ala Met Thr Trp Leu Ile Gly Val Thr Asn Cys Met
 145 150 155 160
 Ile Leu Ser Pro Cys Pro Val Ser Leu Pro Arg Cys Gly Asp His His
 165 170 175
 Leu Asp His Tyr Phe Cys Glu Ile Ser Ala Met Val Lys Ile Ala Cys
 180 185 190
 Gly Ala Thr Thr Val Met Glu Glu Thr Val Arg Val Lys
 195 200 205

<210> 2603

<211> 210

<212> PRT

<213> Unknown (2924249-rev-741-9 conceptual translation of range 74285-74912)

<220>

<221> VARIANT

<222> (1)...(210)

<223> Xaa = Any Amino Acid

<400>2603

```

Ser Val Lys Tyr Leu Asn Glu Ser Phe Pro Glu Asp Phe Ile Leu Met
 1           5           10           15
Gly Phe Val Lys Tyr Pro Trp Leu Asp Phe Leu Leu Phe Cys Val Leu
      20           25           30
Leu Thr Phe Tyr Met Phe Thr Leu Leu Gly Asn Ser Ala Ile Ile Leu
      35           40           45
Val Ser Gln Leu Asp Ser Gln Leu His Ser Pro Met Tyr Phe Leu Leu
      50           55           60
Thr Ser Leu Ser Val Leu Tyr Leu Cys Phe Thr Thr Thr Thr Val Pro
65           70           75           80
Gln Met Leu Phe Asn Leu Gly Gly Thr Asn Lys Asn Ile Thr Xaa Ile
      85           90           95
Gly Cys Met Ala Gln Ala Tyr Val Phe His Trp Leu Ala Cys Ile Glu
      100          105          110
Cys Val Leu Leu Gly Ile Val Ala Leu Asp Cys Tyr Val Ala Val Cys
      115          120          125
Lys Pro Pro Arg Tyr Thr Ile Ile Ile Asp His Lys Val Cys Leu His
130          135          140
Leu Ser Ser Thr Ala Trp Leu Ile Gly Leu Ala Asn Ser Leu Leu Gln
145          150          155          160
Ser Thr Ile Thr Ile Gln Leu Pro Leu Xaa Arg Cys Ile Ala Gln Ile
      165          170          175
Phe Leu Xaa Leu Glu Ser Val Thr Xaa Gln Ser Leu Thr Val Thr Tyr
      180          185          190
Leu Xaa Asp Leu Leu Gln His Ser Ile Xaa Gly Gln Leu His Ala Gly
      195          200          205
Glu Leu
      210

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<210> 2604

<211> 210

<212> PRT

<213> Unknown (4156137-rev-1191-9 conceptual translation of range 119253-119880)

<220>

<221> VARIANT

<222> (1)...(210)

<223> Xaa = Any Amino Acid

<400>2604

```

Ser Val Lys Tyr Leu Asn Glu Ser Phe Pro Glu Asp Phe Ile Leu Met
 1           5           10           15
Gly Phe Val Lys Tyr Pro Trp Leu Asp Phe Leu Leu Phe Cys Val Leu
      20           25           30
Leu Thr Phe Tyr Met Phe Thr Leu Leu Gly Asn Ser Ala Ile Ile Leu
      35           40           45
Val Ser Gln Leu Asp Ser Gln Leu His Ser Pro Met Tyr Phe Leu Leu
      50           55           60
Thr Ser Leu Ser Val Leu Tyr Leu Cys Phe Thr Thr Thr Thr Val Pro
65           70           75           80
Gln Met Leu Phe Asn Leu Gly Gly Thr Asn Lys Asn Ile Thr Xaa Ile
      85           90           95
Gly Cys Met Ala Gln Ala Tyr Val Phe His Trp Leu Ala Cys Thr Glu
      100          105          110
Cys Val Leu Leu Gly Ile Val Ala Leu Asp Cys Tyr Val Ala Val Cys
      115          120          125

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Lys Pro Pro Arg Tyr Thr Ile Ile Ile Asp His Lys Val Tyr Leu His
 130 135 140
 Leu Ser Ser Thr Ala Trp Leu Ile Gly Leu Ala Asn Ser Leu Leu Gln
 145 150 155 160
 Ser Thr Ile Thr Ile Gln Leu Pro Leu Xaa Arg Cys Ile Ala Gln Ile
 165 170 175
 Phe Leu Xaa Leu Glu Ser Val Thr Xaa Gln Ser Leu Thr Val Thr Tyr
 180 185 190
 Leu Xaa Asp Leu Leu Gln His Ser Ile Xaa Gly Gln Leu His Ala Gly
 195 200 205
 Glu Leu
 210

<210> 2605

<211> 216

<212> PRT

<213> Unknown (2921643-dir-0-8 conceptual translation of range 2-649)

<400>2605

Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln Leu Leu Ala
 1 5 10 15
 His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser Cys Ala Ala
 20 25 30
 Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu
 35 40 45
 Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg
 50 55 60
 Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu Ala Ile Thr
 65 70 75 80
 Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr Ala Ile Thr
 85 90 95
 Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His Ile Ser Cys
 100 105 110
 Glu Leu Leu Ala Val Val Arg Leu Ala Arg Val Asp Thr Ser Ser Asn
 115 120 125
 Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe
 130 135 140
 Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys
 145 150 155 160
 Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr Cys Ala Ser
 165 170 175
 His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr
 180 185 190
 Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Phe Ser
 195 200 205
 Val Phe Tyr Ala Ile Leu Thr Pro
 210 215

<210> 2606

<211> 216

<212> PRT

<213> Unknown (2921711-dir-0-8 conceptual translation of range 2-649)

<400>2606

Leu Val Asp Val Ser Cys Ala Thr Ser Val Val Pro Gln Leu Leu Ala
 1 5 10 15
 His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser Cys Ala Ala
 20 25 30
 Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg

50		55		60	
Tyr Ser Ala Ile Met	His Gly Gly Leu Cys	Ala Arg Leu Ala Ile Thr			
65	70	75	80		
Ser Trp Val Ser Gly	Phe Ile Ser Ser	Pro Val Gln Thr Ala Ile Thr			
85	90	95			
Phe Gln Leu Pro Met	Cys Arg Asn Lys	Phe Ile Asp His Ile Ser Cys			
100	105	110			
Glu Leu Leu Ala Val	Val Arg Leu Ala Cys	Val Asp Thr Ser Ser Asn			
115	120	125			
Glu Val Thr Ile Met	Val Ser Ile Val Leu	Leu Met Thr Pro Phe			
130	135	140			
Cys Leu Val Leu Leu	Ser Tyr Ile Gln Ile	Ile Ser Thr Ile Leu Lys			
145	150	155	160		
Ile Gln Ser Arg Glu	Gly Arg Lys Lys	Ala Phe His Thr Cys Ala Ser			
165	170	175			
His Leu Thr Val Ala	Leu Cys Tyr Gly	Val Ala Ile Phe Thr Tyr			
180	185	190			
Ile Gln Pro His Ser	Ser Pro Ser Val	Leu Gln Glu Lys Leu Phe Ser			
195	200	205			
Val Phe Tyr Ala Ile	Leu Thr Pro				
210	215				

<210> 2607

<211> 317

<212> PRT

<213> Unknown (1336042-dir-0-11 conceptual translation of range 1-951)

<400>2607

Met Gly Thr Asp Asn	Gln Thr Trp Val	Ser Glu Phe Ile Leu Leu Gly	
1	5	10	15
Leu Ser Ser Asp Trp	Asp Thr Arg Val	Ser Leu Phe Val Leu Phe Leu	
20	25	30	
Val Met Tyr Val Val	Thr Val Leu Gly	Asn Cys Leu Ile Val Leu Leu	
35	40	45	
Ile Arg Leu Asp Ser	Arg Leu His Thr	Pro Met Tyr Phe Phe Leu Thr	
50	55	60	
Asn Leu Ser Leu Val	Asp Val Ser Tyr	Ala Thr Ser Val Val Pro Gln	
65	70	75	80
Leu Leu Ala His Phe	Leu Ala Glu His	Lys Ala Ile Pro Phe Gln Ser	
85	90	95	
Cys Ala Ala Gln Leu	Phe Phe Ser Leu	Ala Leu Gly Gly Ile Glu Phe	
100	105	110	
Val Leu Leu Ala Val	Met Ala Tyr Asp	Arg Tyr Val Ala Val Cys Asp	
115	120	125	
Ala Leu Arg Tyr Ser	Ala Ile Met His	Gly Gly Leu Cys Ala Arg Leu	
130	135	140	
Ala Ile Thr Ser Trp	Val Ser Gly Phe	Ile Ser Ser Pro Val Gln Thr	
145	150	155	160
Ala Ile Thr Phe Gln	Leu Pro Met Cys	Arg Asn Lys Phe Ile Asp His	
165	170	175	
Ile Ser Cys Glu Leu	Leu Ala Val Val	Arg Leu Ala Cys Val Asp Thr	
180	185	190	
Ser Ser Asn Glu Val	Thr Ile Met Val	Ser Ser Ile Val Leu Leu Met	
195	200	205	
Thr Pro Leu Cys Leu	Val Leu Leu Ser	Tyr Ile Gln Ile Ile Ser Thr	
210	215	220	
Ile Leu Lys Ile Gln	Ser Arg Glu Gly	Arg Lys Lys Ala Phe His Thr	
225	230	235	240
Cys Ala Ser His Leu	Thr Val Val Ala	Leu Cys Tyr Gly Val Ala Ile	
245	250	255	
Phe Thr Tyr Ile Gln	Pro His Ser Ser	Pro Ser Val Leu Gln Glu Lys	

260	265	270
Leu Phe Ser Val Phe Tyr Ala Ile	Leu Thr Pro Met Leu Asn Pro Met	
275	280	285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu		
290	295	300
Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr		
305	310	315

<210> 2608

<211> 216

<212> PRT

<213> Unknown (2921713-dir-0-8 conceptual translation of range 2-649)

<400>2608

Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln Leu Leu Ala	
1	15
His Phe Leu Ala Glu His Lys Ala Thr Pro Phe Gln Ser Cys Ala Ala	
20	30
Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu	
35	45
Ala Val Met Thr Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg	
50	60
Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu Ala Ile Thr	
65	80
Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr Ala Ile Thr	
85	95
Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His Ile Ser Cys	
100	110
Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn	
115	125
Glu Val Thr Ile Met Val Ser Ser Val Val Leu Leu Met Thr Pro Phe	
130	140
Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Asn Ser Thr Ile Leu Lys	
145	160
Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr Cys Ala Ser	
165	175
His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr	
180	190
Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Phe Ser	
195	205
Val Phe Tyr Ala Ile Leu Thr Pro	
210	215

<210> 2609

<211> 301

<212> PRT

<213> Unknown (p161-dir-0-11 conceptual translation of range 2-903)

<400>2609

Trp Val Ser Glu Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Thr	
1	15
Gln Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Val Val Thr Val	
20	30
Leu Gly Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu	
35	45
His Thr Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val	
50	60
Ser Tyr Ala Thr Ser Val Val Pro Gln Leu Leu Ala His Phe Leu Ala	
65	80
Glu His Lys Ala Ile Ser Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe	
85	95

Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala
 100 105 110
 Tyr Asp Arg Tyr Val Ala Val Cys Asp Ala Leu Arg Tyr Ser Ala Ile
 115 120 125
 Met His Gly Gly Leu Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser
 130 135 140
 Gly Phe Ile Asn Ser Leu Val Gln Thr Ala Ile Thr Phe Gln Leu Pro
 145 150 155 160
 Met Cys Thr Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala
 165 170 175
 Val Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile
 180 185 190
 Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu
 195 200 205
 Leu Ser Tyr Ile Gln Ile Thr Ser Thr Ile Leu Lys Ile Gln Ser Arg
 210 215 220
 Glu Gly Arg Arg Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val
 225 230 235 240
 Val Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His
 245 250 255
 Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Phe Ser Val Phe Tyr Ala
 260 265 270
 Ile Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys
 275 280 285
 Glu Val Lys Gly Ala Trp Gln Lys Leu Leu Trp Lys Phe
 290 295 300

<210> 2610

<211> 334

<212> PRT

<213> Unknown (3766130-dir-170-13 conceptual translation of range 17111-18112)

<220>

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400>2610

Phe Cys Phe Phe Leu Thr Leu Ser Thr Asp Xaa Tyr Ser Ser His Phe
 1 5 10 15
 Xaa Met Glu Ile Asp Asn Gln Thr Trp Val Arg Glu Phe Ile Leu Leu
 20 25 30
 Gly Leu Ser Ser Asp Trp Cys Thr Gln Ile Ser Leu Phe Ser Leu Phe
 35 40 45
 Leu Val Thr Tyr Leu Met Thr Val Leu Gly Asn Cys Leu Ile Val Leu
 50 55 60
 Leu Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
 65 70 75 80
 Thr Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro
 85 90 95
 Gln Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln
 100 105 110
 Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu
 115 120 125
 Phe Val Leu Leu Ala Val Met Ala Tyr Asp Arg His Val Ala Val Ser
 130 135 140
 Asp Arg Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg
 145 150 155 160
 Leu Ala Ile Thr Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Val Gln
 165 170 175

Thr Ala Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asp
 180 185 190
 His Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp
 195 200 205
 Thr Ser Ser Asn Glu Ala Ala Ile Met Val Ser Ser Ile Val Leu Leu
 210 215 220
 Met Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Arg Ile Ile Ser
 225 230 235 240
 Thr Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His
 245 250 255
 Thr Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Thr Thr
 260 265 270
 Ile Phe Thr Tyr Ile Gln Pro His Ser Gly Pro Ser Val Leu Gln Glu
 275 280 285
 Lys Leu Ile Ser Val Phe Tyr Ala Ile Val Met Pro Leu Leu Asn Pro
 290 295 300
 Val Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp His Lys
 305 310 315 320
 Leu Leu Glu Lys Phe Ser Gly Leu Thr Ser Lys Leu Gly Thr
 325 330

<210> 2611

<211> 298

<212> PRT

<213> Unknown (p172-dir-0-10 conceptual translation of range 2-895)

<400>2611

Thr Ile Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val Ser
 1 5 10 15
 Leu Phe Val Leu Phe Leu Val Met Cys Met Val Thr Met Leu Gly Asn
 20 25 30
 Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro
 35 40 45
 Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr Ala
 50 55 60
 Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His Lys
 65 70 75 80
 Ser Ile Pro Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala
 85 90 95
 Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp Arg
 100 105 110
 Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met His Gly
 115 120 125
 Ala Pro Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser Gly Phe Ile
 130 135 140
 Asn Ser Leu Val Gln Thr Ala Ile Thr Phe His Leu Pro Met Cys Thr
 145 150 155 160
 Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala Val Ile Arg
 165 170 175
 Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Ala Ala Ile Met Val Ser
 180 185 190
 Ser Ile Val Phe Leu Met Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr
 195 200 205
 Ile Trp Ile Ile Ser Thr Ile Val Lys Ile Gln Ser Thr Glu Gly Arg
 210 215 220
 Lys Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val Ala Leu
 225 230 235 240
 Cys Tyr Gly Leu Ala Ile Phe Thr Tyr Ile Gln Pro His Ser Ser Leu
 245 250 255
 Ser Val Leu Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile Leu Thr
 260 265 270

Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
 275 280 285
 Gly Ala Trp Gln Lys Leu Leu Trp Lys Phe
 290 295

<210> 2612

<211> 298

<212> PRT

<213> Unknown (p171-dir-0-10 conceptual translation of range 3-896)

<220>

<221> VARIANT

<222> (1)...(298)

<223> Xaa = Any Amino Acid

<400>2612

Ser Asp Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val
 1 5 10 15
 Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Met Leu Gly
 20 25 30
 Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr
 35 40 45
 Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr
 50 55 60
 Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His
 65 70 75 80
 Lys Ser Ile Pro Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu
 85 90 95
 Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp
 100 105 110
 Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met His
 115 120 125
 Gly Ala Leu Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser Gly Phe
 130 135 140
 Ile Asn Ser Leu Val Gln Thr Ala Ile Thr Phe His Leu Pro Met Cys
 145 150 155 160
 Thr Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala Val Ile
 165 170 175
 Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Ala Ala Ile Met Val
 180 185 190
 Ser Ser Ile Val Phe Leu Met Thr Pro Phe Cys Leu Val Leu Leu Ser
 195 200 205
 Tyr Ile Xaa Ile Ile Ser Thr Ile Val Lys Ile Gln Ser Thr Glu Gly
 210 215 220
 Arg Lys Lys Ala Phe His Thr Tyr Ala Ser His Leu Thr Val Val Ala
 225 230 235 240
 Leu Cys Tyr Gly Leu Ala Ile Phe Thr Tyr Ile Gln Pro His Ser Ser
 245 250 255
 Leu Ser Val Leu Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile Leu
 260 265 270
 Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val
 275 280 285
 Lys Gly Ala Trp Gln Lys Leu Leu Trp Lys
 290 295

<210> 2613

<211> 299

<212> PRT

<213> Unknown (p173-dir-0-11 conceptual translation of range 4-900)

<400>2613

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Val Thr Ile Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val
1      5      10      15
Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Met Leu Gly
20      25      30
Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr
35      40      45
Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr
50      55      60
Ala Ile Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His
65      70      75      80
Lys Ala Ile Ser Leu Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu
85      90      95
Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp
100     105     110
Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met His
115     120     125
Gly Ala Leu Cys Ala Arg Leu Ala Ile Thr Ser Trp Val Ser Gly Phe
130     135     140
Ile Asn Ser Leu Val Gln Thr Ala Ile Thr Phe His Leu Pro Met Cys
145     150     155     160
Thr Asn Lys Phe Ile Asp His Ile Ser Cys Glu Leu Leu Ala Val Ile
165     170     175
Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Ala Ala Ile Met Val
180     185     190
Ser Ser Ile Val Phe Leu Met Thr Pro Phe Cys Leu Val Leu Leu Ser
195     200     205
Tyr Ile Trp Ile Ile Ser Thr Ile Val Lys Ile Gln Ser Thr Glu Gly
210     215     220
Arg Lys Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val Ala
225     230     235     240
Leu Cys Tyr Gly Leu Ala Ile Phe Thr Tyr Ile Gln Pro His Ser Ser
245     250     255
Leu Ser Val Leu Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile Leu
260     265     270
Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val
275     280     285
Lys Gly Ala Trp Gln Lys Leu Leu Trp Lys Phe
290     295

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<210> 2614

<211> 300

<212> PRT

<213> Unknown (p142-dir-0-11 conceptual translation of range 2-900)

<400>2614

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Val Ser Glu Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln
1      5      10      15
Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Val Val Thr Val Leu
20      25      30
Gly Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His
35      40      45
Thr Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser
50      55      60
Tyr Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu
65      70      75      80
His Lys Ala Ile Ser Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser
85      90      95
Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr
100     105     110
Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met
115     120     125

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His Ala Ala Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly
 130 135 140
 Ser Ile Asn Ser Leu Val His Thr Thr Ile Thr Phe Gln Leu Pro Met
 145 150 155 160
 Cys Ala Asn Lys Phe Ile Asp His Ile Ser Cys Glu Ile Leu Ala Val
 165 170 175
 Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met
 180 185 190
 Val Phe Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu
 195 200 205
 Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu
 210 215 220
 Gly Arg Arg Lys Ala Phe Gln Thr Cys Gly Ser His Leu Thr Met Val
 225 230 235 240
 Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His Ser
 245 250 255
 Ser Pro Ser Val Leu Gln Glu Lys Leu Ile Ser Leu Phe Tyr Ala Ile
 260 265 270
 Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Ser Lys Glu
 275 280 285
 Val Lys Gly Ala Trp Lys Lys Leu Tyr Trp Lys Phe
 290 295 300

<210> 2615

<211> 300

<212> PRT

<213> Unknown (p162-dir-0-10 conceptual translation of range 1-899)

<400>2615

Val Ser Glu Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln
 1 5 10 15
 Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Val Val Thr Val Leu
 20 25 30
 Gly Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His
 35 40 45
 Thr Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser
 50 55 60
 Tyr Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu
 65 70 75 80
 His Lys Ala Ile Ser Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser
 85 90 95
 Leu Ala Leu Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr
 100 105 110
 Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met
 115 120 125
 His Ala Ala Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly
 130 135 140
 Ser Ile Asn Ser Leu Ala His Thr Thr Ile Thr Phe Gln Leu Pro Met
 145 150 155 160
 Cys Ala Asn Lys Phe Ile Asp His Ile Ser Cys Glu Ile Leu Ala Val
 165 170 175
 Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met
 180 185 190
 Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu
 195 200 205
 Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu
 210 215 220
 Gly Arg Arg Lys Ala Phe Gln Thr Cys Gly Ser His Leu Thr Val Val
 225 230 235 240
 Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His Ser
 245 250 255

Ser Pro Ser Val Leu Gln Glu Lys Leu Ile Ser Leu Phe Tyr Ala Thr
 260 265 270
 Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu
 275 280 285
 Val Lys Gly Ala Trp Lys Lys Leu Tyr Trp Lys Phe
 290 295 300

<210> 2616

<211> 300

<212> PRT

<213> Unknown (p160-dir-0-11 conceptual translation of range 3-901)

<400>2616

Val Ser Glu Phe Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln
 1 5 10 15
 Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Val Val Thr Val Leu
 20 25 30
 Gly Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His
 35 40 45
 Thr Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser
 50 55 60
 Tyr Val Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu
 65 70 75 80
 His Lys Ala Ile Ser Phe Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser
 85 90 95
 Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr
 100 105 110
 Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met
 115 120 125
 His Ala Ala Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly
 130 135 140
 Ser Ile Asn Ser Leu Val His Thr Thr Thr Thr Phe Gln Leu Pro Met
 145 150 155 160
 Cys Ala Asn Lys Phe Ile Asp His Ile Ser Cys Glu Ile Leu Ala Val
 165 170 175
 Val Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met
 180 185 190
 Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu
 195 200 205
 Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Lys
 210 215 220
 Gly Arg Arg Lys Ala Phe Gln Thr Cys Gly Ser His Leu Thr Val Val
 225 230 235 240
 Ala Leu Cys Tyr Gly Val Ala Ile Phe Thr Tyr Ile Gln Pro His Ser
 245 250 255
 Asn Pro Ser Val Leu Gln Glu Lys Leu Ile Ser Leu Phe Tyr Ala Ile
 260 265 270
 Leu Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu
 275 280 285
 Val Lys Gly Ala Trp Lys Lys Leu Tyr Trp Lys Phe
 290 295 300

<210> 2617

<211> 298

<212> PRT

<213> Unknown (p165-dir-0-10 conceptual translation of range 1-893)

<400>2617

Val Ser Glu Phe Ile Ile Leu Gly Leu Ser Ser Asp Trp Asp Thr Gln
 1 5 10 15
 Val Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Val Leu

	20		25		30										
Gly	Asn	Cys	Leu	Ile	Val	Leu	Leu	Ile	Arg	Leu	Asp	Ser	Arg	Leu	His
	35		40		45										
Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr	Asn	Leu	Ser	Leu	Val	Asp	Val	Ser
	50		55		60										
Tyr	Ala	Thr	Ser	Ile	Val	Pro	Gln	Leu	Leu	Ala	His	Phe	Leu	Ala	Glu
65			70		75										80
His	Lys	Ala	Ile	Pro	Phe	Gln	Ser	Cys	Ala	Ala	Gln	Leu	Phe	Phe	Ser
			85		90										95
Leu	Ala	Leu	Gly	Gly	Ile	Glu	Phe	Val	Leu	Arg	Ala	Val	Met	Ala	Tyr
			100		105										110
Asp	Arg	Tyr	Val	Ala	Val	Cys	Asp	Pro	Leu	Arg	Tyr	Ser	Ala	Ile	Met
			115		120										125
His	Ala	Ala	Leu	Cys	Ala	Arg	Leu	Ala	Val	Thr	Ser	Trp	Val	Ser	Gly
			130		135										140
Ser	Ile	Asn	Ser	Leu	Val	His	Thr	Thr	Ile	Thr	Phe	Gln	Leu	Pro	Met
145			150		155										160
Cys	Thr	Asn	Lys	Phe	Val	Asp	His	Ile	Ser	Cys	Glu	Ile	Leu	Ala	Val
			165		170										175
Ile	Arg	Leu	Ala	Cys	Val	Asn	Thr	Ser	Ser	Asn	Glu	Val	Thr	Ile	Met
			180		185										190
Val	Ser	Ser	Met	Val	Leu	Leu	Met	Thr	Pro	Phe	Cys	Leu	Val	Leu	Leu
			195		200										205
Ser	Asp	Ile	Gln	Ile	Ile	Ser	Thr	Ile	Leu	Lys	Ile	Gln	Ser	Arg	Glu
			210		215										220
Gly	Arg	Arg	Lys	Ala	Phe	Gln	Thr	Cys	Ala	Ser	His	Leu	Thr	Val	Val
225			230		235										240
Ala	Leu	Cys	Tyr	Gly	Met	Ala	Ile	Phe	Thr	Tyr	Ile	Gln	Pro	His	Ser
			245		250										255
Ser	Pro	Ser	Val	Leu	Gln	Glu	Lys	Leu	Ile	Ser	Leu	Phe	Tyr	Ala	Ile
			260		265										270
Glu	Thr	Pro	Met	Leu	Asn	Pro	Met	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu
			275		280										285
Val	Lys	Gly	Ala	Trp	Lys	Lys	Leu	Leu	Trp						
			290		295										

<210> 2618

<211> 299

<212> PRT

<213> Unknown (p157-dir-0-10 conceptual translation of range 3-898)

<220>

<221> VARIANT

<222> (1)...(299)

<223> Xaa = Any Amino Acid

<400>2618

Val	Ser	Glu	Phe	Ile	Ile	Leu	Gly	Leu	Ser	Ser	Asp	Trp	Asp	Thr	Gln
1			5						10					15	
Val	Ser	Leu	Phe	Val	Leu	Phe	Leu	Val	Met	Tyr	Val	Val	Thr	Val	Leu
			20						25				30		
Gly	Asn	Cys	Leu	Ile	Val	Leu	Leu	Ile	Arg	Leu	Asp	Ser	Arg	Leu	His
	35		40									45			
Thr	Pro	Met	Tyr	Phe	Phe	Leu	Thr	Asn	Leu	Ser	Leu	Val	Asp	Val	Ser
	50		55									60			
Tyr	Ala	Thr	Ser	Val	Val	Pro	Gln	Leu	Leu	Ala	His	Phe	Leu	Ala	Glu
65			70							75					80
His	Lys	Ala	Ile	Pro	Phe	Gln	Ser	Cys	Ala	Ala	Gln	Leu	Phe	Phe	Ser
			85						90						95
Leu	Ala	Leu	Gly	Gly	Ile	Glu	Phe	Val	Leu	Leu	Ala	Val	Met	Ala	Tyr
			100						105						110

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Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Ala Ile Met
    115                120                125
His Ala Gly Leu Cys Ala Arg Leu Ala Val Thr Ser Trp Val Ser Gly
    130                135                140
Ser Ile Asn Ser Leu Val His Thr Ala Ile Thr Phe Gln Leu Pro Arg
    145                150                155                160
Cys Arg Asn Lys Phe Ile Glu His Ile Ser Cys Glu Ile Leu Ala Val
    165                170                175
Ile Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Met
    180                185                190
Val Ser Ser Ile Val Leu Leu Met Thr Pro Phe Cys Leu Val Leu Leu
    195                200                205
Ser Tyr Ile Gln Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu
    210                215                220
Gly Arg Arg Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val
    225                230                235                240
Ala Leu Xaa Tyr Gly Val Ala Ile Phe Thr Xaa Ile Gln Pro His Ser
    245                250                255
Ser Pro Ser Val Ile Gln Glu Lys Leu Phe Ser Leu Phe Tyr Ala Ile
    260                265                270
Val Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Ile Arg Asn Lys Glu
    275                280                285
Val Lys Gly Ala Trp Gln Lys Ile Leu Trp Lys
    290                295

```

<210> 2619

<211> 299

<212> PRT

<213> Unknown (p174-dir-0-11 conceptual translation of range 4-900)

<400>2619

```

Val Thr Ile Ile Leu Leu Gly Leu Ser Ser Asp Trp Asp Ala Gln Val
    1                5                10                15
Ser Leu Phe Val Leu Phe Leu Val Met Tyr Met Val Thr Met Leu Gly
    20                25                30
Asn Cys Leu Ile Val Leu Leu Ile Arg Leu Asp Ser Arg Leu His Thr
    35                40                45
Pro Met Tyr Phe Phe Leu Thr Asn Leu Ser Leu Val Asp Val Ser Tyr
    50                55                60
Ala Thr Ser Ile Val Pro Gln Leu Leu Ala His Phe Leu Ala Glu His
    65                70                75                80
Lys Ala Ile Ser Leu Gln Ser Cys Ala Ala Gln Leu Phe Phe Ser Leu
    85                90                95
Ala Leu Gly Gly Ile Glu Phe Val Leu Leu Ala Val Met Ala Tyr Asp
    100               105               110
Arg Tyr Val Ala Val Cys Asp Pro Leu Arg Tyr Ser Val Ile Met His
    115               120               125
Gly Ala Leu Cys Ala Lys Leu Ala Ile Thr Ser Trp Val Ser Gly Ser
    130               135               140
Ile Asn Ser Arg Met His Thr Thr Ile Thr Phe Gln Leu Pro Met Cys
    145               150               155                160
Thr Asn Lys Phe Ile Asp His Ile Phe Cys Glu Ile Leu Ala Leu Ile
    165               170               175
Arg Leu Ala Cys Val Asp Thr Ser Ser Asn Glu Val Thr Ile Ile Val
    180               185               190
Ser Ser Ile Val Leu Leu Met Thr Pro Leu Cys Leu Val Leu Leu Ser
    195               200               205
Tyr Ile Arg Ile Ile Ser Thr Ile Leu Lys Ile Gln Ser Arg Glu Gly
    210               215               220
Arg Arg Lys Ala Phe His Thr Cys Ala Ser His Leu Thr Val Val Ala
    225               230               235                240

```

Leu Cys Tyr Gly Met Ala Ile Phe Thr Tyr Ile His Pro His Ser Ser
 245 250 255
 Pro Ser Val Leu Gln Glu Lys Leu Ile Ser Leu Phe Tyr Ala Ile Leu
 260 265 270
 Thr Pro Met Leu Asn Pro Met Ile Tyr Ser Leu Arg Asn Lys Glu Val
 275 280 285
 Lys Gly Ala Trp Lys Lys Leu Leu Trp Lys Phe
 290 295

<210> 2620

<211> 317

<212> PRT

<213> Unknown (1314664-dir-0-11 conceptual translation of range 1-951)

<400>2620

Met Gly Thr Gly Asn Gln Thr Trp Val Arg Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Asp Trp Asp Thr Glu Val Ser Leu Phe Val Leu Phe Leu
 20 25 30
 Ile Thr Tyr Met Val Thr Val Leu Gly Asn Phe Leu Ile Ile Leu Leu
 35 40 45
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Ile Ile Pro Gln
 65 70 75 80
 Met Leu Ala His Leu Leu Ala Ala His Lys Ala Ile Pro Phe Val Ser
 85 90 95
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Gly Leu Gly Gly Ile Glu Phe
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
 115 120 125
 Pro Leu Arg Tyr Ser Val Ile Met His Gly Gly Leu Cys Thr Arg Leu
 130 135 140
 Ala Ile Thr Ser Trp Val Ser Gly Ser Met Asn Ser Leu Met Gln Thr
 145 150 155 160
 Val Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Tyr Ile Asp His
 165 170 175
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
 180 185 190
 Ser Ser Asn Glu Ile Ala Ile Met Val Ser Ser Ile Val Leu Leu Met
 195 200 205
 Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
 210 215 220
 Ile Leu Lys Ile Gln Ser Thr Glu Gly Arg Lys Lys Ala Phe His Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Val Leu Cys Tyr Gly Met Ala Ile
 245 250 255
 Phe Thr Tyr Ile Gln Pro Arg Ser Ser Pro Ser Val Leu Gln Glu Lys
 260 265 270
 Leu Ile Ser Leu Phe Tyr Ser Val Leu Thr Pro Met Leu Asn Pro Met
 275 280 285
 Ile Tyr Ser Val Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu
 290 295 300
 Leu Gly Gln Leu Thr Gly Ile Thr Ser Lys Leu Ala Thr
 305 310 315

<210> 2621

<211> 349

<212> PRT

<213> Unknown (3766130-dir-627-13 conceptual translation of range 62771-63818)

<220>

<221> VARIANT

<222> (1)...(349)

<223> Xaa = Any Amino Acid

<400>2621

```

Leu Leu Ile Leu His Phe His Asp Trp Leu Phe Leu His Leu Xaa Cys
 1              5              10              15
Gly Pro Trp Lys Leu Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val
      20              25              30
Ser Glu Phe Ile Leu Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val
      35              40              45
Ser Leu Phe Ala Leu Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly
      50              55              60
Asn Thr Leu Ile Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr
      65              70              75              80
Pro Met Tyr Phe Ser Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr
      85              90              95
Thr Lys Ser Ile Val Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg
      100             105             110
Lys Ser Ile Pro Phe Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser Leu
      115             120             125
Ala Leu Cys Gly Ser Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp
      130             135             140
Arg Tyr Val Ala Val Cys His Pro Leu His Tyr Thr Val Ile Met His
      145             150             155             160
Gly Gly Leu Cys Leu Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe
      165             170             175
Ser Asn Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser
      180             185             190
Arg Phe Ile Asn His Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu
      195             200             205
Ala Cys Val Asp Val Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly
      210             215             220
Phe Leu Val Ile Leu Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala
      225             230             235             240
Cys Ile Val Ala Thr Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys
      245             250             255
Lys Ala Phe Gly Thr Cys Ala Ser His Leu Ile Val Val Cys Met Cys
      260             265             270
Phe Gly Ala Thr Ile Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser
      275             280             285
Ala Glu Glu Glu Lys Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro
      290             295             300
Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala
      305             310             315             320
Ala Val Arg Lys Val Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu
      325             330             335
Arg Thr Ser Cys Tyr Leu Ser Ser Lys Pro Lys Arg Arg
      340             345

```

<210> 2622

<211> 214

<212> PRT

<213> Unknown (hg27-dir-0-8 conceptual translation of range 1-642)

<400>2622

```

Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu Val
 1              5              10              15
His Leu Leu Ser Arg Lys Lys Val Ile Val Phe Thr Leu Cys Ala Ala

```

```

      20      25      30
Arg Leu Leu Phe Leu Leu Ile Gly Cys Thr Gln Cys Ala Leu Leu
   35      40      45
Gly Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
   50      55      60
Tyr Pro Asn Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr Ala
   65      70      75      80
Pro Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe Thr
      85      90      95
Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Trp Cys
   100      105      110
Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala Ser
   115      120      125
Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro Val
   130      135      140
Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val Lys
   145      150      155      160
Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly Ser
      165      170      175
His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr Tyr
      180      185      190
Met Thr Pro Lys Ser Ser Lys Gln Glu Lys Ser Val Ser Val Phe
   195      200      205
Tyr Pro Ile Val Thr Pro
   210

```

<210> 2623

<211> 217

<212> PRT

<213> Unknown (p51-dir-0-8 conceptual translation of range 1-651)

<400>2623

```

Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln Ala Leu
   1      5      10      15
Val His Leu Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu Cys Ala
      20      25      30
Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys Ala Leu
   35      40      45
Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu
   50      55      60
Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu Ala Thr
   65      70      75      80
Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr Thr Phe
      85      90      95
Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His Phe Phe
   100      105      110
Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr His Ala
   115      120      125
Ser Glu Met Ala Ile Phe Leu Thr Gly Val Val Ile Leu Leu Ile Pro
   130      135      140
Val Phe Leu Ile Leu Val Ser Tyr Gly Arg Ile Ile Val Thr Val Val
   145      150      155      160
Lys Met Lys Ser Thr Val Gly Ser Leu Lys Ala Phe Ser Thr Cys Gly
      165      170      175
Ser His Leu Met Val Val Ile Leu Phe Tyr Gly Ser Ala Ile Ile Thr
      180      185      190
Tyr Met Thr Pro Lys Ser Ser Lys Gln Glu Lys Ser Val Ser Val
   195      200      205
Phe Tyr Ala Ile Val Thr Pro Met Leu
   210      215

```

<210> 2624

<211> 158

<212> PRT

<213> Unknown (2564517-dir-0-6 conceptual translation of range 1-474)

<400>2624

```

Ile Ser Phe Pro Leu Arg Tyr Thr Ile Ile Met Ser Arg Ser Ile Cys
 1           5           10           15
Ile Thr Met Val Ser Cys Cys Trp Ile Ser Gly Ser Leu Ile Ala Leu
      20           25           30
Val Val Ile Val Phe Thr Leu Gln Leu Pro Leu Cys Gly Ala Asn Val
      35           40           45
Ile Asn His Phe Phe Cys Glu Ala Thr Thr Leu Val Gly Met Ala Cys
      50           55           60
Val Asp Thr Phe Val Thr Glu Met Val Ile Phe Ser Ala Gly Ile Phe
      65           70           75           80
Thr Leu Leu Leu Pro Ser Ile Leu Thr Leu Leu Ser Tyr Ile Cys Ile
      85           90           95
Ile Val Ala Ile Val Gly Ile Arg Ser Ser Ala Gly Arg Tyr Lys Ala
      100          105          110
Phe Ser Thr Cys Ala Ser His Leu Ile Ile Val Thr Ile Phe Tyr Gly
      115          120          125
Thr Ala Ile Phe Gly Tyr Met Lys Pro Val Ser Lys Asn Ser Gly Asn
      130          135          140
Gln Asp Lys Met Thr Ser Val Phe Tyr Thr Val Thr Pro Pro
      145          150          155

```

<210> 2625

<211> 215

<212> PRT

<213> Unknown (p102-dir-0-8 conceptual translation of range 2-646)

<400>2625

```

Phe Leu Asp Ile Cys Tyr Ile Ser Ala Ser Val Pro Gln Met Ile Val
 1           5           10           15
Asn Cys Leu Val Arg Ile Pro Ile Ile Ser Leu Gly Gln Cys Leu Ala
      20           25           30
Gln Met Cys Ala Gly Leu Tyr Leu Gly Val Val Glu Cys Leu Leu Leu
      35           40           45
Ala Val Met Ala Tyr Asp Arg Cys Ile Ala Ile Gly Asp Pro Leu Arg
      50           55           60
Tyr Ser Val Arg Met Gly Pro Gln Leu Cys Ala Gln Leu Ala Gly Ala
      65           70           75           80
Ser Trp Val Ser Ala Phe Leu Leu Thr Val Val Pro Val Leu Thr Met
      85           90           95
Pro Leu Glu Phe Cys Gly Gln His Ile Ile Asn His Phe Ser Cys Glu
      100          105          110
Leu Leu Ala Val Leu Lys Leu Ala Cys Asn Asp Leu Trp Ile Tyr Glu
      115          120          125
Leu Leu Ile Met Val Thr Ser Ser Leu Thr Leu Leu Ala Pro Phe Ala
      130          135          140
Phe Ile Leu Ala Ser Tyr Gly Cys Ile Leu Gly Ala Val Leu Lys Met
      145          150          155          160
His Ser Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser His
      165          170          175
Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ala Ile Ser Met Tyr Met
      180          185          190
Met Pro Gln Asp Lys Ala Ser Arg Asp Lys Asp Lys Ile Ile Ser Met
      195          200          205
Leu Tyr Gly Ile Val Thr Pro
      210          215

```

<210> 2626

<211> 217

<212> PRT

<213> Unknown (2921715-dir-0-8 conceptual translation of range 2-652)

<400>2626

```

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Lys Val Pro Lys Met Leu Thr
 1             5             10             15
Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
      20             25             30
Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
      35             40             45
Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
      50             55             60
Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
      65             70             75             80
Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
      85             90             95
Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
      100            105            110
Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
      115            120            125
Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro
      130            135            140
Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu
      145            150            155            160
Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
      165            170            175
Ser His Leu Cys Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met
      180            185            190
Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu
      195            200            205
Ser Leu Phe Tyr Ser Leu Phe Asn Pro
      210            215

```

<210> 2627

<211> 217

<212> PRT

<213> Unknown (2921709-dir-0-8 conceptual translation of range 2-652)

<400>2627

```

Ile Ile Asp Ile Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Thr
 1             5             10             15
Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr
      20             25             30
Met Gln Thr Phe Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile
      35             40             45
Leu Val Met Met Ser Tyr Asp Arg Tyr Met Ala Ile Cys His Pro Leu
      50             55             60
Gln Tyr Ser Val Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val
      65             70             75             80
Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu
      85             90             95
Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe
      100            105            110
Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu
      115            120            125
Asn Gln Val Val Ile Phe Ala Ala Ser Val Phe Ile Leu Val Gly Pro
      130            135            140
Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu

```

```

145      150      155      160
Gly Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
      165      170      175
Ser His Leu Cys Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met
      180      185      190
Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu
      195      200      205
Ser Leu Phe Tyr Ser Leu Phe Asn Pro
      210      215

```

<210> 2628

<211> 157

<212> PRT

<213> Unknown (902194-dir-0-6 conceptual translation of range 2-472)

<400>2628

```

Ile Cys His Pro Leu His Tyr Ser Val Ile Met Ser Trp Arg Val Cys
 1      5      10      15
Thr Val Gln Ala Val Thr Ser Trp Ala Cys Gly Ser Leu Leu Ala Leu
      20      25      30
Val His Val Ile Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu
      35      40      45
Ile Asn His Phe Phe Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys
      50      55      60
Ala Asp Thr Arg Leu Asn Gln Val Val Ile Phe Ala Ala Ser Val Ser
      65      70      75      80
Ile Leu Val Gly Pro Leu Cys Leu Val Leu Val Ser Tyr Ser Arg Ile
      85      90      95
Leu Phe Ala Ile Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala
      100      105      110
Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly
      115      120      125
Ser Ala Ile Val Met Tyr Met Ala Pro Lys Ser Asn His Pro Glu Glu
      130      135      140
Gln Gln Lys Ile Leu Ser Leu Phe Tyr Ser Leu Phe Asn
      145      150      155

```

<210> 2629

<211> 215

<212> PRT

<213> Unknown (OST182-dir-0-8 conceptual translation of range 2-646)

<400>2629

```

Ile Val Asp Ile Ser Tyr Ala Ser Asn Tyr Val Pro Lys Met Leu Thr
 1      5      10      15
Asn Leu Met Asn Gln Glu Ser Thr Ile Ser Phe Phe Pro Cys Ile Met
      20      25      30
Gln Thr Phe Leu Tyr Leu Ala Phe Ala His Val Glu Cys Leu Ile Leu
      35      40      45
Val Val Met Ser Tyr Asp Arg Tyr Ala Asp Ile Cys His Pro Leu Arg
      50      55      60
Tyr Asn Ile Leu Met Ser Trp Arg Val Cys Thr Val Leu Ala Val Ala
      65      70      75      80
Ser Trp Val Phe Ser Phe Leu Leu Ala Leu Val Pro Leu Val Leu Ile
      85      90      95
Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Cys Glu
      100      105      110
Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln
      115      120      125
Val Val Ile Phe Ala Ala Cys Val Phe Ile Leu Val Gly Pro Leu Cys
      130      135      140

```

Leu Val Leu Val Ser Tyr Leu Arg Ile Leu Ala Ala Ile Leu Arg Ile
 145 150 155 160
 Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser Ser His
 165 170 175
 Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met
 180 185 190
 Ala Pro Lys Ser Arg His Pro Glu Glu Gln Lys Val Leu Ser Leu
 195 200 205
 Phe Tyr Ser Leu Phe Asn Pro
 210 215

<210> 2630

<211> 352

<212> PRT

<213> Unknown (4156187-rev-1021-13 conceptual translation of range 102238-103293)

<220>

<221> VARIANT

<222> (1)...(352)

<223> Xaa = Any Amino Acid

<400>2630

Leu Leu Val Phe Cys Leu Phe Leu Cys Leu Phe Phe Ser Ser Glu Met
 1 5 10 15
 Val Lys Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly Phe Leu
 20 25 30
 Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu Phe
 35 40 45
 Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile Ser
 50 55 60
 Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His Leu
 65 70 75 80
 Ala Val Val Asn Ile Ala Tyr Ala Cys Asn Thr Val Pro Gln Met Leu
 85 90 95
 Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys Met
 100 105 110
 Thr Xaa Thr Phe Leu Phe Leu Ser Phe Ala His Thr Glu Cys Leu Leu
 115 120 125
 Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
 130 135 140
 Arg Tyr Phe Ile Ile Met Thr Trp Lys Val Cys Ile Thr Leu Ala Ile
 145 150 155 160
 Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Met Val His Val Ser Leu
 165 170 175
 Ile Leu Arg Leu Pro Phe Cys Gly Pro Arg Glu Ile Asn His Phe Phe
 180 185 190
 Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala Asp Thr Trp Leu
 195 200 205
 Asn Gln Val Val Ile Phe Ala Ala Cys Met Phe Ile Leu Val Gly Pro
 210 215 220
 Leu Cys Leu Val Leu Val Ser Tyr Ser His Ile Leu Ala Ala Ile Leu
 225 230 235 240
 Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ser
 245 250 255
 Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val Met
 260 265 270
 Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu
 275 280 285
 Phe Leu Phe Tyr Ser Ser Phe Asn Pro Met Leu Asn Pro Leu Ile Tyr
 290 295 300

Asn Leu Arg Asn Val Glu Val Lys Gly Ala Leu Arg Arg Ala Leu Cys
 305 310 315 320
 Lys Glu Ser His Ser Xaa Glu Val Xaa His Leu Asn Cys Gln Pro Gln
 325 330 335
 Leu Ser Arg Gly Leu Leu Met Pro Asn Tyr Cys Leu Asn Pro Glu Lys
 340 345 350

<210> 2631

<211> 314

<212> PRT

<213> Unknown (4156187-rev-834-13 conceptual translation of range 83640-84581)

<220>

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400>2631

Glu Met Gly Glu Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Phe Leu Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser
 20 25 30
 Leu Phe Tyr Ile Phe Thr Leu Leu Gly Asn Gly Ala Ile Leu Gly Leu
 35 40 45
 Ile Ser Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 His Leu Ala Val Val Asp Ile Ala Tyr Thr Arg Asn Thr Val Pro Gln
 65 70 75 80
 Met Leu Ala Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly
 85 90 95
 Cys Met Thr Gln Thr Phe Leu Cys Leu Ser Phe Gly His Ser Glu Cys
 100 105 110
 Leu Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Ser Val Ile Met Thr Trp Arg Val Cys Ile Thr Leu
 130 135 140
 Ala Val Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Leu Ala His Val
 145 150 155 160
 Val Leu Ile Leu Arg Leu Pro Phe Ser Gly Pro His Glu Ile Asn His
 165 170 175
 Phe Phe Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala Asp Thr
 180 185 190
 Trp Leu Asn Gln Val Val Ile Phe Ala Ala Cys Val Phe Phe Leu Val
 195 200 205
 Gly Pro Pro Ser Leu Val Leu Val Ser Tyr Ser His Ile Leu Ala Ala
 210 215 220
 Ile Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile
 245 250 255
 Ile Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys
 260 265 270
 Val Phe Phe Leu Phe Tyr Ser Phe Phe Asn Pro Thr Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gly Glu Val Lys Gly Ala Leu Arg Arg Ala
 290 295 300
 Leu Gly Lys Glu Ser His Ser Xaa Leu Val
 305 310

<210> 2632

<211> 223

<212> PRT

<213> Unknown (3983369-dir-0-8 conceptual translation of range 1-669)

<400>2632

```

Ser His Leu Ala Ile Val Asp Met Ala Tyr Ala Cys Asn Thr Val Pro
 1          5          10          15
Gln Thr Leu Ile Asn Leu Leu Asp Glu Thr Arg Pro Ile Thr Phe Ala
          20          25          30
Gly Cys Met Thr Gln Thr Tyr Leu Phe Leu Thr Phe Ala Ile Thr Glu
          35          40          45
Cys Leu Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys
          50          55          60
His Pro Leu His Tyr Thr Val Ile Met Asn Trp Arg Val Cys Thr Ile
65          70          75          80
Met Ala Ala Val Ser Trp Ile Val Ser Phe Leu Leu Ser Leu Val His
          85          90          95
Leu Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro His Glu Ile Asn
          100          105          110
His Phe Phe Cys Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp
          115          120          125
Thr Thr Leu Asn Gln Val Val Ile Phe Ala Ala Cys Val Phe Thr Leu
          130          135          140
Val Gly Pro Leu Cys Phe Val Leu Val Ser Tyr Thr Arg Ile Leu Val
145          150          155          160
Ala Ile Leu Arg Ile Gln Ser Gly Glu Arg Arg Arg Lys Ala Phe Ser
          165          170          175
Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala
          180          185          190
Ile Val Met Tyr Met Ala Pro Lys Ser Gln His Pro Gly Glu Gln Gln
          195          200          205
Lys Ile Leu Phe Leu Phe Tyr Ser Phe Phe Asn Pro Met Leu Asn
          210          215          220

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<210> 2633

<211> 216

<212> PRT

<213> Unknown (OST008-dir-0-8 conceptual translation of range 2-649)

<400>2633

```

Ile Ile Asp Met Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Ala
 1          5          10          15
Asn Leu Met Asn Gln Lys Arg Thr Ile Ser Phe Val Pro Cys Ile Met
          20          25          30
Gln Thr Phe Leu Tyr Leu Ala Phe Ala Val Thr Glu Cys Leu Ile Leu
          35          40          45
Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Phe Gln
          50          55          60
Tyr Thr Val Ile Met Ser Trp Arg Val Cys Thr Ile Leu Val Leu Thr
65          70          75          80
Ser Trp Ser Cys Gly Phe Ala Leu Ser Leu Val His Glu Ile Leu Leu
          85          90          95
Leu Arg Leu Pro Phe Cys Gly Pro Arg Asp Val Asn His Leu Phe Cys
          100          105          110
Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Val Asn
          115          120          125
Gln Val Val Ile Phe Ala Thr Cys Val Phe Val Leu Val Gly Pro Leu
          130          135          140
Ser Leu Ile Leu Val Ser Tyr Met His Ile Leu Gly Ala Ile Leu Lys
145          150          155          160
Ile Gln Thr Lys Glu Gly Arg Ile Lys Ala Phe Ser Thr Cys Ser Ser

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165 170 175
 His Leu Cys Val Val Gly Leu Phe Phe Gly Ile Ala Met Val Val Tyr
 180 185 190
 Met Val Pro Asp Ser Asn Gln Arg Glu Glu Gln Glu Lys Met Leu Ser
 195 200 205
 Leu Phe His Ser Val Leu Asn Pro
 210 215

<210> 2634

<211> 310

<212> PRT

<213> Unknown (4156187-dir-87-12 conceptual translation of range 8841-9771)

<400>2634

Met Gly Asp Asn Gln Ser Arg Val Thr Glu Phe Ile Leu Val Gly Phe
 1 5 10 15
 Gln Leu Ser Val Glu Met Glu Val Leu Leu Phe Trp Ile Phe Ser Leu
 20 25 30
 Leu Tyr Leu Phe Ser Leu Leu Ala Asn Gly Met Ile Leu Gly Leu Ile
 35 40 45
 Cys Leu Asp Pro Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Ser His
 50 55 60
 Leu Ala Val Ile Asp Ile Tyr Tyr Ala Ser Ser Asn Leu Leu Asn Met
 65 70 75 80
 Leu Glu Asn Leu Val Lys His Lys Lys Asn Tyr Pro Phe Ile Ser Cys
 85 90 95
 Ile Met Gln Met Ala Leu Tyr Leu Thr Phe Ala Ala Ala Val Cys Met
 100 105 110
 Ile Leu Val Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His Pro
 115 120 125
 Leu His Tyr Thr Val Ile Met Asn Trp Arg Val Cys Thr Val Leu Ala
 130 135 140
 Ile Thr Ser Trp Ala Cys Gly Phe Ser Leu Ala Leu Ile Asn Leu Ile
 145 150 155 160
 Leu Leu Leu Arg Leu Pro Phe Cys Gly Pro Gln Glu Val Asn His Phe
 165 170 175
 Phe Gly Glu Ile Leu Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp
 180 185 190
 Ile Asn Glu Ile Phe Val Phe Ala Gly Gly Val Phe Val Leu Val Gly
 195 200 205
 Pro Leu Ser Leu Met Leu Ile Ser Tyr Met Arg Ile Leu Leu Ala Ile
 210 215 220
 Leu Lys Ile Gln Ser Lys Glu Gly Arg Lys Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Cys Val Val Gly Leu Tyr Phe Gly Met Ala Met Val
 245 250 255
 Val Tyr Leu Val Pro Asp Asn Ser Gln Arg Gln Lys Gln Gln Lys Ile
 260 265 270
 Leu Thr Leu Phe Tyr Ser Leu Phe Asn Pro Leu Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Ala Gln Val Lys Gly Ala Leu Tyr Arg Ala Leu
 290 295 300
 Gln Lys Lys Arg Thr Met
 305 310

<210> 2635

<211> 339

<212> PRT

<213> Unknown (4156187-rev-1102-12 conceptual translation of range 110295-111311)

<220>

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400>2635

```

Ile Cys Phe Xaa Thr Leu Leu Leu Asn His Glu His Xaa Leu Asp Phe
 1          5          10          15
Leu Cys His Arg Asp Met Gly Asp Asn Ile Thr Ser Ile Thr Glu Phe
          20          25          30
Leu Leu Leu Gly Phe Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe
          35          40          45
Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr
          50          55          60
Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr
65          70          75          80
Phe Phe Leu Ser His Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn
          85          90          95
Thr Val Pro Arg Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile
          100          105          110
Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala
          115          120          125
Val Thr Glu Cys Leu Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val
          130          135          140
Ala Ile Cys His Pro Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val
145          150          155          160
Cys Ile Thr Leu Ala Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser
          165          170          175
Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln
          180          185          190
Lys Ile Tyr His Phe Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala
          195          200          205
Cys Ala Asp Thr His Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile
          210          215          220
Ser Gly Leu Val Gly Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys
225          230          235          240
Ile Leu Cys Ala Ile Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys
          245          250          255
Ala Phe Cys Thr Cys Phe Ser His Leu Cys Val Ile Gly Leu Phe Tyr
          260          265          270
Gly Thr Ala Ile Ile Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys
          275          280          285
Glu Gln Lys Lys Tyr Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met
          290          295          300
Leu Asn Pro Leu Ile Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr
305          310          315          320
Leu Lys Arg Val Leu Gly Val Glu Arg Ala Leu Xaa Lys Gly Leu Trp
          325          330          335
His Cys Asp

```

<210> 2636

<211> 339

<212> PRT

<213> Unknown (4156166-dir-1014-13 conceptual translation of range 101536-102552)

<220>

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400>2636

```

Ile Cys Phe Xaa Thr Leu Leu Leu Asn His Glu His Xaa Leu Asp Phe
 1           5           10           15
Leu Cys His Arg Asp Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe
           20           25           30
Leu Leu Leu Gly Phe Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe
           35           40           45
Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr
           50           55           60
Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr
65           70           75           80
Phe Phe Leu Ser His Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn
           85           90           95
Thr Val Pro Arg Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile
           100          105          110
Ser Phe Ala Gly Arg Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala
           115          120          125
Val Thr Glu Cys Leu Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val
           130          135          140
Ala Ile Cys His Pro Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val
145          150          155          160
Cys Ile Thr Leu Ala Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser
           165          170          175
Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln
           180          185          190
Lys Ile Tyr His Phe Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala
           195          200          205
Cys Ala Asp Thr His Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile
           210          215          220
Ser Gly Leu Val Gly Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys
225          230          235          240
Ile Leu Cys Ala Ile Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys
           245          250          255
Ala Phe Arg Thr Cys Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr
           260          265          270
Gly Thr Ala Ile Ile Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys
           275          280          285
Glu Gln Lys Lys Tyr Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met
           290          295          300
Leu Asn Pro Leu Ile Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr
305          310          315          320
Leu Lys Arg Val Leu Gly Val Glu Arg Ala Leu Xaa Lys Gly Leu Trp
           325          330          335
His Cys Asp

```

<210> 2637

<211> 222

<212> PRT

<213> Unknown (293753-dir-0-8 conceptual translation of range 2-667)

<400>2637

```

Phe Phe Leu Ser His Leu Ala Ile Val Asp Ile Ala Tyr Ala Cys Asn
 1           5           10           15
Thr Val Pro Gln Met Leu Val Asn Leu Leu Asp Pro Val Lys Pro Ile
           20           25           30
Ser Tyr Ala Gly Cys Met Thr Gln Thr Phe Leu Phe Leu Thr Phe Ala
           35           40           45
Ile Thr Glu Cys Leu Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val
           50           55           60

```

Ala Ile Cys His Pro Leu Arg Tyr Ser Ala Ile Met Ser Trp Arg Val
65 70 75 80
Cys Ser Thr Met Ala Val Thr Ser Trp Ile Ile Gly Val Leu Leu Ser
85 90 95
Leu Ile His Leu Val Leu Leu Leu Pro Leu Pro Phe Cys Val Ser Gln
100 105 110
Lys Val Asn His Phe Phe Cys Glu Ile Thr Ala Ile Leu Lys Leu Ala
115 120 125
Cys Ala Asp Thr His Leu Asn Glu Thr Met Val Leu Ala Gly Ala Val
130 135 140
Ser Val Leu Val Gly Pro Phe Ser Ser Ile Val Val Ser Tyr Ala Cys
145 150 155 160
Ile Leu Gly Ala Ile Leu Lys Ile Gln Ser Glu Glu Gly Gln Arg Lys
165 170 175
Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Tyr
180 185 190
Gly Thr Ala Ile Val Met Tyr Val Gly Pro Arg His Gly Ser Pro Lys
195 200 205
Glu Gln Lys Lys Tyr Leu Leu Leu Phe His Ser Leu Phe Asn
210 215 220

<210> 2638

<211> 114

<212> PRT

<213> Unknown (892-dir-0-5 conceptual translation of range 2-343)

<400>2638

Ile Cys His Pro Leu Arg Tyr Lys Val Ile Met Ser Arg Trp Met Cys
1 5 10 15
Leu Leu Met Val Gly Ile Cys Gly Val Tyr Gly Val Val Gly Ser Leu
20 25 30
Cys Tyr Thr Phe Phe Ala Met Arg Leu Pro Tyr Cys Gly Pro Asn Glu
35 40 45
Ile Asp His Tyr Phe Cys Glu Val Pro Ala Val Leu Lys Leu Ala Cys
50 55 60
Ala Asp Thr Ser Leu Asn Asp Leu Val Asp Phe Ile Thr Gly Phe Asn
65 70 75 80
Val Ile Val Val Pro Leu Thr Leu Val Val Ile Val Tyr Ala Asn Ile
85 90 95
Phe Ala Thr Ile Met Lys Ile Arg Ser Ala Gln Gly Gln Ile Lys Ala
100 105 110
Phe Ser

<210> 2639

<211> 350

<212> PRT

<213> Unknown (2331266-dir-0-13 conceptual translation of range 111-1160)

<220>

<221> VARIANT

<222> (1)...(350)

<223> Xaa = Any Amino Acid

<400>2639

Leu Ala Gln Asn Ile Lys Arg Lys Thr Ala Met Asn Ser Val Asn Ala
1 5 10 15
Ser Phe Tyr Gln Asn Ile Ser Ile Val Arg Pro Glu Tyr Phe Phe Ile
20 25 30
Ser Gly Leu Ser Gly Ile Pro Tyr Ser Ser Tyr Tyr Tyr Ile Phe Leu
35 40 45

```

Phe Val Val Tyr Phe Ile Ser Val Ile Gly Asn Ser Val Val Leu Leu
 50          55          60
Ile Ile Ala Val Asp Arg Ser Leu His Ser Pro Lys Tyr Ile Gly Val
65          70          75          80
Phe Asn Leu Ala Leu Ala Asp Ile Gly Glu Thr Asn Ala Leu Ile Pro
      85          90          95
Asn Met Met Lys Thr Phe Leu Phe Asn Ser Gln Tyr Ile Ser Tyr Asn
      100          105          110
Gly Cys Met Ala Asn Met Phe Phe Val Val Leu Phe Asn Ser Ile Gln
      115          120          125
Ser Phe Thr Leu Val Ala Leu Ala Tyr Asp Arg Phe Ile Ala Ile Cys
      130          135          140
Leu Pro Leu Arg Tyr His Ala Ile Val Asn Asn Thr Ser Met Ile Leu
145          150          155          160
Ile Phe Leu Ala Ile Trp Ala Phe Asn Ser Ser Val Val Ala Ser Met
      165          170          175
Val Ser Met Ile Thr Arg Leu Ser Ile Cys Lys Ser Asn Val Ile Pro
      180          185          190
Ser Tyr Phe Cys Asp His Gly Pro Ile Phe Arg Leu Ala Cys Asn Asp
      195          200          205
Ile Lys Ile Asn Glu Phe Phe Ala Phe Phe Ile Ser Ile Leu Tyr Leu
      210          215          220
Thr Met Pro Met Val Ile Ile Ala Leu Ser Tyr Leu Asn Ile Phe Leu
225          230          235          240
Ala Leu Ile Lys Ile Thr Thr Trp Glu Gly Arg Leu Lys Ala Leu Lys
      245          250          255
Thr Cys Val Ser His Leu Leu Leu Val Gly Ile Phe Phe Leu Pro Leu
      260          265          270
Leu Cys Thr Tyr Ile Ala Gln Val Leu Leu Ala Leu Thr Pro Asn Ala
      275          280          285
Arg Val Ile Ser Thr Ser Leu Ser Tyr Ala Ile Pro Pro Met Leu Asn
      290          295          300
Pro Ile Ile Tyr Val Leu Asn Thr Ala Glu Ile Lys Tyr Ile Ile Arg
305          310          315          320
Lys Leu Phe Lys Arg Arg Leu Arg Ser Val Ser Asp Asn Ile Ser Lys
      325          330          335
Xaa Phe Cys Ser Cys Trp Gly Leu Tyr Gln Ser Lys Lys Lys
      340          345          350

```

<210> 2640

<211> 353

<212> PRT

<213> Unknown (2331262-dir-1-13 conceptual translation of range 199-1257)

<220>

<221> VARIANT

<222> (1)...(353)

<223> Xaa = Any Amino Acid

<400>2640

```

Val Gln Asn Thr Lys Cys Lys Val Ala Met Ser Ser Leu Asn Ala Ser
 1          5          10          15
Phe Ser Leu Asn Ile Ser Val Val Arg Pro Glu Tyr Phe Phe Ile Leu
      20          25          30
Gly Leu Ser Gly Ile Pro Tyr Ser Asn Leu Tyr Tyr Ile Phe Ile Phe
      35          40          45
Ile Ile Thr Phe Ile Thr Val Ile Gly Asn Phe Leu Val Ile Leu Leu
      50          55          60
Ile Val Leu Asp Arg Ser Leu His Ser Pro Lys Tyr Ile Gly Val Phe
65          70          75          80
Asn Leu Ala Leu Ala Asp Ile Gly Glu Thr Asn Ala Leu Ile Pro Asn

```

```
<210> 2641
<211> 351
<212> PRT
<213> Unknown (4726083-dir-262-12 conceptual translation of range 26289-
27340)

<220>
<221> VARIANT
<222> (1)...(351)
<223> Xaa = Any Amino Acid
```

<400>2641																
Leu	Ser	Pro	Ser	Leu	Lys	Pro	Ser	Cys	Asn	Cys	Asp	Pro	Thr	Met	Trp	
1				5					10					15		
Pro	Asn	Ser	Ser	Asp	Ala	Pro	Phe	Leu	Leu	Thr	Gly	Phe	Leu	Gly	Leu	
			20					25					30			
Glu	Met	Ile	His	His	Trp	Ile	Ser	Ile	Pro	Phe	Phe	Val	Ile	Tyr	Phe	
		35					40					45				
Ser	Ile	Ile	Val	Gly	Asn	Gly	Thr	Leu	Leu	Phe	Ile	Ile	Trp	Ser	Asp	
	50					55					60					
His	Ser	Leu	His	Glu	Pro	Met	Tyr	Tyr	Phe	Leu	Ala	Val	Leu	Ala	Ser	
65					70				75					80		
Met	Asp	Leu	Gly	Met	Thr	Leu	Thr	Thr	Met	Pro	Thr	Val	Leu	Gly	Val	
				85					90					95		
Leu	Val	Leu	Asn	Gln	Arg	Glu	Ile	Val	His	Gly	Ala	Cys	Phe	Ile	Gln	

```

      100      105      110
Ser Tyr Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Val Leu Leu
      115      120      125
Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu His Tyr
      130      135      140
Asn Ser Ile Leu Thr Asn Ser Arg Val Met Lys Met Ala Leu Gly Ala
145      150      155      160
Leu Leu Arg Gly Phe Val Ser Ile Val Pro Pro Ile Met Pro Leu Phe
      165      170      175
Trp Phe Pro Tyr Cys His Ser His Val Leu Ser His Ala Phe Cys Leu
      180      185      190
His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn Leu
      195      200      205
Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp Ala Leu
      210      215      220
Ile Ile Ile Phe Ser Tyr Val Leu Ile Leu Lys Lys Val Met Gly Ile
225      230      235      240
Ala Ser Gly Glu Glu Arg Lys Lys Ser Leu Asn Thr Cys Val Ser His
      245      250      255
Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu Thr Phe
      260      265      270
Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile Thr Met
      275      280      285
Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile Ile Tyr
      290      295      300
Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Leu Arg Leu Leu Ser
305      310      315      320
Lys His Ser Arg Thr Xaa Ile Leu Ile Ile Asp Ser Gln Val Leu Tyr
      325      330      335
Tyr Phe Trp Pro Phe Ile Arg Asn Lys Ser Cys Leu Lys Xaa Tyr
      340      345      350

```

<210> 2642

<211> 159

<212> PRT

<213> Unknown (4680279-dir-0-6 conceptual translation of range 2-478)

<400>2642

```

Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Ser Ala Arg Val Leu Gln
1      5      10      15
Ile Gly Leu Ala Phe Ser Leu Lys Asn Val Leu Leu Ile Leu Pro Phe
      20      25      30
Pro Val Thr Leu Val Arg Leu Arg Tyr Cys Lys Lys Asn Leu Leu Ser
      35      40      45
His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser Asp
      50      55      60
Asn Lys Phe Asn Val Ile Tyr Gly Leu Phe Val Ala Leu Thr Gly Ile
65      70      75      80
Leu Asp Ile Thr Phe Ile Phe Met Ser Tyr Ala Leu Ile Leu Arg Ala
      85      90      95
Val Leu Gly Ile Ala Ser Gln Arg Glu Arg Leu Lys Val Leu Ser Thr
      100      105      110
Cys Val Ser His Ile Cys Ala Val Leu Ile Phe Tyr Val Pro Val Ile
      115      120      125
Ser Leu Ala Val Ile Tyr Arg Leu Ala Ser Arg Ser Ser Pro Ile Ser
      130      135      140
Lys Ile Leu Met Ala Asp Ile Phe Leu Leu Val Pro Pro Val Met
145      150      155

```

<210> 2643

<211> 160

<212> PRT

<213> Unknown (902668-dir-0-6 conceptual translation of range 2-481)

<400>2643

```

Ile Ser Asn Pro Leu Arg Tyr Ala Ser Val Leu Thr Asn Asn Val Ile
 1           5           10           15
Ile Arg Ile Gly Val Ala Ile Thr Thr Arg Ala Thr Leu Ser Leu Leu
          20           25           30
Pro Leu Pro Phe Leu Leu Lys Arg Leu Asn Tyr Cys Pro Gly Lys Ile
          35           40           45
Leu Leu Ser His Ser Phe Cys Phe His Ala Asp Val Met Lys Leu Ala
          50           55           60
Cys Ala Asp Ile Thr Val Asn Ile Leu Tyr Gly Leu Tyr Val Val Leu
65          70          75          80
Ser Thr Val Gly Ile Asp Ser Leu Leu Ile Val Met Ser Tyr Ser Leu
          85          90          95
Ile Leu His Thr Val Met Gly Leu Ala Ser Pro Arg Glu Arg Val Arg
          100          105          110
Thr Leu Asn Thr Cys Val Ser His Ile Ser Ala Val Leu Val Phe Tyr
          115          120          125
Ile Pro Val Ile Gly Val Ser Met Ile His Arg Phe Gly Lys His Leu
          130          135          140
Pro His Ile Val His Ala Leu Val Ala Tyr Val Tyr Leu Val Val Pro
145          150          155          160

```

<210> 2644

<211> 316

<212> PRT

<213> Unknown (3927807-dir-288-13 conceptual translation of range 29007-29954)

<400>2644

```

Leu Asn Met Tyr Pro Arg Asn Ser Ser Gln Ala Gln Pro Phe Leu Leu
 1           5           10           15
Ala Gly Leu Pro Gly Met Ala Gln Phe His His Trp Val Phe Leu Pro
          20           25           30
Phe Gly Leu Met Tyr Leu Val Ala Val Leu Gly Asn Gly Thr Ile Leu
          35           40           45
Leu Val Val Arg Val His Arg Gln Leu His Gln Pro Met Tyr Tyr Phe
          50           55           60
Leu Leu Met Leu Ala Thr Thr Asp Leu Gly Leu Thr Leu Ser Thr Leu
65          70          75          80
Pro Thr Val Leu Arg Val Phe Trp Leu Gly Ala Met Glu Ile Ser Phe
          85          90          95
Pro Ala Cys Leu Ile Gln Met Phe Cys Ile His Val Phe Ser Phe Met
          100          105          110
Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Cys Pro Leu Arg Tyr Ser Ser Ile Leu Thr Gly Ala Arg Val Ala
          130          135          140
Gln Ile Gly Leu Gly Ile Ile Cys Arg Cys Thr Leu Ser Leu Leu Pro
145          150          155          160
Leu Ile Cys Leu Leu Thr Trp Leu Pro Phe Cys Arg Ser His Val Leu
          165          170          175
Ser His Pro Tyr Cys Leu His Gln Asp Ile Ile Arg Leu Ala Cys Thr
          180          185          190
Asp Ala Thr Leu Asn Ser Leu Tyr Gly Leu Ile Leu Val Leu Val Ala
          195          200          205
Ile Leu Asp Phe Val Leu Ile Ala Leu Ser Tyr Ile Met Il Phe Arg
          210          215          220
Thr Val Leu Gly Ile Thr Ser Lys Glu Glu Gln Thr Lys Ala Leu Asn

```



```
<210> 2645
<211> 316
<212> PRT
<213> Unknown (4761596-dir-254-13 conceptual translation of range 25614-26561)
```

Phe 1	His	Asn	Asp	Thr 5	Asn	Pro	Gln	Asp	Val 10	Trp	Tyr	Val	Leu 15	Ile	Gly
Ile	Pro	Gly	Leu	Glu	Asp	Leu	His	Ser 25	Trp	Ile	Ala	Ile	Pro 30	Ile	Cys
Ser	Met	Tyr	Ile	Val	Ala	Val	Ile 40	Gly	Asn	Val	Leu	Leu 45	Ile	Phe	Leu
Ile	Val 50	Thr	Glu	Arg	Ser 55	Leu	His	Glu	Pro	Met	Tyr 60	Phe	Phe	Leu	Ser
Met 65	Leu	Ala	Leu	Ala	Asp 70	Leu	Leu	Leu	Ser	Thr 75	Ala	Thr	Ala	Pro	Lys
Met	Leu	Ala	Ile	Phe 85	Trp	Phe	His	Ser	Arg 90	Gly	Ile	Ser	Phe	Gly	Ser
Cys	Val	Ser	Gln 100	Met	Phe	Phe	Ile	His 105	Phe	Ile	Phe	Val	Ala 110	Glu	Ser
Ala	Ile 115	Leu	Leu	Ala	Met	Ala	Phe 120	Asp	Arg	Tyr	Val	Ala 125	Ile	Cys	Tyr
Pro	Leu 130	Arg	Tyr	Thr	Thr 135	Ile	Leu	Thr	Ser	Ser	Val 140	Ile	Gly	Lys	Ile
Gly 145	Thr	Ala	Ala	Val	Val 150	Arg	Ser	Phe	Leu	Ile 155	Cys	Phe	Pro	Phe	Ile
Phe	Leu	Val	Tyr 165	Arg	Leu	Leu	Tyr	Cys 170	Gly	Lys	His	Ile	Ile	Pro	His
Ser	Tyr	Cys	Glu 180	His	Met	Gly	Ile	Ala 185	Arg	Leu	Ala	Cys	Asp 190	Asn	Ile
Thr	Val 195	Asn	Ile	Ile	Tyr	Gly	Leu 200	Thr	Met	Ala	Leu	Leu 205	Ser	Thr	Gly
Leu	Asp 210	Ile	Leu	Leu	Ile 215	Ile	Ile	Ser	Tyr	Thr 220	Met	Ile	Leu	Arg	Thr
Val 225	Phe	Gln	Ile	Pro	Ser 230	Trp	Ala	Ala	Arg	Tyr 235	Lys	Ala	Leu	Asn	Thr
Cys	Gly	Ser	His 245	Ile	Cys	Val	Ile	Leu 250	Phe	Tyr	Thr	Pro	Ala 255	Phe	
Phe	Ser	Phe 260	Phe	Ala	His	Arg	Phe	Gly 265	Gly	Lys	Thr	Val	Pro 270	Arg	His
Ile	His 275	Ile	Leu	Val	Ala	Asn	Leu 280	Tyr	Val	Val	Val	Pro 285	Pro	Met	Leu
Asn	Pro 290	Ile	Ile	Tyr	Gly	Val	Lys 295	Thr	Lys	Gln	Ile	Gln	Asp	Arg	Val
Val 305	Phe	Leu	Phe	Ser	Ser 310	Val	Ser	Thr	Cys	Gln 315	His				

<210> 2646

<211> 159

<212> PRT

<213> Unknown (2564519-dir-0-6 conceptual translation of range 1-477)

<400>2646

```

Ile Cys Asn Pro Leu Arg Tyr Ala Val Met Leu Thr Asn Ile Val Ile
 1           5           10           15
Arg Lys Ile Ala Ile Leu Ala Val Val Arg Gly Leu Cys Val Val Ala
      20           25           30
Pro Phe Thr Phe Leu Leu His Arg Leu Pro Tyr Cys Gln Asn Asn Val
      35           40           45
Val Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ala Cys
      50           55           60
Ala Asp Val Thr Val Asn Ser Val Tyr Gly Leu Thr Ile Ala Leu Ser
65           70           75           80
Ile Thr Gly Leu Asp Ala Ala Leu Val Val Ala Ser Tyr Val Leu Ile
      85           90           95
Leu Arg Ala Val Leu Asn Met Asn Ser Met Thr Ala Arg His Lys Ala
      100          105          110
Leu Ser Thr Cys Ala Ser His Val Cys Val Ile Ile Leu Phe Cys Val
      115          120          125
Pro Ala Phe Phe Ser Phe Phe Ala His Arg Phe Gly Lys Asn Ile Pro
      130          135          140
Leu Asn Val His Ile Phe Val Ala Asn Leu Tyr Ile Leu Leu Pro
145          150          155

```

<210> 2647

<211> 158

<212> PRT

<213> Unknown (1644474-dir-0-6 conceptual translation of range 1-474)

<400>2647

```

Lys Pro Leu His Tyr Asn Glu Ile Met Asn Ser Ser Met Phe Leu Lys
 1           5           10           15
Leu Phe Leu Phe Thr Leu Ile Arg Ser Gly Thr Ile Met Ser Thr Leu
      20           25           30
Val Ala Leu Ala Ser Pro Leu Ser Phe Cys Gly Ser Asn Val Ile Tyr
      35           40           45
His Cys Tyr Cys Asp His Met Ala Leu Val Ser Leu Ala Cys Asp Ser
      50           55           60
Ile Ala Gln Asn Gln Thr Met Gly Leu Ile Val Ile Ile Cys Phe Val
65           70           75           80
Gly Ile Asp Thr Ser Val Ile Phe Phe Ser Tyr Val Lys Ile Leu His
      85           90           95
Val Val Leu Gly Thr Ala Ala Gly Glu Asp Arg Trp Lys Ala Phe His
      100          105          110
Thr Cys Gly Thr His Leu Met Val Met Ile Cys Phe Tyr Phe Val Gly
      115          120          125
Ser Val Thr Phe Leu Ser Arg Asn Leu Asn Ile Pro Ile Pro Ile Asp
      130          135          140
Val Asn Thr Phe Leu Gly Val Met Tyr Ile Val Phe Pro Ala
145          150          155

```

<210> 2648

<211> 161

<212> PRT

<213> Unknown (4877304-dir-0-6 conceptual translation of range 2-484)

<400>2648

```

Leu Ala Ile Cys Tyr Pro Leu His Tyr Ser Ala Leu Met Thr Asn Lys
 1           5           10           15

```

```

His Ala Ile Arg Leu Ser Cys Leu Cys Trp Ile Ile Gly Phe Leu Ile
      20      25      30
Leu Ile Met Asn Leu Cys Phe Ile Arg Gln Thr Leu Phe Cys Gly Pro
      35      40      45
Asn Glu Val Pro His Tyr Phe Cys Asp Tyr Ser Ala Val Ala Ala Leu
      50      55      60
Ala Cys Asn Asp Ile Ser Ile Tyr Ala Ala Val Gly Phe Ala Ile Ala
      65      70      75      80
Met Cys Val Ile Cys Ser Val Leu Leu Cys Leu Val Tyr Ser Tyr Val
      85      90      95
Lys Ile Val Ala Ser Val Leu Lys Ile Ala Ser Thr Asp Gly Arg Gln
      100     105     110
Lys Ala Phe Ser Thr Cys Val Ser His Leu Phe Val Val Ser Val Phe
      115     120     125
Ser Ile Leu Ala Ala Phe Val Phe Val Ser Tyr Arg Ile Glu Glu Phe
      130     135     140
Ser Glu Asp Ala Arg Met Ile Ile His Val Val Gln Asn Thr Phe Pro
      145     150     155     160
Ser

```

<210> 2649

<211> 168

<212> PRT

<213> Unknown (5262456-dir-284-6 conceptual translation of range 28407-28908)

<220>

<221> VARIANT

<222> (1)...(168)

<223> Xaa = Any Amino Acid

<400>2649

```

Gly Phe Trp Leu Gly Cys Tyr Leu Trp Phe Met Val Val Leu Thr Leu
  1      5      10      15
Ala Ile Arg Leu Arg Pro Phe Gly Leu Gly Gly Phe Leu Leu Lys Xaa
      20      25      30
Thr Ile Glu Xaa Gly Ala Cys Pro Arg Xaa Val Met Leu Leu Cys
      35      40      45
Gln Lys Pro Tyr Leu His Cys Val Val Val Val Val Phe Ile Phe Leu
      50      55      60
Ala Ser Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala Val Ala
      65      70      75      80
Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe Gly Thr
      85      90      95
Cys Phe Ser His Leu Ile Val Val Ser Ile Phe Tyr Gly Thr Val Arg
      100     105     110
Tyr Met Tyr Ile Glu Pro Gly Asn Ser Pro Ser Gln Asp Glu Gly Lys
      115     120     125
Leu Leu His Ile Phe Tyr Ser Ile Val Thr Pro Thr Leu Asn Pro Tyr
      130     135     140
Pro Leu Arg Asn Lys Glu Phe Lys Trp Ala Met Lys Arg Leu Ile Gly
      145     150     155     160
Lys Glu Lys Gly Ser Gly Asp Thr
      165

```

<210> 2650

<211> 312

<212> PRT

<213> Unknown (3941546-dir-0-12 conceptual translation of range 37-972)

<400>2650

```

Asn Val Ser Phe Tyr Asn Phe Lys Cys Thr Leu Ser Glu Leu Thr Gln
 1          5          10          15
Pro Gln Arg Val Leu Ile Trp Val Phe Thr Ile Ile Ile Thr Ile
 20          25          30
Thr Val Val Gly Asn Ile Leu Thr Ile Val Ser Ile Leu Tyr Phe Arg
 35          40          45
Gln Leu Gln Thr Arg Thr Asn Val Leu Ala Leu Ser Leu Ala Leu Ala
 50          55          60
Asp Phe Leu Val Gly Cys Leu Ile Met Pro Phe Ser Val Met Arg Thr
 65          70          75          80
Ala Tyr Ser Cys Trp Phe Tyr Gly Gln Leu Met Cys Arg Ile His Thr
 85          90          95
Trp Leu Asp Tyr Thr Phe Thr Thr Cys Ser Ile Phe Asn Leu Ala Cys
 100          105          110
Ile Ser Ile Asp Arg Tyr Val Ala Ile Ser Asp Pro Leu Arg Tyr Asp
 115          120          125
Gln Arg Val Thr Tyr Arg Ile Leu Ala Val Met Leu Thr Ile Cys Trp
 130          135          140
Gly Asn Ile Ile Pro Tyr Gly Val Ser Tyr Met Leu Lys Leu Asn Ile
 145          150          155          160
Asn Gly Ile Glu Ser Val Val Ala Ala Lys Ser Cys Pro Asp Asn Cys
 165          170          175
Ser Val Phe Met Asn Val Pro Phe Gly Leu Ala Asn Ser Met Gly Ala
 180          185          190
Tyr Val Leu Pro Met Leu Phe Ile Met Ala Ala Tyr Ser Arg Ile Tyr
 195          200          205
Val Met Ala Arg Asn Gln Ala Lys Arg Ile Ser Ser Leu Gly Asp Gln
 210          215          220
Val Arg Ala Ser Asn Ala Ser Asp Leu Thr Met Gln Ser Lys Trp Asn
 225          230          235          240
Ala Met Lys Arg Asp His Asn Ala Thr Lys Thr Leu Gly Met Ile Met
 245          250          255
Val Val Leu Phe Ile Val Trp Leu Pro Phe Ile Val Val Val Ala Thr
 260          265          270
Glu Pro Val Ile Gly Tyr Arg Met Asp Ser Thr Val Trp Asp Val Ala
 275          280          285
Asn Trp Phe Thr Tyr Phe Asn Ser Arg Met Asn Pro Ile Leu Phe Ala
 290          295          300
Ser Phe Asn Asn Ser Phe Arg Ser
305          310

```

<210> 2651

<211> 314

<212> PRT

<213> Unknown (17-2 (HGMP07I 400671 OL1A 438389 P30953 OLFI 1804351A S20572)
 Parmentier-M 92)

<400>2651

```

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1          5          10          15
Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20          25          30
Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35          40          45
Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65          70          75          80
Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85          90          95
Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser

```

100	105	110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe		
115	120	125
Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu		
130	135	140
Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr		
145	150	155
Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His		
165	170	175
Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr		
180	185	190
Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val		
195	200	205
Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser		
210	215	220
Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr		
225	230	235
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile		
245	250	255
Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr		
260	265	270
Val Met Ala Met Met Tyr Thr Val Thr Pro Met Leu Asn Pro Phe		
275	280	285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val		
290	295	300
Ile His Gln Lys Lys Thr Phe Phe Ser Leu		
305	310	

<210> 2652

<211> 312

<212> PRT

<213> Unknown (17-4 (OLFR1 425221 482560 A48413 HSHGM07EG) Schurmans-S 93)

<400>2652

Met Asp Gly Gly Asn Gln Ser Glu Gly Ser Glu Phe Leu Leu Leu Gly	
1	5
Met Ser Glu Ser Pro Glu Gln Gln Gln Ile Leu Phe Trp Met Phe Leu	
20	25
Ser Met Tyr Leu Val Thr Val Val Gly Asn Val Leu Ile Ile Leu Ala	
35	40
Ile Ser Ser Asp Ser Arg Leu His Thr Pro Val Tyr Phe Phe Leu Ala	
50	55
Asn Leu Ser Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys	
65	70
Met Leu Val Asn Leu Gln Ser His Asn Lys Ala Ile Ser Tyr Ala Gly	
85	90
Cys Leu Thr Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn	
100	105
Leu Ile Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys	
115	120
Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu	
130	135
Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr	
145	150
Leu Leu Met Thr Arg Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr	
165	170
Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Met Ala Cys Ser Asn Ile	
180	185
Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe L u	
195	200
Ile Pro Phe Gly Phe Val Ile Ile Ser Tyr Val Leu Ile Ile Arg Ala	
	205

```

      210              215              220
Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr
225              230              235              240
Cys Ala Ser His Leu Gly Ala Val Ser Leu Phe Tyr Gly Thr Leu Cys
      245              250              255
Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val
      260              265              270
Ala Thr Val Met Tyr Ala Val Val Thr Pro Met Met Asn Pro Phe Ile
      275              280              285
Tyr Ser Leu Arg Asn Lys Asp Met His Gly Ala Leu Gly Arg Leu Leu
      290              295              300
Asp Lys His Phe Lys Arg Leu Thr
305              310

```

<210> 2653

<211> 315

<212> PRT

<213> Unknown (17-40 (OL1E 516320 2209308A 1588713))

<400>2653

```

Met Gln Pro Glu Ser Gly Ala Asn Gly Thr Val Ile Ala Glu Phe Ile
1              5              10              15
Leu Leu Gly Leu Leu Glu Ala Pro Gly Leu Gln Pro Val Val Phe Val
      20              25              30
Leu Phe Leu Phe Ala Tyr Leu Val Thr Val Arg Gly Asn Leu Ser Ile
      35              40              45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Thr Pro Met Tyr Phe
      50              55              60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Ser Val Thr
      65              70              75              80
Val Pro Ser Met Leu Ser Arg Leu Leu Ser Arg Lys Arg Ala Val Pro
      85              90              95
Cys Gly Ala Cys Leu Thr Gln Leu Phe Phe Phe His Leu Phe Val Gly
      100              105              110
Val Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Gln Phe Leu Ala
      115              120              125
Ile Cys Arg Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
      130              135              140
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu
      145              150              155              160
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Val
      165              170              175
Ile Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
      180              185              190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Ala Val Gly Phe Ile
      195              200              205
Met Ala Gly Thr Pro Met Ala Leu Ile Val Ile Ser Tyr Ile His Val
      210              215              220
Ala Ala Ala Val Leu Arg Ile Arg Ser Val Glu Gly Arg Lys Lys Ala
      225              230              235              240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Ala Ile Phe Tyr Gly
      245              250              255
Ser Gly Ile Phe Asn Tyr Met Arg Leu Gly Ser Thr Lys Leu Ser Asp
      260              265              270
Lys Asp Lys Ala Val Gly Ile Phe Asn Thr Val Ile Asn Pro Met Leu
      275              280              285
Asn Pro Ile Ile Tyr Ser Phe Arg Asn Pro Asp Val Gln Ser Ala Ile
      290              295              300
Trp Arg Met Leu Thr Gly Arg Arg Ser Leu Ala
305              310              315

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<210> 2654
 <211> 323
 <212> PRT
 <213> Unknown (17-93)

<400>2654

```

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1           5           10           15
Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
      20           25           30
Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
      35           40           45
Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser
 50           55           60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65           70           75           80
Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
      85           90           95
Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser
      100          105          110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
      115          120          125
Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile
      130          135          140
Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu
145          150          155          160
Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys
      165          170          175
Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala
      180          185          190
Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile
      195          200          205
Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu
      210          215          220
Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser
225          230          235          240
Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val
      245          250          255
Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser
      260          265          270
Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr
      275          280          285
Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg
      290          295          300
Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro
305          310          315          320
Phe Leu Leu

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<210> 2655
 <211> 316
 <212> PRT
 <213> Unknown (FAT11 (HUMORLMHC A57069 601919 1097174 1362875) Fan-W 95)

<400>2655

```

Met Asp Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1           5           10           15
Glu His Pro Gly Leu Gly Arg Thr Leu Phe Val Asp Val Ile Thr Ser
      20           25           30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
      35           40           45

```

Leu Asp Thr Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
 65 70 75 80
 Ala Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
 85 90 95
 Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
 100 105 110
 Met Lys Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
 115 120 125
 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
 130 135 140
 Val Ala Trp Val Ile Gly Leu Val Gly Ser Val Val Gln Thr Pro Ser
 145 150 155 160
 Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
 165 170 175
 Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
 180 185 190
 Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
 195 200 205
 Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
 210 215 220
 Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
 225 230 235 240
 Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
 245 250 255
 Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
 260 265 270
 Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
 275 280 285
 Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
 290 295 300
 Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
 305 310 315

<210> 2656

<211> 254

<212> PRT

<213> Unknown (H8 (432510) Selbie-LA 92)

<400>2656

Pro Met Tyr Leu Phe Leu Ser Asn Leu Ser Phe Leu Asp Ile Gly Phe
 1 5 10 15
 Ile Ser Thr Ile Ile Pro Lys Met Leu Asp His Ile Ser Ser Gly Ile
 20 25 30
 Lys Leu Ile Ser Tyr Gly Glu Cys Leu Thr Gln Leu Tyr Phe Ser Gly
 35 40 45
 Leu Phe Ala Asp Leu Asp Asn Asn Phe Leu Leu Ala Val Met Ala Ile
 50 55 60
 Asp Arg Tyr Val Ala Ile Ser His Pro Leu His Tyr Ala Leu Thr Met
 65 70 75 80
 Asn Ser Gln Arg Cys Val Leu Leu Val Ala Val Ser Trp Val Ile Thr
 85 90 95
 Ile Leu His Ala Leu Val His Thr Leu Leu Val Thr Arg Leu Ser Phe
 100 105 110
 Cys Gly Pro Asn Ile Ile Pro His Phe Phe Cys Asp Leu Val Pro Leu
 115 120 125
 Leu Lys Leu Ala Cys Ser Ser Thr Cys Val Asn Asp Leu Val Leu Ile
 130 135 140
 Leu Val Pro Gly Thr Leu Leu Ile Ala Pro Phe Val Cys Ile Leu Met
 145 150 155 160

Ser Tyr Phe Tyr Ile Ala Leu Ala Ile Leu Arg Ile Asp Ser Pro Arg
 165 170 175
 Gly Lys Gln Arg Ala Phe Ser Ser Cys Thr Ser His Leu Ser Val Val
 180 185 190
 Ser Leu Phe Tyr Ser Thr Ala Ile Gly Val Tyr Leu Cys Pro Pro Ser
 195 200 205
 Ser His Ser Asp Gly Lys Asp Arg Val Phe Ser Val Met Tyr Thr Val
 210 215 220
 Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp
 225 230 235 240
 Met Lys Gly Ala Leu Gly Lys Leu Leu Gly Ile Lys Thr Ser
 245 250

<210> 2657

<211> 195

<212> PRT

<213> Unknown (G3 (432509) Selbie-LA 92)

<400>2657

Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Asp Leu Gln Pro Val
 1 5 10 15
 Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu
 20 25 30
 Arg Asn Leu Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His
 35 40 45
 Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp Pro Asp Ile Gly
 50 55 60
 Phe Thr Ser Ala Met Val Pro Lys Met Ile Val Asp Thr Gln Ser His
 65 70 75 80
 Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu
 85 90 95
 Leu Leu Val Ala Cys Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr
 100 105 110
 Asp Cys Phe Val Ala Ile Cys Arg Pro Leu His Tyr Pro Ile Ile Val
 115 120 125
 Asn Pro His Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser
 130 135 140
 Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu Gln Leu Thr Ile
 145 150 155 160
 Ile Lys Asn Val Glu Ile Ser Asn Leu Val Cys Asp Pro Ser Gln Leu
 165 170 175
 Leu Lys Leu Ala Cys Ser Asp Ser Val Leu Thr Asn Ile Phe Ile Tyr
 180 185 190
 Ser Ile Gly
 195

<210> 2658

<211> 314

<212> PRT

<213> Unknown (HsOLF1 (1336041 HSU56420) Issel-Tarver-L 97 11q11)

<400>2658

Met Glu Phe Thr Asp Arg Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu
 1 5 10 15
 Leu Gly Phe Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Met
 20 25 30
 Phe Leu Thr Leu Tyr Ala Ile Ile Leu Ile Gly Asn Ile Gly Leu Met
 35 40 45
 Leu Leu Ile Arg Ile Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Ser Phe Val Asp Leu Cys Tyr Phe Ser Asp Il Val

```

65          70          75          80
Pro Lys Met Leu Val Asn Phe Leu Ser Glu Asn Lys Ser Ile Ser Tyr
      85          90          95
Tyr Gly Cys Ala Leu Gln Phe Tyr Phe Phe Cys Thr Phe Ala Asp Thr
      100        105        110
Glu Ser Phe Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile
      115        120        125
Cys Asn Pro Leu Leu Tyr Thr Val Val Met Ser Arg Gly Ile Cys Met
      130        135        140
Arg Leu Ile Val Leu Ser Tyr Leu Gly Gly Asn Met Ser Ser Leu Val
      145        150        155        160
His Thr Ser Phe Ala Phe Ile Leu Lys Tyr Cys Asp Lys Asn Val Ile
      165        170        175
Asn His Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Thr
      180        185        190
Asp Thr Thr Ile Asn Glu Trp Leu Leu Ser Thr Tyr Gly Ser Ser Val
      195        200        205
Glu Ile Ile Cys Phe Ile Ile Ile Ile Ser Tyr Phe Phe Ile Leu
      210        215        220
Leu Ser Val Leu Lys Ile Arg Ser Phe Ser Gly Arg Lys Lys Thr Phe
      225        230        235        240
Ser Thr Cys Ala Ser His Leu Thr Ser Val Thr Ile Tyr Gln Gly Thr
      245        250        255
Leu Leu Phe Ile Tyr Ser Arg Pro Ser Tyr Leu Tyr Ser Pro Asn Thr
      260        265        270
Asp Lys Ile Ile Ser Val Phe Tyr Thr Ile Phe Ile Pro Val Leu Asn
      275        280        285
Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ala Glu
      290        295        300
Lys Val Leu Arg Ser Lys Val Asp Ser Ser
      305        310

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<210> 2659

<211> 317

<212> PRT

<213> Unknown (HsOLF3 (1336043 HSU56421) Issel-Tarver-L 97 7q35)

<400>2659

```

Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly
1      5      10      15
Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu
      20      25      30
Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
      35      40      45
Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50      55      60
Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
      65      70      75      80
Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
      85      90      95
Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
      100     105     110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
      115     120     125
Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
      130     135     140
Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr
      145     150     155     160
Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His
      165     170     175
Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr

```

Met 1	Ser	Gly	Thr	Asn 5	Gln	Ser	Ser	Val 10	Ser	Glu	Phe	Leu	Leu 15	Gly	
Leu	Ser	Arg	Gln	Pro	Gln	Gln	Gln	His 25	Leu	Leu	Phe	Val	Phe 30	Phe	Leu
Ser	Met	Tyr	Leu	Ala	Thr	Val	Leu	Gly 40	Asn	Leu	Leu	Ile 45	Ile	Leu	Ser
Val	Ser	Ile	Asp	Ser	Cys	Leu	His 55	Thr	Pro	Met	Tyr 60	Phe	Phe	Leu	Ser
Asn 65	Leu	Ser	Phe	Val	Asp	Ile	Cys 70	Phe	Ser	Phe	Thr 75	Thr	Val	Pro	Lys 80
Met	Leu	Ala	Asn	His 85	Ile	Leu	Glu	Thr 90	Gln	Thr	Ile	Ser	Phe 95	Cys	Gly
Cys	Leu	Thr	Gln	Met 100	Tyr	Phe	Val	Phe 105	Met	Phe	Val	Asp	Met 110	Asp	Asn
Phe	Leu	Leu	Ala	Val	Met	Ala	Tyr 120	Asp	His	Phe	Val	Ala 125	Val	Cys	His
Pro	Leu	His	Tyr	Thr	Ala	Lys 135	Met	Thr	His	Gln	Leu 140	Cys	Ala	Leu	Leu
Val 145	Ala	Gly	Leu	Trp	Val	Val	Ala	Asn	Leu	Asn 155	Val	Leu	Leu	His	Thr 160
Leu	Leu	Met	Ala	Pro 165	Leu	Ser	Phe	Cys 170	Ala	Asp	Asn	Ala	Ile 175	Thr	His
Phe	Phe	Cys	Asp	Val 180	Thr	Pro	Leu	Leu 185	Lys	Leu	Ser	Cys 190	Ser	Asn	Thr
His	Leu	Asn	Glu	Val 195	Ile	Ile	Leu 200	Ser	Glu	Gly	Ala 205	Leu	Val	Met	Ile
Thr	Pro	Phe	Leu	Cys	Ile	Leu 215	Ala	Ser	Tyr	Met 220	His	Ile	Thr	Cys	Thr
Val 225	Leu	Lys	Val	Pro	Ser	Thr	Lys	Gly	Arg	Trp 235	Lys	Ala	Phe	Ser	Thr 240
Cys	Gly	Ser	His	Leu 245	Ala	Val	Val	Leu	Leu	Phe 250	Tyr	Ser	Thr	Ile	Ile
Ala	Val	Tyr	Phe	Asn 260	Pro	Leu	Ser	Ser 265	His	Ser	Ala	Glu	Lys 270	Asp	Thr
Met	Ala	Thr	Val	Leu 275	Tyr	Thr	Val	Val 280	Thr	Pro	Met 285	Leu	Asn	Pro	Phe
Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Tyr	Leu	Lys	Gly	Ala	Leu	Lys	Lys	Val

290 295 300
 Ile Gly Arg Val Val Phe Ser Val
 305 310

<210> 2661

<211> 315

<212> PRT

<213> Unknown (OLFMF2 gi|2808536|emb|AJ003145|HSAJ03145 Homo sapiens mRNA for)

<400>2661

Val Gln Thr Tyr Glu Arg Asp Lys Pro Val Ser Val Ser Glu Phe Leu
 1 5 10 15
 Leu Leu Gly Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val
 20 25 30
 Phe Phe Leu Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile
 35 40 45
 Ile Leu Ala Ile Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val
 65 70 75 80
 Pro Lys Met Leu Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe
 85 90 95
 Ser Gly Cys Leu Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met
 100 105 110
 Asp Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val
 115 120 125
 Cys Arg Pro Leu His Tyr Thr Ala Lys Met Ile His Gln Leu Cys Ala
 130 135 140
 Leu Leu Val Thr Gly Ser Trp Val Val Ala Asn Ser Asn Ala Leu Leu
 145 150 155 160
 His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile
 165 170 175
 Pro His Ile Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser
 180 185 190
 Asp Thr His Leu Ser Glu Val Met Ile Leu Thr Glu Ala Ala Leu Val
 195 200 205
 Thr Ile Thr Pro Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr
 210 215 220
 Cys Val Val Leu Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr
 245 250 255
 Ile Met Ser Pro Tyr Phe Arg Thr Ser Ser Ser His Ser Ala Gln Arg
 260 265 270
 Asp Ile Ala Ala Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val
 290 295 300
 Lys Val Val Ala Val Lys Phe Phe Ser Val Gln
 305 310 315

<210> 2662

<211> 313

<212> PRT

<213> Unknown (CFDTMT)

<400>2662

Met Thr Glu Lys Asn Gln Thr Val Val Ser Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Asp Pro Asp Gln Arg Asp Leu Phe Tyr Ala Leu Phe Leu

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<210> 2663
<211> 309
<212> PRT
<213> Unknown (CfOLF4 (CFU53682) Issel-Tarver-L 97)
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Met	Glu	Leu	Glu	Asn	Asp	Thr	Arg	Ile	Pro	Glu	Phe	Leu	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Glu	Glu	Pro	Lys	Leu	Gln	Pro	Phe	Leu	Phe	Gly	Leu	Phe	Leu
			20					25					30		
Ser	Met	Tyr	Leu	Val	Thr	Ile	Leu	Gly	Asn	Leu	Leu	Leu	Ile	Leu	Ala
		35				40						45			
Val	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala
	50					55					60				
Asn	Leu	Ser	Phe	Val	Asp	Ile	Cys	Phe	Thr	Cys	Thr	Thr	Ile	Pro	Lys
65					70					75				80	
Met	Leu	Val	Asn	Ile	Gln	Thr	Gln	Arg	Lys	Val	Ile	Thr	Tyr	Glu	Ser
			85						90					95	
Cys	Ile	Ile	Gln	Met	Tyr	Phe	Phe	Glu	Leu	Phe	Ala	Gly	Ile	Asp	Asn
			100					105					110		
Phe	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Met	Ala	Ile	Cys	Tyr
		115					120					125			
Pro	Leu	His	Tyr	Met	Val	Ile	Met	Asn	Pro	Gln	Leu	Cys	Ser	Leu	Leu

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      130              135              140
Leu Leu Val Ser Trp Ile Met Ser Ala Leu His Ser Leu Leu Gln Thr
145              150              155              160
Leu Met Val Leu Arg Leu Ser Phe Cys Thr His Phe Gln Ile Pro His
      165              170              175
Phe Phe Cys Glu Leu Asn Gln Met Ile Gln Leu Ala Cys Ser Asp Thr
      180              185              190
Phe Leu Asn Asn Met Met Leu Tyr Phe Ala Ala Ile Leu Leu Gly Val
      195              200              205
Ala Pro Leu Val Gly Val Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser
      210              215              220
Ile Arg Gly Ile Ser Ser Ala His Ser Lys Tyr Lys Ala Phe Ser Thr
225              230              235              240
Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ser Leu
      245              250              255
Gly Val Tyr Leu Ser Ser Ala Ala Pro Gln Ser Thr His Thr Ser Ser
      260              265              270
Val Ala Ser Val Met Tyr Thr Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Asn Val Phe
      290              295              300
Phe Arg Gly Lys Pro
305

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<210> 2664

<211> 317

<212> PRT

<213> Unknown (CfOLF3 (CFU53681) Issel-Tarver-L 97)

<400>2664

```

Met Gly Thr Gly Asn Gln Thr Trp Val Arg Glu Phe Val Leu Leu Gly
1      5      10      15
Leu Ser Ser Asp Trp Asp Thr Glu Val Ser Leu Phe Val Leu Phe Leu
      20      25      30
Ile Thr Tyr Met Val Thr Val Leu Gly Asn Phe Leu Ile Ile Leu Leu
      35      40      45
Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50      55      60
Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Ile Ile Pro Gln
65      70      75      80
Met Leu Ala His Leu Leu Ala Ala His Lys Ala Ile Pro Phe Val Ser
      85      90      95
Cys Ala Ala Gln Leu Phe Phe Ser Leu Gly Leu Gly Gly Ile Glu Phe
      100      105      110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
      115      120      125
Pro Leu Arg Tyr Ser Val Ile Met His Gly Gly Leu Cys Thr Arg Leu
      130      135      140
Ala Ile Thr Ser Trp Val Ser Gly Ser Met Asn Ser Leu Met Gln Thr
145      150      155      160
Val Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Tyr Ile Asp His
      165      170      175
Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
      180      185      190
Ser Ser Asn Glu Ile Ala Ile Met Val Ser Ser Ile Val Leu Leu Met
      195      200      205
Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
      210      215      220
Ile Leu Lys Ile Gln Ser Thr Glu Gly Arg Lys Lys Ala Phe His Thr
225      230      235      240
Cys Ala Ser His Leu Thr Val Val Val Leu Cys Tyr Gly Met Ala Ile

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<213> Unknown (CfOLF2 (1314663 CFU53680) Issel-Tarver-L 97)

<213> Unknown (CfOLF1 (1314661 CFU53679) Issel-Tarver-L 97)

<400>2666

```

Met Asp Gly Asn Tyr Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Phe
 1          5          10          15
Pro Thr Arg Pro Glu Leu Gln Ile Val Leu Phe Leu Val Phe Leu Thr
      20          25          30
Leu Tyr Gly Ile Ile Leu Thr Gly Asn Ile Gly Leu Met Met Leu Ile
      35          40          45
Arg Thr Asp Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn
      50          55          60
Leu Ser Phe Ala Asp Leu Cys Phe Ser Ser Ala Ile Val Pro Lys Met
      65          70          75          80
Leu Val Asn Phe Leu Ser Glu Asn Lys Ser Ile Ser Leu Tyr Gly Cys
      85          90          95
Ala Leu Gln Phe Tyr Phe Ser Cys Ala Phe Ala Asp Thr Glu Ser Phe
      100          105          110
Ile Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
      115          120          125
Leu Leu Tyr Thr Val Val Met Ser Arg Gly Ile Cys Val Trp Leu Ile
      130          135          140
Val Leu Ser Tyr Ile Gly Gly Asn Met Ser Ser Leu Val His Thr Ser
      145          150          155          160
Phe Ala Phe Ile Leu Lys Tyr Cys Asp Lys Asn Val Ile Asn His Phe
      165          170          175
Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr Ser
      180          185          190
Val Asn Glu Trp Leu Leu Ser Thr Tyr Gly Ser Ser Val Glu Ile Phe
      195          200          205
Cys Phe Ile Val Ile Val Ile Ser Tyr Tyr Phe Ile Leu Arg Ser Val
      210          215          220
Leu Arg Ile Arg Ser Ser Ser Gly Arg Lys Lys Thr Phe Ser Thr Cys
      225          230          235          240
Ala Ser His Leu Thr Ser Val Ala Ile Tyr Gln Gly Thr Leu Leu Phe
      245          250          255
Ile Tyr Ser Arg Pro Thr Tyr Leu Tyr Thr Pro Asn Thr Asp Lys Ile
      260          265          270
Ile Ser Val Phe Tyr Thr Ile Ile Ile Pro Val Leu Asn Pro Leu Ile
      275          280          285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ala Lys Arg Ala Val
      290          295          300
Arg Leu Lys Val Asp Ser Ser
      305          310

```

<210> 2667

<211> 155

<212> PRT

<213> Unknown (DRU42392)

<400>2667

```

Asn Pro Leu Arg Tyr Pro Ala Val Met Thr Ser Asn Met Val Val His
 1          5          10          15
Leu Ser Ala Ala Ala Trp Gly Val Ala Val Val Leu Val Gly Ile Leu
      20          25          30
Ile Gly Leu Thr Val Arg Leu Ser Phe Cys Arg Ser Val Ile Glu Asn
      35          40          45
Pro Phe Cys Asp Asn Ala Ser Leu Phe Lys Leu Ser Cys Glu Ser Thr
      50          55          60
Ala Ile Asn Asn Ile Tyr Gly Leu Ser Phe Thr Val Val Leu Leu Thr
      65          70          75          80
Ser Ser Leu Gly Ser Ile Ala Leu Thr Tyr Leu Arg Ile Ala Ile Val
      85          90          95

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Cys Phe Lys Ser Lys Asn Lys Ala Thr Asn Ser Lys Ala Ile Lys Thr
 100 105 110
 Cys Ser Thr His Leu Ala Val Tyr Leu Ile Met Met Val Ser Gly Leu
 115 120 125
 Thr Thr Ile Thr Leu His Arg Phe Pro Glu Leu Ser Asp Ser Arg Lys
 130 135 140
 Leu Ser Ser Ile Ile Lys His Ile Val Pro Pro
 145 150 155

<210> 2668

<211> 155

<212> PRT

<213> Unknown (DRU42394)

<400>2668

Asn Pro Leu Arg Tyr Gln Thr Ile Met Thr Asn Lys Thr Val Ile Thr
 1 5 10 15
 Leu Ser Ala Leu Ala Trp Gly Ile Ala Leu Leu Phe Ile Ser Ile Leu
 20 25 30
 Ile Gly Leu Thr Leu Arg Leu Ser Arg Cys Arg Thr Phe Ile Ser Asn
 35 40 45
 Pro Phe Cys Asp Asn Ala Ser Leu Phe Lys Leu Ser Cys Glu Asp Val
 50 55 60
 Thr Ile Asn Asn Leu Tyr Gly Leu Ile Tyr Thr Val Leu Leu Phe Gly
 65 70 75 80
 Ser Ser Met Gly Ser Ile Ala Val Thr Tyr Ile Lys Ile Thr Ala Val
 85 90 95
 Cys Leu Val Thr Lys Ser Lys Met Leu Asn Ser Arg Ala Leu Lys Thr
 100 105 110
 Cys Ser Thr His Leu Ser Leu Tyr Leu Ile Met Leu Ile Ser Gly Leu
 115 120 125
 Ile Ile Ile Val Leu His Arg Phe Pro Ala Tyr Ser Asp Tyr Arg Lys
 130 135 140
 Ile Ala Ser Leu Leu Phe His Ile Ile Pro Ser
 145 150 155

<210> 2669

<211> 157

<212> PRT

<213> Unknown (DRU42395)

<400>2669

Leu Pro Leu Arg Tyr His Ala Ile Val Asn Asn Ser Ser Ile Thr Leu
 1 5 10 15
 Ile Leu Ser Ala Lys Trp Ala Phe Asn Ser Ser Ile Val Ala Leu Met
 20 25 30
 Val Ser Leu Ile Thr Arg Ile Ser Phe Cys Asp Ser Asn Val Ile Gln
 35 40 45
 Ser Tyr Phe Cys Asp His Gly Pro Val Tyr Arg Leu Ala Cys Asn Asp
 50 55 60
 Asn Ser Ile Asn Arg Phe Met Gly Ser Phe Ile Thr Cys Leu Tyr Leu
 65 70 75 80
 Val Val Pro Leu Gly Ile Ile Ile Leu Ser Tyr Ile Gly Ile Phe Leu
 85 90 95
 Ala Leu Asn Lys Ile Thr Thr Trp Glu Ser Arg Leu Lys Ala Leu Lys
 100 105 110
 Thr Cys Val Ser His Leu Leu Leu Val Gly Ile Tyr Phe Leu Pro Met
 115 120 125
 Ser Cys Thr Tyr Ile Ala Ala Trp Leu Leu Ala Leu Ala Pro Asn Ala
 130 135 140
 Arg Val Ile Thr Thr Ser Leu Ala Tyr Thr Ile Ser Gln

145

150

155

<210> 2670

<211> 150

<212> PRT

<213> Unknown (DRU42396)

<400>2670

```

Leu Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Val Ile Val Asn Asn
1           5           10           15
Thr Ser Met Ile Ser Ile Phe Ser Ala Val Phe Met Phe Asn Ser Ile
20           25           30
Ile Val Ala Ser Met Val Ser Leu Val Thr Asn Ile Ser Phe Cys Lys
35           40           45
Ser Asn Val Ile Gln Ser Tyr Phe Cys Asp His Gly Pro Met Phe Arg
50           55           60
Met Ala Cys Asn Asp Asn Asn Ile Asn Lys Ile Met Gly Phe Leu Tyr
65           70           75           80
Thr Thr Leu Tyr Leu Ile Ala Pro Met Leu Val Ile Phe Leu Ser Tyr
85           90           95
Leu Gly Ile Phe Leu Val Val Ser Lys Ile Ala Thr Trp Glu Arg Arg
100          105          110
Leu Lys Ala Leu Lys Thr Cys Val Ser His Leu Leu Leu Val Gly Ile
115          120          125
Tyr Phe Leu Pro Ile Phe Phe Thr Tyr Leu Thr Ser Leu Leu Leu Phe
130          135          140
Ser Thr Ser Asn Ser Arg
145          150

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<210> 2671

<211> 158

<212> PRT

<213> Unknown (DRU42397 (odorant receptor 8; 1644478) Weth-F 96)

<400>2671

```

Asn Pro Leu Arg Tyr Pro Asn Ile Val Thr Lys Trp Asn Ile Phe Tyr
1           5           10           15
Leu Cys Leu Ile Ser Trp Val Ile Ala Asn Val Thr Pro Leu Met Met
20           25           30
Val Ile Arg Ala Tyr Pro Leu Pro Tyr Cys Ala Glu Asn Thr Ile Ile
35           40           45
Gln Cys Tyr Cys Asp His Ile Ser Ile Thr Ser Leu Ala Cys Thr Asn
50           55           60
Arg Ala Pro Tyr Ser Ile Pro Ala Phe Val Leu Ala Met Val Ala Leu
65           70           75           80
Leu Thr Pro Leu Ala Phe Ile Val Phe Ser Tyr Cys Ala Ile Ile Leu
85           90           95
Ala Val Leu Arg Ile Ser Ser Thr Gln Ala Arg Leu Lys Thr Phe Ser
100          105          110
Thr Cys Ser Pro Gln Leu Ile Ile Ala Leu Tyr Phe Leu Pro Arg
115          120          125
Cys Phe Ile Tyr Leu Ser Ser Asn Ile Gly Ile Tyr Phe Ser Thr Asp
130          135          140
Leu Arg Leu Ala Ile Ile Met Met Tyr Ser Leu Phe Pro Pro
145          150          155

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<210> 2672

<211> 155

<212> PRT

<213> Unknown (DRU42398 (1151131))

<400>2672

```

Arg Pro Leu Glu Tyr His Ser Ile Met Thr Asp Gln Arg Ile Ile Glu
 1           5           10           15
Cys Ile Leu Phe Cys Trp Leu Thr Pro Phe Phe Cys Met Ala Val Leu
          20           25           30
Ile Gly Leu Thr Ala Arg Leu Thr Leu Cys Gly Ser Ala Ile Glu Lys
          35           40           45
Leu Tyr Cys Glu Asn Trp Ser Val Val Lys Leu Ser Cys Phe Ser Thr
          50           55           60
Thr Val Asn Asn Val Val Gly Tyr Val Ile Ile Val Tyr Phe Gly
65           70           75           80
His Ala Val Leu Ile Phe Cys Ser Tyr Ile Tyr Leu Val Val Lys Cys
          85           90           95
Arg Lys Ser Thr Glu Ser Arg His Lys Phe Ile Gln Thr Cys Val Pro
          100          105          110
His Leu Leu Ala Leu Leu Asn Val Thr Val Ala Leu Leu Phe Asp Val
          115          120          125
Leu Tyr Ser Arg Tyr Gly Ser Lys Ser Leu Pro Gln Asp Leu Arg Asn
          130          135          140
Phe Met Ser Leu Glu Phe Leu Leu Val Pro Pro
145           150           155

```

<210> 2673

<211> 174

<212> PRT

<213> Unknown (DRU44439)

<400>2673

```

Met Ala Tyr Asp Arg Leu Ile Ala Ile Cys Trp Pro Leu Arg Tyr Ser
 1           5           10           15
Thr Ile Asn Thr Asn Leu Arg Met Leu Leu Ile Ile Ala Leu Ile Trp
          20           25           30
Ile Leu Val Thr Leu Leu Asp Ile Phe Pro Val Ile Phe Ala Ser Arg
          35           40           45
Leu Pro Tyr Cys Ser Ser Arg Ala Val Leu Ser Cys Cys Cys Glu His
          50           55           60
Gly Pro Val Tyr Arg Leu Ala Cys Thr Asp Thr Tyr Asn Arg Gln
65           70           75           80
Leu Gly Thr Val Lys Thr Met Ile Thr Leu Leu Gly Pro Leu Phe Phe
          85           90           95
Ile Val Phe Thr Tyr Val Ile Val Val Ile Ala Val Met Arg Ile Ala
          100          105          110
Ser Val Thr Gln Arg Trp Lys Ala Phe His Thr Cys Leu Thr His Met
          115          120          125
Met Leu Val Met Leu Tyr Tyr Met Pro Ile Ile Ile Ala Cys Val Leu
          130          135          140
Gly Asn Leu Arg Leu Val Gln Asn Val Asp Leu Leu Thr Ala Ile Leu
145           150           155           160
Thr Arg Ser Val Thr Val Pro Ala Met Leu Asn Pro Ile Ile
          165           170

```

<210> 2674

<211> 173

<212> PRT

<213> Unknown (DRU44440)

<400>2674

```

Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys Leu Pro Leu Arg Tyr His
 1           5           10           15
Ser Ile Val Asn Asn Ser Asn Met Ile Leu Ile Phe Ser Ala Ile Trp
          20           25           30

```

Ala Phe Asn Ser Ser Val Val Ala Leu Met Val Ser Leu Ile Asp Arg
 35 40 45
 Leu Ser Phe Cys Glu Ser Asn Met Ile Gln Ser Tyr Phe Cys Asp His
 50 55 60
 Gly Pro Val Tyr Arg Leu Ala Cys Ser Asp Ile Ser Lys Asn Lys Ile
 65 70 75 80
 Met Ala Tyr Val Ile Ser Ala Met Tyr Ile Ala Pro Met Val Val
 85 90 95
 Ile Val Phe Ser Tyr Leu Gly Ile Phe Leu Ala Leu Ile Lys Ile Thr
 100 105 110
 Thr Trp Glu Gly Arg Leu Lys Ala Leu Lys Thr Cys Val Ser His Leu
 115 120 125
 Leu Leu Val Gly Ile Phe Phe Leu Pro Leu Phe Cys Thr Tyr Leu Ala
 130 135 140
 Gln Leu Leu Leu Ser Leu Asn Pro Asn Ala Arg Val Ile Ser Thr Ser
 145 150 155 160
 Leu Ser Tyr Ala Ile Pro Pro Met Leu Asn Pro Ile Ile
 165 170

<210> 2675

<211> 173

<212> PRT

<213> Unknown (DRU44441)

<400>2675

Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys Leu Pro Leu Arg Tyr His
 1 5 10 15
 Val Ile Val Asn Asn Thr Ser Met Ile Ser Ile Phe Ser Ala Val Phe
 20 25 30
 Met Phe Asn Ser Ile Ile Val Ala Ser Met Val Ser Leu Val Thr Asn
 35 40 45
 Ile Ser Phe Cys Lys Ser Asn Val Ile Gln Ser Tyr Phe Cys Asp His
 50 55 60
 Gly Pro Met Phe Arg Met Ala Cys Asn Asp Asn Ile Ile His Glu Ile
 65 70 75 80
 Met Gly Phe Leu Tyr Thr Thr Leu Tyr Leu Ile Ala Pro Met Leu Val
 85 90 95
 Ile Phe Leu Ser Tyr Leu Gly Ile Phe Leu Val Val Ser Lys Ile Ala
 100 105 110
 Thr Trp Glu Arg Arg Leu Lys Ala Leu Lys Thr Cys Val Ser His Leu
 115 120 125
 Leu Phe Val Gly Ile Tyr Phe Leu Pro Ile Phe Phe Thr Tyr Leu Thr
 130 135 140
 Ser Leu Leu Leu Phe Ser Thr Ser Asn Ser Arg Val Ile Ser Thr Ser
 145 150 155 160
 Leu Ala Tyr Ala Ile Pro Pro Met Leu Asn Pro Ile Ile
 165 170

<210> 2676

<211> 344

<212> PRT

<213> Unknown (ICTORDA (fish1 L09217 1079242) Ngai-J 93)

<400>2676

Met Thr Ser Val Leu Asn Ala Leu Ser Ala Asn Ala Thr Phe Ile Arg
 1 5 10 15
 Pro Ser Thr Phe Tyr Ile Asn Gly Phe Tyr Asn Ile Pro His Thr Lys
 20 25 30
 Tyr Tyr Tyr Ala Phe Leu Cys Ile Ala Tyr Ala Val Thr Val Leu Gly
 35 40 45
 Asn Ser Phe Ile Met Cys Thr Ile Tyr Leu Ala Arg Ser Leu His Thr

50 55 60
 Ala Lys Tyr Ile Thr Val Phe Asn Leu Ala Leu Ser Asp Leu Gly Gly
 65 70 75 80
 Ser Ser Ala Leu Ile Pro Lys Leu Ile Asp Thr Phe Leu Phe Glu Asn
 85 90 95
 Gln Val Ile Ser Tyr Glu Ala Cys Leu Ala Asn Met Phe Phe Val Leu
 100 105 110
 Phe Phe Met Thr Val Gln Ser Leu Thr Leu Leu Val Met Ala Tyr Asp
 115 120 125
 Arg Val Val Ala Ile Cys Phe Pro Leu Arg Tyr Asn Val Ile Val Thr
 130 135 140
 Lys Glu Ala Met Thr Leu Ile Ile Val Ile Thr Trp Ile Phe Ser Ile
 145 150 155 160
 Ser Ile Ile Ala Leu Leu Val Ala Leu Ile Thr Arg Leu Ser Phe Cys
 165 170 175
 Arg Ser Val Ile Ile Asn Ser Tyr Phe Cys Asp His Gly Pro Ile Leu
 180 185 190
 Ile Leu Ala Cys Asn Asp Lys Phe Ile Asn Arg Val Met Ala Ile Gly
 195 200 205
 Cys Phe Val Val Leu Asp Cys Val Pro Phe Leu Leu Ile Ile Val Ser
 210 215 220
 Tyr Ile Cys Ile Gly Ile Ala Leu Met Asn Ile Ser His Gly Leu Glu
 225 230 235 240
 Arg Arg Lys Ala Met Lys Thr Cys Thr Ser His Leu Ile Leu Val Ala
 245 250 255
 Leu Phe Tyr Leu Pro Phe Ile Gly Thr Asn Ile Thr Ser Leu Thr Ser
 260 265 270
 Ser Ile Asn Ala Asn Asp Arg Ile Leu Asn Ser Thr Leu Thr Gln Ile
 275 280 285
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Lys Thr Glu Glu
 290 295 300
 Val Met Gln Ala Val Lys Val Leu Tyr Lys Arg Ala Lys Ala Val Val
 305 310 315 320
 Ile Cys Asp Ile Pro Asn Gly Gln Val Phe Gln Pro Trp Val Gly Val
 325 330 335
 Asp Ser Lys Lys Lys Thr Phe Cys
 340

<210> 2677

<211> 321

<212> PRT

<213> Unknown (ICTORDB (fish3 L09218 1079244) Ngai-J 93)

<400>2677

Met Ala Asp Asn Ile Thr Ser Ile Leu Ser Leu Thr Ser Thr Asn Ala
 1 5 10 15
 Thr Phe Ile Arg Pro Ser Thr Phe Tyr Ile Thr Gly Leu Tyr Asn Ile
 20 25 30
 Pro His Ala Lys Tyr Tyr Tyr Leu Phe Leu Cys Phe Val Tyr Thr Val
 35 40 45
 Thr Phe Leu Gly Asn Ser Phe Ile Met Gly Thr Ile Tyr Leu Ala Arg
 50 55 60
 Ser Leu His Thr Ala Lys Tyr Ile Ala Val Phe Asn Leu Ala Leu Ser
 65 70 75 80
 Asp Leu Cys Gly Ser Ser Ala Leu Ile Pro Lys Leu Leu Asp Met Leu
 85 90 95
 Leu Phe Glu Asn Gln Ser Ile Ser Tyr Glu Ala Cys Leu Ser Asn Met
 100 105 110
 Phe Phe Val Tyr Cys Phe Met Thr Leu Gln Cys Leu Thr Leu Leu Ala
 115 120 125
 Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys Tyr Pro Leu Arg Tyr His

130 135 140
 Ala Ile Val Thr Lys Ala Ala Met Ile Phe Ile Ile Gly Ala Met Trp
 145 150 155 160
 Val Leu Ser Val Ser Val Asn Ala Val Leu Val Ala Leu Ile Thr Arg
 165 170 175
 Leu Ser Phe Cys Arg Ser Thr Thr Val Tyr Ser Tyr Phe Cys Asp His
 180 185 190
 Gly Pro Ile Tyr Lys Leu Ala Cys Asn Asp Asn Thr Ile Asn Ser Ile
 195 200 205
 Met Gly Asn Val Cys Thr Ala Thr Leu Leu Tyr Phe Pro Leu Ile Leu
 210 215 220
 Ile Ile Ala Ser Tyr Val Cys Ile Gly Phe Ala Leu Gln Lys Ile Ala
 225 230 235 240
 His Gly Val Glu Gln Val Lys Ala Met Lys Thr Cys Thr Ser His Leu
 245 250 255
 Ile Leu Val Ala Met Phe Tyr Leu Pro Ile Ile Ser Val Tyr Thr Val
 260 265 270
 Ala Leu Thr Thr Arg Ile Asp Thr Asn Ile Arg Ile Ile Asn Thr Ala
 275 280 285
 Leu Thr Gln Thr Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu
 290 295 300
 Lys Thr Glu Glu Val Met Gln Ala Ile Lys Leu Tyr Lys His Ile
 305 310 315 320
 Arg

<210> 2678

<211> 328

<212> PRT

<213> Unknown (ICTORDC (fish32A L09219 1079245) Ngai-J 93)

<400>2678

Met Ser Ala Leu Asn Ser Ser Leu Leu Gln Asn Val Ser Phe Val Arg
 1 5 10 15
 Pro Glu Tyr Phe Phe Ile Ser Gly Phe Ser Gly Ile Pro Phe Ser Gln
 20 25 30
 Tyr Tyr Phe Ala Phe Leu Ile Phe Ile Tyr Ile Ile Ser Leu Cys Gly
 35 40 45
 Asn Ser Ile Val Leu Phe Met Ile Leu Val Asp Arg Thr Leu His Ile
 50 55 60
 Pro Lys Tyr Met Gly Ile Phe Asn Leu Ala Leu Ser Asp Phe Gly Glu
 65 70 75 80
 Thr Asn Val Leu Ile Pro Ser Leu Val Lys Thr Leu Phe Phe Asp Ser
 85 90 95
 Gln Tyr Ile Ser Tyr Asp Ala Cys Leu Ala Asn Met Phe Leu Thr Phe
 100 105 110
 Phe Phe Ser Ser Gly Gln Ala Leu Thr Leu Val Ala Leu Ala Tyr Asp
 115 120 125
 Arg Phe Ile Ala Ile Cys Leu Pro Leu Arg Tyr Asn Ala Ile Val Asn
 130 135 140
 Asn Ser Phe Met Phe Ala Ser Leu Thr Ala Ile Trp Ile Phe Asn Val
 145 150 155 160
 Val Met Asn Gly Thr Leu Val Val Leu Ile Thr Arg Leu Ser Phe Cys
 165 170 175
 Lys Thr Asn Glu Ile Lys Ser Phe Phe Cys Asp His Gly Pro Val Tyr
 180 185 190
 Thr Ile Ala Cys Asn Asp Asn Ser Ile Asn Ser Phe Met Ala Lys Leu
 195 200 205
 Cys Thr Ala Val Tyr Leu Tyr Ala Pro Leu Thr Ala Ile Val Phe Ser
 210 215 220
 Tyr Leu Gly Ile Leu Leu Ala Leu Thr Lys Ile Thr Thr Trp Glu Ser

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225          230          235          240
Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly
          245          250          255
Val Phe Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Val Thr Phe
          260          265          270
Ser Leu His Pro Asn Ala Arg Ile Ile Asn Thr Ser Leu Ser Arg Thr
          275          280          285
Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp
          290          295          300
Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Ile Ile
305          310          315          320
Ser Gln Val His Ala Leu Ala Lys
          325

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<210> 2679

<211> 328

<212> PRT

<213> Unknown (ICTORDD (fish22 fish202 L09220 1079243) Ngai-J 93)

<400>2679

```

Met Pro Glu Gly Asn Ile Thr Asn Val Lys Asn Phe Val Ile Leu Gly
1          5          10          15
Phe Pro Gly Leu Pro Pro Asn Tyr Tyr Gly Leu Val Ser Val Val Met
          20          25          30
Phe Phe Val Tyr Val Cys Thr Leu Ile Gly Asn Cys Thr Phe Phe Thr
          35          40          45
Leu Phe Leu Arg Glu Lys Ser Leu Gln Lys Pro Met Tyr Tyr Ile Met
          50          55          60
Leu Asn Leu Ala Ala Ser Asp Val Leu Phe Ser Thr Thr Thr Leu Pro
65          70          75          80
Lys Ile Ile Ala Arg Tyr Trp Phe Gly Asp Gly Ser Ile Ser Phe Val
          85          90          95
Gly Cys Phe Ile Gln Met Gln Phe Val His Tyr Phe Ala Thr Val Asn
          100          105          110
Ala Leu Val Leu Ala Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys
          115          120          125
Asn Pro Leu Arg Tyr Val Asn Ile Val Lys Glu Ser Thr Ile Leu Gly
          130          135          140
Leu Cys Val Val Ser Trp Leu Leu Ala Glu Pro Thr Val Leu Thr Thr
145          150          155          160
Val Ile Arg Ala Thr Ser Leu Pro Tyr Cys Ala Ser Asn Thr Val Ile
          165          170          175
Gln Cys Tyr Cys Asp His Val Ser Val Thr Lys Leu Ala Cys Ile Asp
          180          185          190
Arg Thr Pro Tyr Ala Phe Pro Ala Leu Val Ser Ala Leu Val Met Leu
195          200          205
Leu Thr Pro Leu Ala Phe Ile Leu Phe Ser Tyr Gly Ser Ile Ile Val
210          215          220
Thr Val Phe Arg Thr Ser Ser Thr Arg Gly Arg Leu Lys Thr Leu Ser
225          230          235          240
Thr Cys Ser Ser Gln Leu Ile Ile Ile Thr Leu Phe Phe Leu Pro Arg
          245          250          255
Cys Leu Asn Tyr Leu Ser Ser Ser Leu Gly Ile His Ile Asn Ala Asp
          260          265          270
Ile Gln Ile Leu Val Ile Met Leu Tyr Ser Leu Leu Pro Pro Met Ile
          275          280          285
Asn Pro Val Ile Tyr Cys Leu Arg Thr Lys Glu Ala Lys Glu Cys Leu
290          295          300
Lys Arg Ser Leu Asn Arg Ser Ser Phe Val Gln Phe Leu Lys Ile Asn
305          310          315          320
Val Gln Val Ser Thr Leu Ser Asn

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325

<210> 2680

<211> 317

<212> PRT

<213> Unknown (ICTORDE (fish47 L09221 1079249) Ngai-J 93)

<400>2680

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Met Asn Ser Thr Asn Ser Thr Asp Ser Phe Asp Lys Gly Phe Tyr Leu
1          5          10          15
Ile Ala Tyr Asn Ser Leu Gly Asn Lys Asn Tyr Leu Ile Leu Ala Leu
20          25          30
Gly Ile Ile Tyr Leu Ile Thr Leu Leu Cys Asn Phe Thr Leu Leu Ala
35          40          45
Ile Ile Leu Met Asn Ser Ser Leu Gln Asn Pro Lys Phe Leu Ala Val
50          55          60
Phe Asn Leu Ala Val Val Asp Ile Ser Ile Asn Ser Val Ile Ile Pro
65          70          75          80
Gln Met Val Pro Val Phe Val Phe Asn Leu Asn His Ile Ser Phe Glu
85          90          95
Ser Cys Phe Ser Gln Met Phe Phe Met His Phe Phe Gly Asp Met Glu
100         105         110
Ser Phe Ser Leu Ala Leu Leu Ala Tyr Asp Arg Leu Ile Ala Ile Cys
115         120         125
Phe Pro Leu Arg Tyr Pro Thr Ile Asn Thr Asn Met Arg Met Val Leu
130         135         140
Ile Ile Ala Ser Leu Trp Phe Leu Val Phe Leu Ile Glu Leu Tyr Pro
145         150         155         160
Val Ala Leu Ala Ser Gly Leu Ser Tyr Cys Arg Ser Arg Val Val Pro
165         170         175
Ser Cys Cys Cys Glu His Gly Pro Val Tyr Asn Leu Ala Cys Gly Asp
180         185         190
Ile Ser Tyr Asn Lys Arg Leu Ala Leu Ala Lys Thr Leu Val Val Leu
195         200         205
Leu Gly Pro Leu Thr Phe Ile Ile Cys Ser Tyr Val Ile Val Val Val
210         215         220
Ala Val Leu Arg Ile Ala Ser Pro Thr Gln Cys Trp Lys Ala Phe Asn
225         230         235         240
Thr Cys Leu Thr His Met Ile Leu Val Leu Ile Tyr Tyr Leu Pro Ile
245         250         255
Ile Leu Ala Tyr Ile Leu Gly Asn Leu Lys Leu Leu Gln Ser Ala Asp
260         265         270
Leu Tyr Thr Ala Gly Leu Thr Val Cys Val Thr Leu Pro Ala Met Leu
275         280         285
Asn Pro Ile Ile Tyr Ser Leu Lys Thr Glu Glu Leu Gln Asp Lys Leu
290         295         300
Leu Lys Phe Ile Lys Pro Gln Lys Val Ser Asn Thr Val
305         310         315

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<210> 2681

<211> 313

<212> PRT

<213> Unknown (ICTORDF (fish8 L09222 1079250) Ngai-J 93)

<400>2681

```

Met Leu Ala Pro Val Gln Asn Ile Ser Phe Thr Thr Phe Thr Leu Thr
1          5          10          15
Gly Phe His Asp Leu Gly Glu Trp Gly Pro Ile Leu Ser Ile Pro Tyr
20          25          30
Leu Leu Met Phe Leu Leu Ser Ser Thr Ser Asn Leu Thr Leu Ile Tyr
35          40          45

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Leu Ile Ile Ser Gln Arg Ala Leu His Ser Pro Met Cys Ile Leu Ile
 50 55 60
 Gly Leu Met Ala Val Val Asp Leu Ser Met Pro Ile Phe Cys Val Pro
 65 70 75 80
 Asn Met Leu Leu Ser Phe Leu Phe Asn Trp Lys Gly Ile Ser Leu Val
 85 90 95
 Gly Cys Leu Val Gln Met Phe Cys Ile His Cys Ala Gly Thr Phe Gln
 100 105 110
 Ser Thr Ile Leu Leu Trp Met Ala Leu Asp Arg Phe Phe Ala Ile Cys
 115 120 125
 Arg Pro Leu Tyr Tyr Gln Lys Tyr Met Gly Met Pro Asn Phe Leu Lys
 130 135 140
 Phe Ile Ile Phe Pro Val Ile Arg Asn Leu Phe Phe Ile Thr Thr Ile
 145 150 155 160
 Val Ser Trp Ala Gly Lys Leu Thr Phe Cys Glu Thr Asn Glu Ile Asp
 165 170 175
 His Cys Val Cys Glu His Met Ala Leu Val Gln Leu Ala Cys Gly Asp
 180 185 190
 Ile Ser Ile Asn Asn Ala Leu Gly Leu Leu Thr Val Phe Leu Thr Ile
 195 200 205
 Thr Ala Asp Phe Ile Phe Ile Thr Ile Ser Tyr Ile Val Ile Leu Val
 210 215 220
 Ser Ile Leu Arg Ser Gly Lys Ala Cys Leu Lys Ala Val Asn Thr Cys
 225 230 235 240
 Ile Thr His Ile Ile Val Met Thr Val Ser Leu Thr Phe Ala Leu Ile
 245 250 255
 Ala Phe Leu Ser Tyr Arg Ile Arg Asn Phe Ser Pro Ser Ser Arg Val
 260 265 270
 Phe Leu Ser Thr Met Tyr Leu Phe Ile Pro Ser Cys Phe Asn Pro Ile
 275 280 285
 Ile Tyr Gly Val Arg Thr Lys Glu Ile Arg Glu Gln Phe Leu Lys Leu
 290 295 300
 Met Lys Tyr Val Lys Val Phe Pro Lys
 305 310

<210> 2682

<211> 328

<212> PRT

<213> Unknown (ICTORDG (fish32D L09223 1079248) Ngai-J 93)

<400>2682

Met Asn Ala Leu Asn Ser Ser Leu Leu Gln Asn Val Ser Phe Val Arg
 1 5 10 15
 Pro Glu Tyr Phe Phe Ile Ser Gly Phe Ser Gly Ile Pro Phe Ser Gln
 20 25 30
 Tyr Tyr Phe Val Phe Leu Ile Phe Ile Tyr Ile Ile Ser Leu Cys Gly
 35 40 45
 Asn Ser Ile Val Leu Phe Met Ile Leu Val Asp Arg Thr Leu His Ile
 50 55 60
 Pro Lys Tyr Met Gly Ile Phe Asn Leu Ala Leu Ser Asp Phe Gly Glu
 65 70 75 80
 Thr Asn Ala Leu Ile Pro Ser Leu Val Lys Thr Leu Phe Phe Asp Ser
 85 90 95
 Gln Tyr Ile Ser Tyr Asp Ala Cys Leu Ala Asn Met Phe Phe Thr Phe
 100 105 110
 Phe Phe Phe Gly Gly Gln Ala Leu Thr Leu Val Ala Leu Ala Tyr Asp
 115 120 125
 Arg Phe Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Ala Ile Val Asn
 130 135 140
 Asn Ser Phe Met Phe Ala Thr Leu Thr Ala Ile Trp Val Phe Asn Leu
 145 150 155 160

Val Met Ile Gly Thr Leu Val Val Leu Ile Thr Arg Leu Ser Phe Cys
 165 170 175
 Lys Thr Asn Glu Ile Lys Ser Phe Phe Cys Asp His Gly Pro Val Tyr
 180 185 190
 Thr Ile Ala Cys Asn Asp Asn Ser Ile Asn Ser Phe Met Ala Lys Leu
 195 200 205
 Cys Thr Ala Val Tyr Leu Tyr Ala Pro Leu Thr Ala Ile Val Leu Ser
 210 215 220
 Tyr Ile Gly Ile Leu Leu Ala Leu Thr Lys Ile Thr Thr Trp Glu Ser
 225 230 235 240
 Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly
 245 250 255
 Val Phe Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Leu Thr Phe
 260 265 270
 Ser Leu His Pro Asn Ala Arg Ile Ile Asn Thr Ser Leu Ser Arg Thr
 275 280 285
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp
 290 295 300
 Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Lys Ile
 305 310 315 320
 Ser Gln Val His Ala Leu Ala Lys
 325

<210> 2683

<211> 328

<212> PRT

<213> Unknown (ICTORDH (fish32C L09224 1079247) Ngai-J 93)

<400>2683

Met Ser Ala Leu Asn Ser Ser Leu Leu Gln Asn Val Ser Phe Val Arg
 1 5 10 15
 Pro Glu Tyr Phe Phe Ile Ser Gly Phe Ser Gly Ile Pro Phe Ser Gln
 20 25 30
 Tyr Tyr Phe Val Phe Leu Ile Phe Ile Tyr Ile Ile Ser Leu Cys Gly
 35 40 45
 Asn Ser Ile Val Leu Phe Met Ile Leu Val Asp Arg Thr Leu His Ile
 50 55 60
 Pro Lys Tyr Met Gly Ile Phe Asn Leu Ala Leu Ser Asp Ile Gly Glu
 65 70 75 80
 Thr Asn Ala Leu Ile Pro Ser Leu Val Lys Thr Leu Phe Phe Asp Ser
 85 90 95
 Gln Tyr Ile Ser Tyr Asp Ala Cys Leu Thr Asn Met Phe Phe Thr Phe
 100 105 110
 Phe Phe Ser Gly Gly Gln Ala Leu Thr Leu Val Ala Leu Ala Tyr Asp
 115 120 125
 Arg Phe Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Ala Ile Val Asn
 130 135 140
 Asn Ser Phe Met Phe Ala Thr Leu Thr Ala Ile Trp Val Phe Asn Leu
 145 150 155 160
 Val Ile Phe Gly Thr Thr Val Val Phe Ile Thr Arg Leu Ser Phe Cys
 165 170 175
 Lys Thr Asn Glu Ile Lys Ser Phe Phe Cys Asp His Gly Pro Val Tyr
 180 185 190
 Thr Ile Ala Cys Asn Asp Asn Ser Ile Asn Ser Phe Met Ala Lys Leu
 195 200 205
 Cys Thr Ala Val Tyr Leu Tyr Ala Pro Leu Thr Ala Ile Val Leu Ser
 210 215 220
 Tyr Ile Gly Ile Leu Leu Ala Leu Thr Lys Ile Thr Thr Trp Glu Ser
 225 230 235 240
 Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly
 245 250 255

Val Phe Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Leu Thr Phe
 260 265 270
 Ser Leu His Pro Asn Ala Arg Ile Ile Asn Thr Ser Leu Ser Arg Thr
 275 280 285
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp
 290 295 300
 Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Lys Ile
 305 310 315 320
 Ser Gln Val His Ala Leu Ala Lys
 325

<210> 2684

<211> 328

<212> PRT

<213> Unknown (ICTORDII (fish32B L09225 1079246) Ngai-J 93)

<400>2684

Met Ser Ala Leu Asn Ser Ser Leu Leu Gln Asn Val Ser Phe Val Arg
 1 5 10 15
 Pro Glu Tyr Phe Phe Ile Ser Gly Phe Ser Gly Ile Pro Phe Ser Gln
 20 25 30
 Tyr Tyr Phe Val Phe Leu Ile Phe Ile Tyr Ile Ile Ser Leu Cys Gly
 35 40 45
 Asn Ser Ile Val Leu Phe Met Ile Leu Val Asp Arg Thr Leu His Ile
 50 55 60
 Pro Lys Tyr Met Gly Ile Phe Asn Leu Ala Leu Ser Asp Phe Gly Glu
 65 70 75 80
 Thr Asn Ala Leu Ile Pro Ser Leu Val Lys Thr Leu Phe Phe Asp Ser
 85 90 95
 Gln Tyr Ile Ser Tyr Asp Ala Cys Leu Ala Asn Met Phe Phe Thr Phe
 100 105 110
 Phe Phe Ala Gly Gly Gln Ala Leu Thr Leu Val Ala Leu Ala Tyr Asp
 115 120 125
 Arg Phe Ile Ala Ile Cys Leu Pro Leu Arg Tyr His Ala Ile Val Asn
 130 135 140
 Asn Ser Phe Met Phe Val Thr Leu Ile Ala Ile Trp Val Phe Asn Val
 145 150 155 160
 Val Ile Ile Gly Thr Thr Val Val Phe Ile Thr Arg Leu Ser Phe Cys
 165 170 175
 Lys Thr Asn Glu Ile Lys Ser Phe Phe Cys Asp His Gly Pro Val Tyr
 180 185 190
 Thr Ile Ala Cys Asn Asp Asn Ser Ile Asn Ser Phe Met Ala Tyr Phe
 195 200 205
 Cys Thr Ala Val Tyr Leu Tyr Ala Pro Leu Thr Ala Ile Val Leu Ser
 210 215 220
 Tyr Ile Gly Ile Leu Leu Ala Leu Thr Lys Ile Thr Thr Trp Glu Ser
 225 230 235 240
 Arg Leu Lys Ala Leu Lys Thr Cys Ile Ser His Leu Leu Val Val Gly
 245 250 255
 Val Phe Phe Leu Pro Ile Val Gly Thr Tyr Leu Ala Ala Val Thr Phe
 260 265 270
 Ser Leu His Pro Asn Ala Arg Ile Ile Asn Thr Ser Leu Ser Arg Thr
 275 280 285
 Ile Pro Pro Met Leu Asn Pro Ile Ile Tyr Val Leu Asn Thr Lys Asp
 290 295 300
 Phe Arg Val Phe Ile Val Lys Met Leu Lys Lys Lys Thr Thr Ile Ile
 305 310 315 320
 Ser Gln Val His Ala Leu Ala Lys
 325

<210> 2685

<211> 313

<212> PRT

<213> Unknown (ol1 (RATOL1RECE L34074) Guillaume-D 94)

<400>2685

```

Met Ser Val Ala Asn Glu Ser Ile Ser Arg Glu Phe Ile Leu Leu Gly
 1          5          10          15
Phe Ser Asp Arg Pro Trp Leu Glu Leu Pro Leu Phe Val Val Phe Leu
 20          25          30
Val Ser Tyr Ile Leu Thr Ile Phe Gly Asn Met Met Ile Ile Leu Val
 35          40          45
Ser Arg Leu Asp Ser Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50          55          60
Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln
 65          70          75          80
Met Leu Ile Asn Ile Cys Ser Thr Arg Lys Val Ile Ser Tyr Gly Gly
 85          90          95
Cys Val Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Ser Thr Glu Cys
 100         105         110
Phe Leu Leu Gly Val Met Ser Leu Asp Arg Phe Leu Ala Ile Cys Arg
 115         120         125
Pro Leu His Tyr Ser Val Ile Met His Gln Arg Arg Cys Leu His Leu
 130         135         140
Ala Ala Ala Cys Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln Ser
 145         150         155         160
Thr Trp Thr Leu Gln Met Pro Leu Cys Gly His Lys Glu Val Asp His
 165         170         175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp Thr
 180         185         190
Thr Ala Asn Glu Ala Glu Leu Phe Ile Ser Val Leu Phe Leu Leu
 195         200         205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln Ala
 210         215         220
Val Leu Lys Ile Arg Ser Ala Glu Cys Arg Arg Lys Ala Phe Gly Thr
 225         230         235         240
Cys Gly Ser His Leu Ile Val Val Val Leu Phe Tyr Gly Thr Ala Ile
 245         250         255
Tyr Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly Lys
 260         265         270
Met Val Ser Leu Phe Tyr Gly Ile Ile Thr Pro Met Leu Asn Pro Leu
 275         280         285
Ile Tyr Thr Leu Arg Asn Glu Glu Val Lys Gly Ala Phe Lys Arg Leu
 290         295         300
Met Lys Arg Ile Ile Leu Ile Gly Lys
 305         310

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<210> 2686

<211> 333

<212> PRT

<213> Unknown (F3 (RATOLFPROB M64376 RNOLFPP15 A23701) Buck-L 91)

<400>2686

```

Met Asp Ser Ser Asn Arg Thr Arg Val Ser Glu Phe Leu Leu Leu Gly
 1          5          10          15
Phe Val Glu Asn Lys Asp Leu Gln Pro Leu Ile Tyr Gly Leu Phe Leu
 20          25          30
Ser Met Tyr Leu Val Thr Val Ile Gly Asn Ile Ser Ile Ile Val Ala
 35          40          45
Ile Ile Ser Asp Pro Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50          55          60
Asn Leu Ser Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys

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65          70          75          80
Met Leu Val Asn Ile Gln Thr Gln Asn Asn Val Ile Thr Tyr Ala Gly
      85          90          95
Cys Ile Thr Gln Ile Tyr Phe Phe Leu Leu Phe Val Glu Leu Asp Asn
      100          105          110
Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Met His Tyr Thr Val Ile Met Asn Tyr Lys Leu Cys Gly Phe Leu
      130          135          140
Val Leu Val Ser Trp Ile Val Ser Val Leu His Ala Leu Phe Gln Ser
145          150          155          160
Leu Met Met Leu Ala Leu Pro Phe Cys Thr His Leu Glu Ile Pro His
      165          170          175
Tyr Phe Cys Glu Pro Asn Gln Val Ile Gln Leu Thr Cys Ser Asp Ala
      180          185          190
Phe Leu Asn Asp Leu Val Ile Tyr Phe Thr Leu Val Leu Leu Ala Thr
      195          200          205
Val Pro Leu Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Val Ser Ser
      210          215          220
Ile Cys Ala Ile Ser Ser Val His Gly Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu
      245          250          255
Gly Val Tyr Leu Ser Ser Ala Ala Asn Asn Ser Ser Gln Ala Ser Ala
      260          265          270
Thr Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Val Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ser Val Leu Lys Lys Thr
      290          295          300
Leu Cys Glu Glu Val Ile Arg Ser Pro Pro Ser Leu Leu His Phe Phe
305          310          315          320
Leu Val Leu Cys His Leu Pro Cys Phe Ile Phe Cys Tyr
      325          330

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<210> 2687

<211> 313

<212> PRT

<213> Unknown (F5 (RATOLFPROC M64377 RNOLFPP17 OLF5 P23266 B23701) Buck-L 91)

<400>2687

```

Met Ser Ser Thr Asn Gln Ser Ser Val Thr Glu Phe Leu Leu Leu Gly
1          5          10          15
Leu Ser Arg Gln Pro Gln Gln Gln Gln Leu Leu Phe Leu Leu Phe Leu
      20          25          30
Ile Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      35          40          45
Ile Gly Thr Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50          55          60
Asn Leu Ser Phe Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys
65          70          75          80
Val Leu Ala Asn His Ile Leu Gly Ser Gln Ala Ile Ser Phe Ser Gly
      85          90          95
Cys Leu Thr Gln Leu Tyr Phe Leu Ala Val Phe Gly Asn Met Asp Asn
      100          105          110
Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His
      115          120          125
Pro Leu His Tyr Thr Thr Lys Met Thr Arg Gln Leu Cys Val Leu Leu
      130          135          140
Val Val Gly Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His Ile
145          150          155          160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His

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      165      170      175
Phe Phe Cys Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
      180      185      190
His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val
      195      200      205
Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala
      210      215      220
Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr
      225      230      235      240
Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile
      245      250      255
Ala Val Tyr Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met
      260      265      270
Ala Ala Ala Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu Arg Asn Ser Asp Met Lys Ala Ala Leu Arg Lys Val
      290      295      300
Leu Ala Met Arg Phe Pro Ser Lys Gln
      305      310

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<210> 2688

<211> 311

<212> PRT

<213> Unknown (F6 (RATOLFFPROD RNOLFP01 M64378) Buck-L 91)

<400>2688

```

Met Ala Trp Ser Thr Gly Gln Asn Leu Ser Thr Pro Gly Pro Phe Ile
  1      5      10      15
Leu Leu Gly Phe Pro Gly Pro Arg Ser Met Arg Ile Gly Leu Phe Leu
      20      25      30
Leu Phe Leu Val Met Tyr Leu Leu Thr Val Val Gly Asn Leu Ala Ile
      35      40      45
Ile Ser Leu Val Gly Ala His Arg Cys Leu Gln Thr Pro Met Tyr Phe
      50      55      60
Phe Leu Cys Asn Leu Ser Phe Leu Glu Ile Trp Phe Thr Thr Ala Cys
      65      70      75      80
Val Pro Lys Thr Leu Ala Thr Phe Ala Pro Arg Gly Gly Val Ile Ser
      85      90      95
Leu Ala Gly Cys Ala Thr Gln Met Tyr Phe Val Phe Ser Leu Gly Cys
      100      105      110
Thr Glu Tyr Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala
      115      120      125
Ile Cys Leu Pro Leu Arg Tyr Gly Gly Ile Met Thr Pro Gly Leu Ala
      130      135      140
Met Arg Leu Ala Leu Gly Ser Trp Leu Cys Gly Phe Ser Ala Ile Thr
      145      150      155      160
Val Pro Ala Thr Leu Ile Ala Arg Leu Ser Phe Cys Gly Ser Arg Val
      165      170      175
Ile Asn His Phe Phe Cys Asp Ile Ser Pro Trp Ile Val Leu Ser Cys
      180      185      190
Thr Asp Thr Gln Val Val Glu Leu Val Ser Phe Gly Ile Ala Phe Cys
      195      200      205
Val Ile Leu Gly Ser Cys Gly Ile Thr Leu Val Ser Tyr Ala Tyr Ile
      210      215      220
Ile Thr Thr Ile Ile Lys Ile Pro Ser Ala Arg Gly Arg His Arg Ala
      225      230      235      240
Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp Tyr Gly
      245      250      255
Ser Thr Ile Phe Leu His Val Arg Thr Ser Val Glu Ser Ser Leu Asp
      260      265      270
Leu Thr Lys Ala Ile Thr Val Leu Asn Thr Ile Val Thr Pro Val Leu

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275 280 285
 Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Glu Ala Leu
 290 295 300
 Arg Arg Thr Val Lys Gly Lys
 305 310

<210> 2689

<211> 317

<212> PRT

<213> Unknown (F12 (RATOLFPROG OLF2 P23268 M64381 D23701) Buck-L 91)

<400>2689

Met Glu Ser Gly Asn Ser Thr Arg Arg Phe Ser Ser Phe Phe Leu Leu
 1 5 10 15
 Gly Phe Thr Glu Asn Pro Gln Leu His Phe Leu Ile Phe Ala Leu Phe
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Met
 35 40 45
 Ala Ile Ile Thr Gln Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ala Asn Leu Ser Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro
 65 70 75 80
 Lys Met Leu Val Asn Ile Tyr Thr Gln Ser Lys Ser Ile Thr Tyr Glu
 85 90 95
 Asp Cys Ile Ser Gln Met Cys Val Phe Leu Val Phe Ala Glu Leu Gly
 100 105 110
 Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Arg Cys
 115 120 125
 His Pro Leu Cys Tyr Thr Val Ile Val Asn His Arg Leu Cys Ile Leu
 130 135 140
 Leu Leu Leu Leu Ser Trp Val Ile Ser Ile Phe His Ala Phe Ile Gln
 145 150 155 160
 Ser Leu Ile Val Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro
 165 170 175
 His Phe Phe Cys Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp
 180 185 190
 Asn Phe Pro Ser His Leu Ile Met Asn Leu Val Pro Val Met Leu Ala
 195 200 205
 Ala Ile Ser Phe Ser Gly Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser
 210 215 220
 Ser Ile His Ser Ile Ser Thr Val Gln Gly Lys Tyr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly
 245 250 255
 Leu Gly Val Tyr Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala
 260 265 270
 Ala Ser Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Arg Ala Leu Glu Arg
 290 295 300
 Leu Leu Glu Gly Asn Cys Lys Val His His Trp Thr Gly
 305 310 315

<210> 2690

<211> 310

<212> PRT

<213> Unknown (I3 (RATOLFPROK OLF0 P23269 M64385 RNOLFPO8 E23701) Buck-L 91)

<400>2690

Met Asn Asn Gln Thr Phe Ile Thr Gln Phe Leu Leu Leu Gly Leu Pro
 1 5 10 15

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Ile Pro Glu Glu His Gln His Leu Phe Tyr Ala Leu Phe Leu Val Met
      20      25      30
Tyr Leu Thr Thr Ile Leu Gly Asn Leu Leu Ile Ile Val Leu Val Gln
      35      40      45
Leu Asp Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu
      50      55      60
Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu
      65      70      75      80
Gln Asn Met Arg Ser Gln Asp Thr Ser Ile Pro Tyr Gly Gly Cys Leu
      85      90      95
Ala Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu
      100      105      110
Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu
      115      120      125
His Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Thr Cys Leu Val Leu
      130      135      140
Leu Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu
      145      150      155      160
Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Val Leu Asn Phe Phe
      165      170      175
Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Ile
      180      185      190
Asn Glu Leu Met Ile Phe Ile Met Ser Thr Leu Leu Ile Ile Ile Pro
      195      200      205
Phe Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu
      210      215      220
Lys Val Pro Ser Thr Gln Gly Ile Cys Lys Val Phe Ser Thr Cys Gly
      225      230      235      240
Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu
      245      250      255
Tyr Leu Cys Pro Ala Gly Asn Asn Ser Thr Val Lys Glu Met Val Met
      260      265      270
Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
      275      280      285
Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val Ile Cys
      290      295      300
Ser Met Lys Ile Thr Leu
      305      310

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<210> 2691

<211> 312

<212> PRT

<213> Unknown (I8 (RATOLFPPROM M64387 RNOLFPO9) Buck-L 91)

<400>2691

```

Met Asn Asn Lys Thr Val Ile Thr His Phe Leu Leu Leu Gly Leu Pro
      1      5      10      15
Ile Pro Pro Glu His Gln Gln Leu Phe Phe Ala Leu Phe Leu Ile Met
      20      25      30
Tyr Leu Thr Thr Phe Leu Gly Asn Leu Leu Ile Val Val Leu Val Gln
      35      40      45
Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu
      50      55      60
Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Leu Lys Leu Leu
      65      70      75      80
Gln Asn Ile Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala Gly Cys Leu
      85      90      95
Thr Gln Ile Phe Phe Phe Leu Leu Phe Gly Tyr Leu Gly Asn Phe Leu
      100      105      110
Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu
      115      120      125

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His Tyr Thr Asn Ile Met Ser His Lys Leu Cys Thr Cys Leu Leu Leu
 130 135 140
 Val Phe Trp Ile Met Thr Ser Ser His Ala Met Met His Thr Leu Leu
 145 150 155 160
 Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Leu Leu Asn Phe Phe
 165 170 175
 Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val
 180 185 190
 Asn Glu Leu Met Ile His Ile Met Gly Val Ile Ile Ile Val Ile Pro
 195 200 205
 Phe Val Leu Ile Val Ile Ser Tyr Ala Lys Ile Ile Ser Ser Ile Leu
 210 215 220
 Lys Val Pro Ser Thr Gln Ser Ile His Lys Val Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu
 245 250 255
 Tyr Leu Cys Pro Ser Gly Asp Asn Phe Ser Leu Lys Gly Ser Ala Met
 260 265 270
 Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
 275 280 285
 Ser Leu Arg Asn Arg Asp Met Lys Gln Ala Leu Ile Arg Val Thr Cys
 290 295 300
 Ser Lys Lys Ile Ser Leu Pro Trp
 305 310

<210> 2692

<211> 314

<212> PRT

<213> Unknown (I9 (RATOLFPRON OLF9 H23701 M64388 RNOLFP10 P23272) Buck-L 91)

<400>2692

Met Thr Arg Arg Asn Gln Thr Ala Ile Ser Gln Phe Phe Leu Leu Gly
 1 5 10 15
 Leu Pro Phe Pro Pro Glu Tyr Gln His Leu Phe Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Ile Ile Ile Leu
 35 40 45
 Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly
 85 90 95
 Cys Leu Ala Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
 130 135 140
 Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Ser Val Ile Pro His
 165 170 175
 Tyr Phe Cys Asp Met Ser Thr Leu Leu Lys Val Ala Cys Ser Asp Thr
 180 185 190
 His Asp Asn Glu Leu Ala Ile Phe Ile Leu Gly Gly Pro Ile Val Val
 195 200 205
 Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala Arg Ile Val Ser Ser
 210 215 220
 Ile Phe Lys Val Pro Ser Ser Gln Ser Ile His Lys Ala Phe Ser Thr
 225 230 235 240

<212> PRT

<213> Unknown (I15 (RATOLFPROR A37286 M64391 RNOLFP16) Buck-L 91)

<400>2694

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Met Thr Glu Glu Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Phe
 1          5          10          15
Leu Pro Ile Pro Ser Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
          20          25          30
Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
          35          40          45
Ile His Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65          70          75          80
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Phe Ala Gly
          85          90          95
Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu Ser
          100          105          110
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
          115          120          125
Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
          130          135          140
Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
145          150          155          160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His
          165          170          175
Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
          180          185          190
His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile Val
          195          200          205
Ile Pro Phe Val Leu Ile Ile Val Ser Tyr Ala Arg Val Val Ala Ser
          210          215          220
Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser Thr
225          230          235          240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
          245          250          255
Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr
          260          265          270
Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Ile Arg Val
          290          295          300
Leu Cys Lys Lys Lys Ile Thr Phe Cys Leu
305          310

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<210> 2695

<211> 309

<212> PRT

<213> Unknown (RNOLP4 (517366 631861 1083741 S51356) Gat-U 94)

<400>2695

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Met Met Gly Thr Gly Asn His Ser Ala Val Val Val Phe Val Leu Val
 1          5          10          15
Gly Leu Thr Lys Gln Pro Glu Leu Leu Leu Pro Leu Phe Phe Leu Phe
          20          25          30
Leu Val Ile Tyr Val Leu Thr Val Val Gly Asn Leu Gly Met Ile Leu
          35          40          45
Leu Ile Ile Val Ser Pro Leu Leu His Thr Pro Met Tyr Tyr Phe Leu
          50          55          60
Ser Ser Leu Ser Phe Val Asp Leu Cys Tyr Ser Thr Val Ile Thr Pro
65          70          75          80
Lys Met Leu Val Asn Phe Leu Gly Lys Lys Asn Phe Ile Thr Tyr Ser

```

85 90 95
 Glu Cys Met Ala Gln Phe Phe Phe Phe Ala Ile Phe Val Val Thr Glu
 100 105 110
 Gly Tyr Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Arg Pro Leu Leu Tyr Asn Val Ile Met Ser Ser Arg Ile Cys Ser Leu
 130 135 140
 Leu Val Leu Val Ala Phe Ser Leu Gly Leu Phe Ser Ala Val Val His
 145 150 155 160
 Thr Ser Ala Met Met Asn Leu Ser Phe Cys Lys Ser Tyr Ile Ile Ser
 165 170 175
 His Tyr Phe Cys Asp Ala Leu Pro Leu Leu Lys Leu Ala Cys Ser Asn
 180 185 190
 Thr His Leu Asn Glu Leu Leu Ile Phe Ile Ile Gly Gly Leu Asn Thr
 195 200 205
 Leu Val Pro Thr Leu Ala Val Ala Ile Ser Tyr Val Phe Ile Phe Cys
 210 215 220
 Ser Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Ser Lys Ala Phe Gly
 225 230 235 240
 Thr Cys Ser Ser His Leu Met Ala Val Gly Ile Phe Phe Gly Ser Ile
 245 250 255
 Thr Phe Met Tyr Leu Lys Pro Ser Ser Ser Asn Ser Leu Glu Gln Glu
 260 265 270
 Lys Val Ser Ser Val Phe Tyr Thr Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Gly Arg
 290 295 300
 Phe Ser Val Arg Ser
 305

<210> 2696

<211> 318

<212> PRT

<213> Unknown (TB641 (RNU50949 1256393) Thomas-MB 96)

<400>2696

Met Arg Arg Asn Arg Asn Thr Ser Leu Asp Thr Val Val Thr Asp Phe
 1 5 10 15
 Leu Leu Leu Gly Leu Ala His Pro Pro Asn Leu Arg Thr Phe Leu Phe
 20 25 30
 Leu Val Phe Leu Leu Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu
 35 40 45
 Ile Leu Leu Thr Val Trp Ala Asp Pro Lys Leu His Ala Arg Pro Met
 50 55 60
 Tyr Ile Leu Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser
 65 70 75 80
 Val Ile Val Pro Arg Ile Ile Leu Asn Phe Thr Pro Ala Asn Lys Ala
 85 90 95
 Ile Ala Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu
 100 105 110
 Gly Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr
 115 120 125
 Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Lys
 130 135 140
 Leu Cys Thr Ile Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His
 145 150 155 160
 Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
 165 170 175
 Lys Glu Val Asp Tyr Phe Phe Cys Asp Ile Pro Ala Val Leu Arg Leu
 180 185 190
 Ala Cys Ala Asp Thr Ala Ile Asn Glu Leu Val Thr Phe Val Asp Ile

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<210> 2697
<211> 315
<212> PRT
<213> Unknown (TB567 (RNU50948 1256391) Thomas-MB 96)
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<400>2697																
Met	Thr	Gln	Arg	Asn	Ala	Thr	Glu	Val	Thr	Asp	Phe	Tyr	Leu	Leu	Gly	
1				5					10					15		
Phe	Gly	Val	Gln	Gln	Asn	Thr	Gln	Cys	Val	Leu	Phe	Ile	Val	Phe	Phe	
		20						25					30			
Val	Ile	Tyr	Val	Thr	Ser	Met	Val	Gly	Asn	Thr	Gly	Met	Ile	Leu	Leu	
		35					40					45				
Ile	Asn	Thr	Asn	Ser	Arg	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gln	
	50					55					60					
Asn	Leu	Ala	Phe	Val	Asp	Ile	Cys	Tyr	Thr	Ser	Ala	Ile	Thr	Pro	Lys	
65					70					75					80	
Met	Leu	Gln	Ser	Phe	Met	Val	Glu	Asp	Cys	Ser	Ile	Ser	Tyr	Thr	Gly	
				85					90					95		
Cys	Val	Ile	Gln	Leu	Leu	Val	Tyr	Ala	Thr	Phe	Ala	Thr	Ser	Asp	Cys	
			100					105					110			
Tyr	Leu	Leu	Ala	Val	Met	Ala	Val	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys	
	115					120						125				
Pro	Leu	Arg	Tyr	Pro	Ile	Ile	Met	Ser	Arg	Gln	Val	Cys	Leu	Leu	Leu	
	130				135						140					
Val	Ala	Leu	Ser	Tyr	Leu	Met	Gly	Ser	Ile	Asn	Ser	Ser	Val	His	Thr	
145					150					155				160		
Gly	Phe	Thr	Phe	Ser	Leu	Ser	Tyr	Cys	Asn	Ser	Lys	Asn	Ile	Asn	His	
			165						170					175		
Phe	Phe	Cys	Asp	Val	Val	Pro	Ile	Ile	Ser	Leu	Ser	Cys	Ser	Asn	Thr	
		180						185					190			
Asp	Ile	Asn	Ile	Met	Leu	Leu	Ile	Val	Phe	Val	Gly	Phe	Asn	Leu	Thr	
	195					200						205				
Phe	Thr	Val	Leu	Val	Ile	Ile	Phe	Ser	Tyr	Ile	Tyr	Ile	Met	Ala	Ala	
	210				215						220					
Ile	Leu	Lys	Met	Ser	Ser	Thr	Ala	Gly	Arg	Lys	Lys	Thr	Phe	Ser	Thr	
225					230					235				240		
Cys	Ala	Ser	His	Leu	Thr	Ala	Val	Thr	Ile	Phe	Tyr	Gly	Thr	Leu	Ser	
			245						250					255		
Tyr	Met	Tyr	Leu	Gln	Pro	His	Ser	Asp	Asn	Ser	Glu	Glu	Asn	Met	Lys	
		260						265					270			
Val	Ala	Ser	Val	Phe	Tyr	Gly	Ile	Val	Ile	Pro	Met	Leu	Asn	Pro	Leu	
	275					280						285				
Il	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Val	Lys	Glu	Gly	Phe	Lys	Ala	Met	
	290				295						300					
Ser	Arg	Arg	Phe	Leu	Arg	Met	Lys	Ser	Asn	Pro						

305

310

315

<210> 2698

<211> 311

<212> PRT

<213> Unknown (TB334 (RNU50947 1256389) Thomas-MB 96)

<400>2698

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Met Glu Asn Gln Ser Ser Val Ser Glu Phe Phe Leu Arg Gly Ile Ser
 1              5              10              15
Gly Phe Pro Glu Gln Gln Gln Leu Leu Tyr Gly Leu Phe Leu Cys Met
              20              25              30
Tyr Leu Val Thr Leu Thr Gly Asn Val Leu Ile Ile Leu Ala Ile Gly
              35              40              45
Ser Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu
              50              55              60
Ser Phe Ala Asp Met Gly Leu Ile Ser Ser Thr Val Thr Lys Met Leu
65              70              75              80
Phe Asn Val Gln Thr Gln Cys His Thr Ile Ser Tyr Thr Gly Cys Leu
              85              90              95
Thr Gln Met Tyr Leu Phe Met Met Phe Gly Asp Leu Asp Ser Phe Phe
              100              105              110
Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
              115              120              125
His Tyr Ser Thr Ile Met Asn Ala Arg Ile Cys Val Leu Met Leu Ile
              130              135              140
Leu Cys Trp Ile Leu Thr Asn Val Val Ala Leu Thr His Thr Leu Leu
145              150              155              160
Met Ala Arg Leu Ser Phe Cys Val Val Gly Glu Ile Ala His Phe Phe
              165              170              175
Cys Asp Val Thr Ser Val Met Lys Leu Ser Cys Ser Asp Thr His Val
              180              185              190
Asn Glu Leu Val Leu Ser Gly Phe Gly Gly Thr Val Leu Met Val Pro
              195              200              205
Phe Val Ser Ile Val Ile Ser Tyr Val His Ile Val Phe Ala Val Leu
              210              215              220
Arg Ile Gln Ser Ser Gly Gly Ser Ser Lys Ala Phe Ser Thr Cys Ser
225              230              235              240
Ser His Leu Cys Val Val Cys Val Phe Tyr Gly Thr Leu Phe Ser Val
              245              250              255
Tyr Leu Phe Pro Ser Ser Val Glu Thr Thr Glu Lys Asp Val Ala Ala
              260              265              270
Ala Ala Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
              275              280              285
Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Lys Arg Leu Leu Ser
              290              295              300
His Arg Arg Ile Leu Ser Ser
305              310

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<210> 2699

<211> 312

<212> PRT

<213> Unknown (OR12 (423700 S29708) Raming-K 93)

<400>2699

```

Met Ile Met Asn Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly
 1              5              10              15
Leu Pro Ile Pro Pro Glu His Trp His Leu Phe Tyr Thr Leu Leu Leu
              20              25              30
Ala Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile Ile Ile Leu
              35              40              45

```

Ile Leu Leu Asp Ser Asn Leu His Ile Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Thr Ser Ile Thr Tyr Thr Gly
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Ser Met Val Phe Ala Gly Met Glu Ile
 100 105 110
 Phe Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu
 115 120 125
 Pro Leu His Tyr Thr Ser Ile Met Ser Pro Lys Phe Cys Val Cys Leu
 130 135 140
 Gly Ser Leu Ser Trp Val Phe Asn Val Leu Tyr Ser Met Leu His Thr
 145 150 155 160
 Leu Leu Leu Ala Arg Leu Ser Phe Cys Lys Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Tyr Ile Asn Glu Leu Met Ile Phe Ile Leu Gly Gly Leu Leu Ile Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Val Met Thr Tyr Val Gln Ile Val Cys Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Thr Arg Ala Ile Tyr Lys Ile Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Thr Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr
 260 265 270
 Val Met Ala Met Met Ile Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Glu Ala Leu Val Arg Val
 290 295 300
 Leu Ile Lys Lys Lys Ile Ser Leu
 305 310

<210> 2700

<211> 304

<212> PRT

<213> Unknown (OR14 (423701) Raming-K 93)

<400>2700

Ser Val Thr Glu Phe Ile Leu Ala Gly Leu Thr Asp Gln Pro Gly Leu
 1 5 10 15
 Arg Met Pro Leu Phe Phe Leu Phe Leu Gly Phe Tyr Met Val Thr Val
 20 25 30
 Val Gly Asn Leu Ile Gly Leu Phe Leu Ile Gly Leu Asn Ser His Leu
 35 40 45
 His Thr Pro Met Tyr Phe Phe Leu Phe Asn Leu Ser Val Val Asp Phe
 50 55 60
 Cys Phe Ser Ser Thr Ile Ile Pro Lys Met Leu Met Ser Phe Ile Ser
 65 70 75 80
 Lys Lys Asn Ile Ile Ser His Ser Gly Cys Met Thr Gln Leu Phe Phe
 85 90 95
 Phe Cys Phe Phe Val Val Ser Glu Thr Phe Ile Leu Ser Ala Met Ala
 100 105 110
 Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Met Tyr Thr Val Thr
 115 120 125
 Met Ser Pro Gln Val Cys Leu Leu Leu Leu Gly Ala Tyr Val Met
 130 135 140
 Gly Phe Ser Glu Ala Met Ala His Thr Gly Asn Leu Met Asn Leu Thr
 145 150 155 160

Phe Cys Ala Asp Asn Leu Val Asn His Phe Met Cys Asp Ile Leu Pro
 165 170 175
 Leu Leu Glu Leu Ser Cys Asn Ser Thr Phe Ile Asn Glu Leu Val Val
 180 185 190
 Phe Ile Val Val Ala Ile Asp Ile Ala Val Pro Ile Val Ser Ile Phe
 195 200 205
 Ile Ser Tyr Ala Leu Ile Leu Ser Ser Ile Leu Arg Met His Ser Thr
 210 215 220
 Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Val
 225 230 235 240
 Val Cys Leu Leu Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Leu Pro
 245 250 255
 Ser Ile Leu Pro Leu Asp Gln Gly Lys Val Ser Ser Leu Phe Tyr Thr
 260 265 270
 Ile Val Val Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys
 275 280 285
 Asp Val Lys Val Ala Leu Arg Lys Thr Leu Gly Lys Ile Ile Leu Ser
 290 295 300

<210> 2701

<211> 307

<212> PRT

<213> Unknown (OR18 (423702) Raming-K 93)

<400>2701

Met Gly Glu Asn Asn Asn Ile Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1 5 10 15
 Gln Asp Pro Asp Gly Arg Lys Ala Leu Phe Val Ile Phe Phe Leu Ile
 20 25 30
 Tyr Ile Val Thr Met Met Gly Asn Leu Leu Ile Val Val Thr Val Ile
 35 40 45
 Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Phe Phe Leu Ala Ser Leu
 50 55 60
 Ser Leu Leu Asp Ala Leu Phe Ser Thr Ala Ile Ser Pro Lys Leu Ile
 65 70 75 80
 Ala Asp Leu Leu Tyr Asp Gln Lys Thr Ile Ser Phe Arg Ala Cys Met
 85 90 95
 Ser Gln Leu Phe Ile Glu His Leu Phe Gly Gly Val Asp Ile Val Ile
 100 105 110
 Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Leu Ala Ile Met Asn Arg Arg Val Cys Ile Thr Leu Leu Ile
 130 135 140
 Phe Ala Trp Thr Gly Gly Phe Thr His Ser Leu Ile Gln Ile Val Phe
 145 150 155 160
 Val Tyr Asn Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile
 165 170 175
 Cys Asp Met Ser Pro Leu Leu Val Leu Ala Cys Thr Asp Thr Tyr Phe
 180 185 190
 Ile Gly Leu Thr Val Ile Ala Asn Gly Gly Val Asn Cys Ile Val Ile
 195 200 205
 Phe Thr Leu Leu Leu Gly Ser Tyr Gly Ile Ile Leu Arg Ser Leu Lys
 210 215 220
 Thr Gln Ser Gln Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys Ser Ser
 225 230 235 240
 His Ile Leu Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Met Tyr
 245 250 255
 Ala Arg Pro Val Tyr Asn Phe Pro Ile Asp Lys Cys Ile Thr Val Phe
 260 265 270
 Tyr Thr Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285

Asn Ser Glu Ile Lys Ser Cys Met Lys Lys Leu Trp Cys Lys Met Leu
 290 295 300
 His Ala Asp
 305

<210> 2702
 <211> 314
 <212> PRT
 <213> Unknown (OR5 (423703 444281) Raming-K 93)

<400>2702
 Met Thr Glu Arg Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Pro Pro Glu His Gln His Val Gly Tyr Ala Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile Ile Leu
 35 40 45
 Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly
 85 90 95
 Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
 130 135 140
 Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu Val
 195 200 205
 Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser
 210 215 220
 Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser Ser
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
 245 250 255
 Pro Leu Tyr Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Glu Thr
 260 265 270
 Val Met Ser Leu Met Tyr Thr Leu Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Ala Met Glu Ile Ile
 290 295 300
 Phe Cys Lys Arg Lys Ile Gln Leu Asn Leu
 305 310

<210> 2703
 <211> 305
 <212> PRT
 <213> Unknown (OR37 (423699 S29711 265086) Raming-K 93)

<400>2703
 Leu Leu Leu Gly Leu Ser Gly Tyr Pro Lys Thr Glu Ile Leu Tyr Phe
 1 5 10 15
 Val Ile Val Leu Val Met Tyr Leu Val Ile His Thr Gly Asn Gly Val

20 25 30
 Leu Ile Ile Ala Ser Ile Phe Asp Ser His Leu His Thr Pro Met Tyr
 35 40 45
 Phe Phe Leu Gly Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser
 50 55 60
 Ser Val Pro Ser Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile
 65 70 75 80
 Ser Phe Ser Gly Cys Thr Val Gln Met Phe Val Gly Phe Ala Met Gly
 85 90 95
 Ser Thr Glu Cys Leu Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val
 100 105 110
 Ala Ile Cys Asn Pro Leu Arg Tyr Ser Val Ile Met Ser Lys Glu Val
 115 120 125
 Tyr Val Ser Met Ala Ser Ala Ser Trp Phe Ser Gly Gly Ile Asn Ser
 130 135 140
 Val Val Gln Thr Ser Leu Ala Met Arg Leu Pro Phe Cys Gly Asn Asn
 145 150 155 160
 Val Ile Asn His Phe Thr Cys Glu Val Leu Ala Val Leu Lys Leu Ala
 165 170 175
 Cys Ala Asp Ile Ser Leu Asn Ile Val Thr Met Val Ile Ser Asn Met
 180 185 190
 Ala Phe Leu Val Leu Pro Leu Leu Leu Ile Phe Phe Ser Tyr Val Leu
 195 200 205
 Ile Leu Tyr Thr Ile Leu Arg Met Asn Ser Ala Ser Gly Arg Arg Lys
 210 215 220
 Ala Phe Ser Thr Cys Ser Ala His Leu Thr Val Val Val Ile Phe Tyr
 225 230 235 240
 Gly Thr Ile Phe Ser Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Thr
 245 250 255
 Gly Lys Asp Lys Phe Gln Thr Ser Asp Lys Ile Ile Ser Leu Phe Tyr
 260 265 270
 Gly Val Val Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn
 275 280 285
 Lys Asp Val Lys Ala Ala Val Lys Tyr Ile Leu Lys Gln Lys Tyr Ile
 290 295 300
 Pro
 305

<210> 2704

<211> 314

<212> PRT

<213> Unknown (RNOLFRECP (1504112) Raming-K 93)

<400>2704

Met Thr Glu Arg Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Pro Pro Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
 35 40 45
 Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly
 85 90 95
 Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu

130		135		140
Val Val Leu Ser Trp	Val Leu Thr Thr Phe His Ala Met Leu His Thr			
145	150	155		160
Leu Leu Met Ala Arg	Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His			
	165	170		175
Phe Phe Cys Asp Met	Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr			
	180	185		190
Arg Val Asn Glu Val	Val Ile Phe Ile Val Val Ser Leu Phe Leu Val			
	195	200		205
Leu Pro Phe Ala Leu	Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser			
	210	215		220
Ile Leu Lys Val Pro	Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser Thr			
225	230	235		240
Cys Gly Ser His Leu	Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile			
	245	250		255
Gly Leu Tyr Leu Cys	Pro Ser Ser Asn Asn Ser Thr Val Lys Glu Thr			
	260	265		270
Val Met Ser Leu Met	Tyr Thr Val Thr Pro Met Leu Asn Pro Phe			
	275	280		285
Ile Tyr Ser Leu Arg	Asn Arg Asp Ile Lys Gly Ala Met Glu Arg Ile			
	290	295		300
Phe Cys Lys Arg Lys	Ile Gln Leu Asn Leu			
305	310			

<210> 2705

<211> 314

<212> PRT

<213> Unknown (1906335A (444281) Raming-K 93)

<400>2705

Met Thr Glu Arg Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Gly	
1	5
Leu Pro Ile Pro Pro Glu His Gln His Val Phe Tyr Ala Leu Phe Leu	10
	20
Ser Met Tyr Leu Thr Thr Ile Leu Gly Asn Leu Ile Ile Ile Leu	25
	30
	35
Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser	40
	45
	50
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys	55
65	60
	70
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly	75
	80
	85
Cys Leu Ser Gln Ile Tyr Phe Phe Leu Phe Gly Asp Leu Gly Asn	90
	95
	100
Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe	105
	110
	115
Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu	120
	125
	130
Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr	135
145	140
	150
Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His	155
	160
	165
Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr	170
	175
	180
Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu Val	185
	190
	195
Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser	200
	205
	210
Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys Ala Phe Ser Ser	215
225	220
	230
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile	235
	240

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<210> 2706
<211> 185
<212> PRT
<213> Unknown (PTE01 (544449) Abe-K 93)
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Met	Tyr	Leu	Phe	Leu	Ser	Asn	Leu	Ser	Leu	Ala	Asp	Ile	Ser	Phe	Thr
1				5					10					15	
Ser	Thr	Thr	Leu	Pro	Lys	Met	Ile	Val	Asp	Ile	Gln	Thr	Asn	Asn	Arg
			20					25					30		
Ala	Ile	Ser	Tyr	Ser	Gly	Cys	Leu	Thr	Gln	Met	Ser	Phe	Phe	Met	Leu
		35					40					45			
Phe	Gly	Cys	Leu	Asp	Ser	Leu	Leu	Leu	Thr	Ala	Met	Ala	Tyr	Asp	Arg
	50					55					60				
Phe	Val	Ala	Ile	Cys	His	Pro	Leu	His	Tyr	Gln	Val	Ile	Met	Asn	Pro
65					70					75				80	
Arg	Leu	Cys	Gly	Leu	Leu	Val	Phe	Leu	Ser	Ile	Leu	Ile	Ser	Leu	Leu
				85					90					95	
Val	Ser	Gln	Leu	His	Asn	Ser	Val	Val	Leu	Gln	Leu	Thr	Tyr	Phe	Lys
			100					105					110		
Ser	Val	Asp	Ile	Ser	His	Phe	Phe	Cys	Asp	Pro	Ser	Leu	Leu	Leu	Asn
		115					120					125			
Leu	Ala	Cys	Ser	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Val	Met	Tyr	Phe	Val
	130					135					140				
Gly	Ala	Ile	Ser	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Ile	Phe	Phe	Ser	Tyr
145					150					155				160	
Tyr	Lys	Ile	Val	Ser	Ser	Ile	Leu	Arg	Met	Pro	Ser	Pro	Gly	Gly	Lys
				165					170					175	
Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser							
		180						185							

<210> 2707
<211> 168
<212> PRT
<213> Unknown (PTE03 (544450) Abe-K 93)

Thr	Thr	Val	Pro	Lys	Met	Leu	Ile	Asn	Leu	Gln	Lys	Gln	Asn	Lys	Ala
1				5				10					15		
Ile	Ser	Tyr	Ala	Gly	Cys	Ile	Thr	Gln	Leu	Ser	Phe	Val	Leu	Leu	Phe
			20					25				30			
Ala	Gly	Met	Glu	Asn	Phe	Leu	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Tyr
		35				40					45				
Val	Ala	Ile	Cys	Lys	Pro	Leu	Arg	Tyr	Thr	Ala	Ile	Met	Lys	Ala	His
	50					55				60					
Leu	Cys	Leu	Val	Met	Thr	Leu	Leu	Ser	Leu	Cys	Ile	Ser	Ile	Val	Asp
65					70				75					80	
Ala	Leu	Leu	His	Gly	Leu	Met	Ile	Leu	Arg	Leu	Ser	Phe	Cys	Thr	Phe
			85					90					95		
Leu	Glu	Ile	Pro	His	Tyr	Phe	Cys	Glu	Leu	Tyr	Gln	Val	Ile	Lys	Leu
			100					105				110			

Ser Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Val Tyr Thr Met Thr
 115 120 125
 Ser Thr Leu Gly Gly Val Pro Leu Gly Gly Ile Ile Phe Ser Tyr Phe
 130 135 140
 Lys Ile Ile Ser Ser Ile Leu Arg Met Pro Ser Ser Gly Ser Arg His
 145 150 155 160
 Arg Ala Phe Ser Thr Cys Gly Ser
 165

<210> 2708

<211> 234

<212> PRT

<213> Unknown (PTE33 (544451) Abe-K 93)

<400>2708

Met Tyr Leu Phe Phe Ser Asn Leu Ser Phe Val Asp Ile Tyr Phe Ile
 1 5 10 15
 Ser Gly Thr Ile Pro Lys Ile Leu Val Asn Met Gln Ser Lys Thr Lys
 20 25 30
 Asp Ile Ser Tyr Ile Glu Cys Leu Thr Gln Val Tyr Phe Phe Asn Thr
 35 40 45
 Phe Val Gly Met Asp Asp Val Leu Arg Thr Leu Met Ala Tyr Asp Arg
 50 55 60
 Phe Val Ala Ile Cys Met Pro Leu Lys Tyr Thr Val Ile Met Asn Pro
 65 70 75 80
 Arg Val Cys Thr Leu Leu Val Leu Met Phe Trp Ile Ile Met Phe Cys
 85 90 95
 Ile Ser Leu Ile His Val Leu Leu Met Asn Glu Leu Asn Phe Ser Arg
 100 105 110
 Gly Thr Lys Ile Pro His Phe Phe Cys Glu Leu Ala Gln Val Leu Lys
 115 120 125
 Val Ser Asn Ser Asp Thr His Ile Asn Asn Ile Phe Met Tyr Val Leu
 130 135 140
 Ser Ser Leu Leu Gly Val Ile Pro Met Thr Gly Ile Leu Met Ser Tyr
 145 150 155 160
 Ser Gln Ile Val Ser Ser Leu Leu Arg Met Ser Ser Thr Val Ser Lys
 165 170 175
 Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Cys Val Val Cys Leu
 180 185 190
 Phe Tyr Gly Ser Val Ile Gly Val Tyr Phe Ser Ser Ser Val Val Leu
 195 200 205
 Ser Thr Gln Arg Ile Met Val Ala Ser Leu Met Tyr Thr Val Ile Ser
 210 215 220
 Pro Met Phe Asn Pro Phe Ile Tyr Ser Leu
 225 230

<210> 2709

<211> 234

<212> PRT

<213> Unknown (PTE38 (544452) Abe-K 93)

<400>2709

Met Tyr Leu Phe Phe Ser Asn Leu Ser Phe Asn Asp Ile Cys Ile Ile
 1 5 10 15
 Thr Thr Thr Ile Pro Lys Met Leu Met Asn Val Gln Ser His Asp Gln
 20 25 30
 Ser Ile Thr Tyr Leu Gly Cys Leu Ser Gln Val Tyr Leu Ile Val Asn
 35 40 45
 Phe Gly Ser Ile Glu Ser Cys Leu Leu Ala Val Met Ala Tyr Asp Arg
 50 55 60
 Tyr Val Ala Ile Cys His Pro Leu Lys Tyr Thr Val Ile Met Asn His

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65          70          75          80
Tyr Phe Cys Val Met Leu Leu Leu Phe Ala Cys Ser Leu Ala Leu His
      85          90          95
Met Cys Leu Phe His Ile Leu Met Val Leu Ile Leu Thr Phe Cys Thr
      100         105         110
Lys Thr Glu Ile Pro His Phe Phe Cys Glu Leu Ala His Ile Ile Lys
      115         120         125
Leu Thr Cys Ser Asp Asn Phe Ile Asn Tyr Leu Leu Ile Tyr Thr Val
      130         135         140
Ser Val Leu Phe Phe Gly Val His Ile Val Gly Ile Ile Leu Ser Tyr
145         150         155         160
Ile Tyr Thr Val Ser Ser Val Leu Arg Met Ser Leu Leu Gly Gly Met
      165         170         175
Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu
      180         185         190
Phe Tyr Gly Thr Gly Phe Gly Val His Ile Ser Ser Pro Leu Thr Asp
      195         200         205
Ser Pro Arg Lys Thr Val Val Ala Ser Val Met Tyr Thr Val Val Thr
      210         215         220
Gln Met His Gly Pro Phe Ile Tyr Ser Leu
225         230

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<210> 2710

<211> 234

<212> PRT

<213> Unknown (PTE45 (544453) Abe-K 93)

<400>2710

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Met Tyr Leu Phe Phe Ser Asn Leu Ser Phe Ala Asp Ile Cys Leu Ile
1          5          10          15
Ser Thr Thr Ile Pro Lys Met Leu Ala Asn Glu His Leu Asn His Lys
      20         25         30
Ala Ile Thr Tyr Glu Gly Cys Ile Met Gln Ile Tyr Phe Phe Thr Leu
      35         40         45
Phe Val Gly Leu Asp Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg
      50         55         60
Phe Val Ala Ile Cys His Pro Leu Arg Tyr Thr Ser Ile Met Thr Pro
65         70         75         80
His Leu Cys His Ser Leu Val Leu Val Ser Trp Ile Thr Ser Val Leu
      85         90         95
Asn Ser Ser Leu Gln Ser Phe Leu Val Leu Gln Leu Ser Phe Cys Thr
      100        105        110
Glu Val Glu Ile Pro His Phe Phe Cys Glu Leu Ser Met Leu Val His
      115        120        125
Leu Ala Cys Ser Asp Thr Phe Leu Ser Asp Met Ala Met Asn Val Leu
      130        135        140
Ala Ala Leu Leu Gly Gly Gly Cys Leu Val Gly Ile Leu Tyr Ser Tyr
145        150        155        160
Ser Lys Ile Val Ser Ser Ile Gln Ala Ile Ser Ser Ala Glu Gly Lys
      165        170        175
Tyr Lys Ala Phe Ser Thr Cys Val Ser His Leu Ser Val Val Ser Leu
      180        185        190
Phe Tyr Cys Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Val Thr Gln
      195        200        205
Asn Ser His Ser Thr Ala Ala Thr Ser Leu Met Tyr Thr Val Val Thr
      210        215        220
Pro Met Leu Asn Pro Phe Ile Tyr Phe Phe
225        230

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<210> 2711

<211> 232

<212> PRT

<213> Unknown (PTE58 (544454) Abe-K 93)

<400>2711

```

Leu Leu Met Cys Asn Leu Cys Phe Ala Asp Ile Cys Phe Thr Ser Ala
 1           5           10           15
Ser Ile Pro Thr Asn Leu Val Asn Ile Gln Thr Lys Asn Lys Val Ile
      20           25           30
Thr Tyr Glu Gly Cys Ile Ser Gln Val Tyr Phe Phe Ile Leu Phe Gly
      35           40           45
Val Leu Asp Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val
      50           55           60
Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Asn Arg Arg Leu
      65           70           75           80
Cys Gly Leu Leu Val Leu Gly Ser Trp Val Thr Thr Ala Leu Asn Ser
      85           90           95
Leu Leu Gln Ser Ser Met Ala Leu Arg Leu Ser Phe Cys Thr Asp Leu
      100          105          110
Lys Ile Pro His Phe Val Cys Glu Leu Asn Gln Leu Val Leu Leu Ala
      115          120          125
Cys Asn Asp Thr Phe Pro Asn Asp Met Val Met Tyr Phe Ala Ala Val
      130          135          140
Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser Lys
      145          150          155          160
Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ser Gln Gly Lys Tyr Lys
      165          170          175
Ala Phe Ser Thr Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr
      180          185          190
Ser Thr Leu Leu Gly Val Tyr Leu Ser Ser Ser Phe Thr Gln Asn Ser
      195          200          205
His Ser Thr Ala Arg Ala Ser Val Met Tyr Ser Val Val Thr Pro Met
      210          215          220
Leu Asn Pro Phe Ile Tyr Phe Phe
      225          230

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<210> 2712

<211> 312

<212> PRT

<213> Unknown (RATGUST27 (D12820 P34987 A46750) Abe-K 93)

<400>2712

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Met Ile Leu Asn Cys Asn Pro Phe Ser Gly Leu Phe Leu Ser Met Tyr
 1           5           10           15
Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Val Ser Ser
      20           25           30
Asn Ser His Leu His Asn Leu Met Tyr Phe Phe Leu Ser Asn Leu Ser
      35           40           45
Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Ile Pro Lys Met Leu Val
      50           55           60
Asn Ile His Ser Gln Thr Lys Asp Ile Ser Tyr Ile Glu Cys Leu Ser
      65           70           75           80
Gln Val Tyr Phe Leu Thr Thr Phe Gly Gly Met Asp Asn Phe Leu Leu
      85           90           95
Thr Leu Met Ala Cys Asp Arg Tyr Val Ala Ile Cys His Pro Leu Asn
      100          105          110
Tyr Thr Val Ile Met Asn Leu Gln Leu Cys Ala Leu Leu Ile Leu Met
      115          120          125
Phe Trp Leu Ile Met Phe Cys Val Ser Leu Ile His Val Leu Leu Met
      130          135          140
Asn Glu Leu Asn Phe Ser Arg Gly Thr Glu Ile Pro His Phe Phe Cys
      145          150          155          160

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<210> 2713
<211> 222
<212> PRT
<213> Unknown (K7 (MUSODORECA L14566 293754 464305 C40745) Ressler-KJ 93)
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Phe 1	Phe	Leu	Ser	His 5	Leu	Ala	Ile	Val	Asp 10	Ile	Ala	Tyr	Ala	Cys 15	Asn
Thr	Val	Pro	Gln	Met	Leu	Val	Asn	Leu	Leu	Asp	Pro	Val	Lys	Pro	Ile
		20						25					30		
Ser	Tyr	Ala	Gly	Cys	Met	Thr	Gln	Thr	Phe	Leu	Phe	Leu	Thr	Phe	Ala
		35					40					45			
Ile	Thr	Glu	Cys	Leu	Leu	Leu	Val	Val	Met	Ser	Tyr	Asp	Arg	Tyr	Val
	50					55					60				
Ala	Ile	Cys	His	Pro	Leu	Arg	Tyr	Ser	Ala	Ile	Met	Ser	Trp	Arg	Val
65					70				75						80
Cys	Ser	Thr	Met	Ala	Val	Thr	Ser	Trp	Ile	Ile	Gly	Val	Leu	Leu	Ser
			85					90					95		
Leu	Ile	His	Leu	Val	Leu	Leu	Leu	Pro	Leu	Pro	Phe	Cys	Val	Ser	Gln
		100						105					110		
Lys	Val	Asn	His	Phe	Phe	Cys	Glu	Ile	Thr	Ala	Ile	Leu	Lys	Leu	Ala
		115					120					125			
Cys	Ala	Asp	Thr	His	Leu	Asn	Glu	Thr	Met	Val	Leu	Ala	Gly	Ala	Val
	130					135				140					
Ser	Val	Leu	Val	Gly	Pro	Phe	Ser	Ser	Ile	Val	Val	Ser	Tyr	Ala	Cys
145					150					155					160
Ile	Leu	Gly	Ala	Ile	Leu	Lys	Ile	Gln	Ser	Glu	Glu	Gly	Gln	Arg	Lys
			165					170					175		
Ala	Phe	Ser	Thr	Cys	Ser	Ser	His	Leu	Cys	Val	Val	Gly	Leu	Phe	Tyr
			180					185					190		
Gly	Thr	Ala	Ile	Val	Met	Tyr	Val	Gly	Pro	Arg	His	Gly	Ser	Pro	Lys
		195					200					205			
Glu	Gln	Lys	Lys	Tyr	Leu	Leu	Leu	Phe	His	Ser	Leu	Phe	Asn		
	210					215					220				

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<210> 2714
<211> 222
<212> PRT
<213> Unknown (M50 (MUSODORECB L14567 293756 P34986 OLF5) Buck 93)
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<400>2714

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Tyr Phe Leu Ser Thr Met Ser Phe Leu Glu Ala Trp Tyr Ile Ser Val
 1           5           10           15
Thr Val Pro Lys Met Leu Ala Gly Phe Leu Phe His Pro Asn Thr Ile
      20           25           30
Ser Phe Leu Gly Cys Met Thr Gln Leu Tyr Phe Phe Met Ser Leu Ala
      35           40           45
Cys Thr Glu Cys Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
      50           55           60
Ala Ile Cys Trp Pro Leu Arg Tyr Pro Val Met Met Thr Thr Gly Phe
      65           70           75           80
Cys Val Gln Leu Thr Ile Ser Ser Trp Val Ser Gly Phe Thr Ile Ser
      85           90           95
Met Ala Lys Val Tyr Phe Leu Ser Arg Val Ala Phe Cys Gly Asn Asn
      100          105          110
Val Leu Asn His Phe Phe Cys Asp Val Ser Pro Ile Leu Lys Leu Ala
      115          120          125
Cys Met Asn Leu Ser Met Ala Glu Thr Val Asp Phe Ala Leu Ala Ile
      130          135          140
Val Ile Leu Ile Phe Pro Leu Ser Ala Thr Val Leu Ser Tyr Gly Phe
      145          150          155          160
Ile Val Ser Thr Val Leu Gln Ile Pro Ser Ala Thr Gly Gln Arg Lys
      165          170          175
Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Val Ile Phe Tyr
      180          185          190
Thr Ala Val Ile Phe Met Tyr Val Arg Pro Arg Ala Ile Ala Ser Phe
      195          200          205
Asn Ser Asn Lys Leu Ile Ser Ala Ile Tyr Ala Val Phe Thr
      210          215          220

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<210> 2715

<211> 161

<212> PRT

<213> Unknown (K18 (MUSODORECC L14568 293758 B40745) Buck 93)

<400>2715

```

Arg Tyr Val Ala Ile Cys Lys Pro Leu Thr Tyr Lys Val Ile Met Ser
 1           5           10           15
Pro Lys Ile Cys Cys Leu Leu Ile Phe Ser Ser Tyr Leu Met Gly Phe
      20           25           30
Ala Ser Ala Met Ala His Thr Gly Cys Met Ile Arg Leu Ser Phe Cys
      35           40           45
Asp Ser Asn Ile Ile Asn His Tyr Met Cys Asp Ile Phe Pro Leu Leu
      50           55           60
Pro Leu Ser Cys Ser Ser Thr Tyr Val Asn Glu Leu Met Ser Ser Val
      65           70           75           80
Val Val Gly Ser Ala Ile Ile Leu Cys Cys Leu Ile Ile Leu Ile Ser
      85           90           95
Tyr Ala Met Ile Leu Phe Asn Ile Ile His Met Ser Ser Gly Lys Gly
      100          105          110
Trp Ser Lys Ala Leu Gly Thr Cys Gly Ser His Ile Ile Thr Val Ser
      115          120          125
Leu Phe Tyr Gly Ser Gly Leu Leu Ala Tyr Val Lys Pro Ser Ser Ala
      130          135          140
Lys Thr Val Gly Gln Gly Lys Phe Phe Ser Val Phe Tyr Thr Leu Leu
      145          150          155          160
Val

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<210> 2716

<211> 222

<212> PRT

<213> Unknown (K4 (MUSODORECD L14569 293760 464303 OLF4 P34983) Ressler-KJ 93)

<400>2716

```

Tyr Phe Leu Ser Ser Leu Ser Phe Ile Asp Phe Cys Gln Ser Thr Val
 1          5          10          15
Val Ile Pro Lys Met Leu Val Ser Phe Leu Thr Glu Met Asn Ile Ile
      20          25          30
Ser Tyr Ser Glu Cys Met Ala Gln Leu Tyr Phe Phe Leu Thr Phe Gly
      35          40          45
Ile Ala Gly Cys Tyr Thr Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val
      50          55          60
Ala Ile Cys Asn Pro Leu Leu Tyr Asn Val Thr Met Ser Tyr Gln Ile
      65          70          75          80
Tyr Ser Ser Leu Ile Ser Gly Val Tyr Ile Phe Ala Val Ile Cys Ser
      85          90          95
Ser Phe Asn Thr Gly Phe Met Leu Arg Thr Gln Phe Cys Asn Leu Asp
      100          105          110
Val Ile Asn His Tyr Phe Cys Asp Leu Leu Pro Leu Leu Asn Leu Ala
      115          120          125
Ser Ser Asn Thr Tyr Ile Asn Glu Ile Leu Ile Leu Phe Phe Ala Thr
      130          135          140
Leu Asn Ser Phe Val Pro Val Leu Thr Ile Ile Thr Ser Tyr Ile Phe
      145          150          155          160
Ile Ile Val Thr Ile Leu Ser Ile His Ser Arg Glu Gly Lys Phe Lys
      165          170          175
Ala Phe Ser Thr Cys Ser Thr His Ile Ser Ala Val Ala Ile Phe Tyr
      180          185          190
Gly Ser Gly Ala Phe Thr Tyr Leu Gln Pro Ser Ser Leu Asn Ser Met
      195          200          205
Gly Gln Ala Lys Val Ser Ser Val Phe Tyr Thr Thr Val Val
      210          215          220

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<210> 2717

<211> 312

<212> PRT

<213> Unknown (olf3 (MUSOR3X OR3 M84005 200154 P23275 A46247) Nef 92)

<400>2717

```

Met Glu Val Asp Ser Asn Ser Ser Ser Gly Thr Phe Ile Leu Met Gly
 1          5          10          15
Val Ser Asp His Pro His Leu Glu Ile Ile Phe Phe Ala Val Ile Leu
      20          25          30
Ala Ser Tyr Leu Leu Thr Leu Val Gly Asn Leu Thr Ile Ile Leu Leu
      35          40          45
Ser Arg Leu Asp Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50          55          60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Thr Thr Ser Ser Val Pro Gln
      65          70          75          80
Met Leu Lys Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Gly Gly
      85          90          95
Cys Val Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
      100          105          110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
      115          120          125
Pro Leu His Tyr Met Thr Val Met Asn Pro Arg Leu Cys Trp Gly Leu
      130          135          140
Ala Ala Ile Ser Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
      145          150          155          160
Thr Phe Thr Leu Gln Leu Pro Phe Cys Gly His Arg Lys Val Asp Asn

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      165      170      175
Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr
      180      185      190
Ser Leu Asn Glu Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Val
      195      200      205
Val Pro Val Ser Val Ile Leu Val Ser Tyr Cys Phe Ile Ala Gln Ala
      210      215      220
Val Met Lys Ile Arg Ser Val Glu Gly Arg Arg Lys Ala Phe Asn Thr
225      230      235      240
Cys Val Ser His Leu Val Val Val Phe Leu Phe Tyr Gly Ser Ala Ile
      245      250      255
Tyr Gly Tyr Leu Leu Pro Ala Lys Ser Ser Asn Gln Ser Gln Gly Lys
      260      265      270
Phe Ile Ser Leu Phe Tyr Ser Val Val Thr Pro Met Val Asn Pro Leu
      275      280      285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Gly Arg Leu
      290      295      300
Leu Gly Lys Gly Arg Gly Ala Ser
305      310

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<210> 2718

<211> 309

<212> PRT

<213> Unknown (MMOR23 (X92969))

<400>2718

```

Met Gln Arg Asn Asn Phe Thr Glu Val Ile Glu Phe Val Phe Leu Gly
 1      5      10      15
Phe Ser Ser Phe Gly Lys His Gln Ile Thr Leu Phe Val Val Phe Leu
      20      25      30
Thr Ile Tyr Ile Leu Thr Leu Ala Gly Asn Ile Ile Ile Val Thr Ile
      35      40      45
Thr His Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg
      65      70      75      80
Met Leu Ser Ser Leu Ile Phe Tyr Asn Leu Pro Ile Ser Leu Ala Gly
      85      90      95
Cys Ala Thr Gln Met Phe Phe Phe Val Thr Leu Ala Thr Asn Asn Cys
      100      105      110
Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115      120      125
Pro Leu Arg Tyr Thr Ile Ile Met Ser Lys Gly Met Cys Ala Leu Leu
      130      135      140
Val Cys Gly Ser Leu Gly Thr Gly Leu Val Met Ala Val Leu His Val
      145      150      155      160
Pro Ala Met Phe His Leu Pro Phe Cys Gly Thr Val Val Glu His Phe
      165      170      175
Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Val Asp Thr Thr
      180      185      190
Val Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Leu Val
      195      200      205
Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Ile Val Ser Ser Ile
      210      215      220
Leu Lys Ile Val Ser Thr Glu Gly Gln Lys Lys Ala Phe Ala Thr Cys
      225      230      235      240
Ala Ser His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile
      245      250      255
Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Val Glu Lys Asp Leu Leu
      260      265      270
Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val

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275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Ala Val
 290 295 300
 Gly Arg Asn Thr Ser
 305

<210> 2719

<211> 332

<212> PRT

<213> Unknown (GGCOR2GEN)

<400>2719

Met Leu Val Leu Cys Phe Ser Ala Ser Leu Leu Ser Asn Cys Asn Cys
 1 5 10 15
 Val Val Met Met Ala Lys Gly Asn His Ser Ser Ile Thr Glu Phe Val
 20 25 30
 Leu Leu Gly Phe Ser Glu Lys Arg Ala Ile Gln Ala Val Leu Phe Met
 35 40 45
 Gly Phe Leu Leu Ile Tyr Leu Ile Thr Leu Leu Gly Asn Val Gly Met
 50 55 60
 Ile Thr Leu Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe
 65 70 75 80
 Phe Leu Ser Ser Leu Ser Phe Leu Asp Ile Cys Tyr Ser Ser Thr Ile
 85 90 95
 Thr Pro Arg Val Leu Ser Asp Leu Pro Ala Ser Gln Lys Val Ile Ser
 100 105 110
 His Ser Ala Cys Leu Ala Gln Phe Tyr Phe Tyr Ala Val Phe Ala Thr
 115 120 125
 Thr Glu Cys Tyr Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala
 130 135 140
 Ile Cys Ser Pro Leu Leu Tyr Val Phe Ser Met Ser Ser Arg Val Cys
 145 150 155 160
 Val Leu Leu Val Ala Gly Ser Tyr Leu Val Gly Val Val Asn Ala Thr
 165 170 175
 Ile His Thr Gly Leu Ala Leu Gln Leu Ser Phe Cys Gly Pro Asn Ile
 180 185 190
 Ile Asn His Phe Tyr Cys Asp Gly Pro Pro Leu Tyr Ala Ile Ser Cys
 195 200 205
 Thr Asp Pro Thr Thr Asn Glu Ile Ala Ile Phe Leu Val Val Gly Phe
 210 215 220
 Asn Met Leu Ile Thr Ser Val Thr Ile Phe Ile Ser Tyr Thr Tyr Ile
 225 230 235 240
 Leu Phe Ala Val Leu Arg Met His Thr Ala Ala Gly Lys Arg Lys Thr
 245 250 255
 Phe Ser Thr Cys Ala Ser His Leu Ala Thr Val Thr Leu Phe Tyr Ala
 260 265 270
 Ser Ala Gly Ser Met Tyr Ser Arg Pro Ser Ser Arg His Ser Gln Asp
 275 280 285
 Leu Asp Lys Val Ala Ser Val Phe Tyr Thr Met Val Thr Pro Met Leu
 290 295 300
 Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Asp Val Leu
 305 310 315 320
 Gly Lys Val Met Gly Arg Lys Ser Val Ser Asp Lys
 325 330

<210> 2720

<211> 312

<212> PRT

<213> Unknown (GGCOR3GEN)

<400>2720

```

Met Ala Leu Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
 1          5          10          15
Leu Thr Asp Asn Pro Arg Leu Gln Met Pro Leu Phe Met Val Phe Leu
          20          25          30
Val Ile Tyr Thr Thr Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
          35          40          45
Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
          50          55          60
Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
65          70          75          80
Met Leu Ala Thr Phe Leu Glu Glu Arg Lys Thr Ile Ser Tyr Val Gly
          85          90          95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Thr Ser Glu Cys
          100          105          110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Leu Leu Tyr Pro Ser Ile Met Thr Lys Ala Val Cys Trp Arg Leu
          130          135          140
Val Lys Gly Leu Tyr Phe Leu Ala Phe Leu Asn Ser Leu Val His Thr
          145          150          155          160
Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His
          165          170          175
Phe Phe Cys Asp Asn Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr
          180          185          190
Thr Leu Asn Glu Leu Leu Val Ile Ile Phe Gly Ser Leu Phe Val Met
          195          200          205
Ser Ser Ile Ile Thr Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
          210          215          220
Val Val Arg Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
          225          230          235          240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
          245          250          255
Phe Met Tyr Leu Arg Ser Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
          260          265          270
Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu
          290          295          300
Thr Ala Thr Ser Ile Trp Leu His
          305          310

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<210> 2721

<211> 312

<212> PRT

<213> Unknown (GGCOR4GEN)

<400>2721

```

Met Ala Glu Gly Asn His Thr Leu Ala Ser Glu Phe Ile Leu Val Gly
 1          5          10          15
Leu Ser Asp His Pro Lys Met Lys Ala Ala Leu Phe Val Val Phe Leu
          20          25          30
Leu Ile Tyr Val Ile Thr Phe Gln Gly Asn Leu Gly Ile Ile Ile Leu
          35          40          45
Ile Gln Gly Asp Pro Arg Leu His Thr Ser Met Tyr Phe Phe Leu Ser
          50          55          60
Ser Leu Ser Val Val Asp Ile Cys Phe Ser Ser Val Ile Ala Pro Arg
          65          70          75          80
Thr Leu Val Asn Phe Leu Ser Glu Arg Arg Thr Ile Ser Phe Thr Gly
          85          90          95
Cys Thr Gly Gln Thr Phe Phe Tyr Ile Val Phe Val Thr Thr Glu Cys
          100          105          110

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Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Ser Thr Ile Met Thr Arg Arg Gln Cys Met Gln Leu
 130 135 140
 Val Val Gly Ser Tyr Ile Gly Gly Ile Leu Asn Ala Ile Il Gln Thr
 145 150 155 160
 Thr Phe Ile Ile Arg Leu Pro Phe Cys Gly Ser Asn Ile Ile Asn His
 165 170 175
 Phe Phe Cys Asp Val Pro Pro Leu Leu Ala Leu Ser Leu Ala Ser Thr
 180 185 190
 Tyr Ile Ser Glu Met Ile Leu Phe Ser Leu Ala Gly Ile Ile Glu Leu
 195 200 205
 Ser Thr Val Thr Ser Ile Leu Val Ser Tyr Ile Phe Ile Ser Cys Ala
 210 215 220
 Ile Leu Arg Ile Arg Ser Ala Glu Gly Arg Gln Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Ala Val Thr Leu Leu Tyr Gly Thr Thr Ile
 245 250 255
 Phe Thr Tyr Leu Arg Pro Ser Ser Ser Tyr Ser Leu Asn Thr Asp Lys
 260 265 270
 Val Val Ser Val Phe Tyr Thr Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Gly Ala Leu Ser Arg Val
 290 295 300
 Val Glu Arg Ile Thr Val Arg Val
 305 310

<210> 2722

<211> 318

<212> PRT

<213> Unknown (GGCOR1)

<400>2722

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
 1 5 10 15
 Leu Thr Asp Asn Pro Gly Leu Gln Met Pro Leu Phe Met Val Phe Leu
 20 25 30
 Ala Ile Tyr Thr Ile Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
 35 40 45
 Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
 50 55 60
 Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Ala Thr Phe Leu Glu Glu Arg Lys Thr Ile Ser Tyr Val Gly
 85 90 95
 Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Val Thr Glu Ser
 100 105 110
 Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu Leu Tyr Pro Ser Ile Met Thr Lys Ala Val Cys Trp Arg Leu
 130 135 140
 Val Glu Ser Leu Tyr Phe Leu Ala Phe Leu Asn Ser Leu Val His Thr
 145 150 155 160
 Ser Gly Leu Leu Lys Leu Ser Phe Cys Tyr Ser Asn Val Val Asn His
 165 170 175
 Phe Phe Cys Asp Ile Ser Pro Leu Phe Gln Ile Ser Ser Ser Ile
 180 185 190
 Ala Ile Ser Glu Leu Leu Val Ile Ile Ser Gly Ser Leu Phe Val Met
 195 200 205
 Ser Ser Ile Ile Ile Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
 210 215 220

Val Val Met Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
 245 250 255
 Phe Met Tyr Leu Arg Pro Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
 260 265 270
 Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu
 290 295 300
 Thr Ala Thr Thr Phe Gly Phe Ile Asp Ser Lys Ala Val Gln
 305 310 315

<210> 2723

<211> 312

<212> PRT

<213> Unknown (GGCOR2)

<400>2723

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
 1 5 10 15
 Leu Thr Asp Asn Pro Arg Leu Gln Met Pro Leu Phe Met Val Phe Leu
 20 25 30
 Val Ile Tyr Thr Thr Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
 35 40 45
 Ile Gly Met Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
 50 55 60
 Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
 65 70 75 80
 Met Leu Ala Thr Phe Leu Glu Glu Arg Arg Thr Ile Ser Tyr Val Gly
 85 90 95
 Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Thr Ser Glu Trp
 100 105 110
 Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu Leu Tyr Pro Ser Ile Met Thr Lys Ala Val Cys Trp Arg Leu
 130 135 140
 Val Lys Gly Leu Tyr Ser Leu Ala Phe Leu Asn Ser Leu Val His Thr
 145 150 155 160
 Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His
 165 170 175
 Phe Phe Cys Asp Asn Arg Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr
 180 185 190
 Thr Leu Asn Glu Leu Leu Val Ile Ile Ser Gly Ser Leu Phe Val Met
 195 200 205
 Ser Ser Ile Ile Thr Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
 210 215 220
 Val Val Met Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
 245 250 255
 Phe Met Tyr Leu Arg Ser Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
 260 265 270
 Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu
 290 295 300
 Thr Ala Thr Ser Val Trp Leu His
 305 310

<210> 2724

<211> 318
 <212> PRT
 <213> Unknown (GGCOR3)

<400>2724

```

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
1          5          10          15
Leu Thr Asp Asn Pro Gly Leu Gln Met Pro Leu Phe Met Val Phe Leu
20          25          30
Ala Ile Tyr Thr Ile Thr Leu Leu Thr Asn Leu Gly Leu Ile Arg Leu
35          40          45
Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
50          55          60
Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
65          70          75          80
Met Leu Ala Thr Phe Leu Glu Glu Arg Lys Thr Ile Ser Tyr Val Gly
85          90          95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Thr Ser Glu Cys
100          105          110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
115          120          125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Lys Ala Val Cys Trp Arg Leu
130          135          140
Val Glu Ser Leu Tyr Phe Leu Ala Phe Leu Asn Ser Leu Val His Thr
145          150          155          160
Cys Gly Leu Leu Lys Leu Ser Phe Cys Tyr Ser Asn Val Val Asn His
165          170          175
Phe Phe Cys Asp Ile Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Ile
180          185          190
Ala Ile Ser Glu Leu Leu Val Ile Ile Ser Gly Ser Leu Phe Val Met
195          200          205
Ser Ser Ile Ile Ile Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
210          215          220
Val Val Met Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
225          230          235          240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
245          250          255
Phe Met Tyr Leu Arg Pro Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
260          265          270
Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
275          280          285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Leu
290          295          300
Thr Ala Thr Thr Phe Gly Phe Ile Asp Ser Lys Ala Val Gln
305          310          315

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<210> 2725
 <211> 312
 <212> PRT
 <213> Unknown (GGCOR4)

<400>2725

```

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
1          5          10          15
Leu Thr Asp Asn Pro Gly Leu Gln Met Pro Leu Phe Met Val Phe Leu
20          25          30
Ala Ile Tyr Thr Ile Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
35          40          45
Ile Ser Val Asp Leu His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
50          55          60
Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys

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65          70          75          80
Met Leu Ala Thr Phe Leu Glu Glu Arg Lys Thr Ile Ser Tyr Ile Gly
      85          90          95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Val Thr Glu Ser
      100         105         110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
      115         120         125
Pro Leu Leu Tyr Pro Ser Ile Met Thr Lys Ala Val Cys Trp Arg Leu
      130         135         140
Val Lys Gly Leu Tyr Ser Leu Ala Phe Leu Asn Ser Leu Val His Thr
      145         150         155         160
Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His
      165         170         175
Phe Phe Cys Asp Asn Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr
      180         185         190
Thr Leu Asn Glu Leu Leu Val Phe Ile Phe Gly Ser Leu Phe Ala Met
      195         200         205
Ser Ser Ile Ile Thr Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
      210         215         220
Val Val Arg Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
      225         230         235         240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
      245         250         255
Phe Met Tyr Leu Arg Pro Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
      260         265         270
Ile Ala Ser Leu Phe Tyr Thr Val Ile Pro Met Leu Asn Pro Leu
      275         280         285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Val
      290         295         300
Ile Ala Thr Asn Val Trp Ile His
305          310

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<210> 2726

<211> 312

<212> PRT

<213> Unknown (GGCOR5)

<400>2726

```

Met Ala Leu Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
1          5          10          15
Leu Thr Asp Asn Pro Arg Leu Gln Met Pro Leu Phe Met Val Phe Leu
      20         25         30
Ala Ile Tyr Thr Ile Thr Leu Leu Ala Asn Leu Gly Leu Ile Ala Leu
      35         40         45
Ile Ser Val Asp Phe His Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
      50         55         60
Asn Leu Ser Phe Thr Asp Ala Ala Tyr Ser Thr Val Ile Thr Pro Lys
65          70          75          80
Met Leu Ala Thr Phe Leu Glu Glu Arg Arg Thr Ile Ser Tyr Val Gly
      85          90          95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Ser Ser Glu Cys
      100         105         110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
      115         120         125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Lys Ala Val Cys Trp Arg Leu
      130         135         140
Val Glu Gly Leu Tyr Ser Leu Ala Phe Leu Asn Ser Leu Val His Thr
      145         150         155         160
Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His
      165         170         175
Phe Phe Cys Asp Asn Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr

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      180      185      190
Thr Leu Asn Glu Leu Leu Val Phe Ile Phe Gly Ser Trp Phe Ala Met
      195      200      205
Ser Ser Ile Ile Thr Thr Pro Ile Ser Tyr Val Phe Ile Ile Leu Thr
      210      215      220
Val Val Arg Ile Arg Ser Lys Asp Gly Lys Tyr Lys Ala Phe Ser Thr
      225      230      235      240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Val Ile
      245      250      255
Phe Met Tyr Leu Arg Pro Val Lys Leu Phe Ser Leu Asp Thr Asp Lys
      260      265      270
Ile Ala Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
      275      280      285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu Arg Arg Val
      290      295      300
Ile Ala Thr Asn Val Trp Ile His
      305      310

```

<210> 2727

<211> 312

<212> PRT

<213> Unknown (GGCOR6)

<400>2727

```

Met Ala Ser Gly Asn Cys Thr Thr Pro Thr Thr Phe Ile Leu Ser Gly
  1      5      10      15
Leu Thr Asp Asn Pro Gly Leu Gln Met Pro Leu Phe Met Val Phe Leu
      20      25      30
Ala Ile Tyr Thr Ile Thr Leu Leu Thr Asn Leu Gly Leu Ile Ala Leu
      35      40      45
Ile Ser Ile Asp Leu Gln Leu Gln Thr Pro Met Tyr Ile Phe Leu Gln
      50      55      60
Asn Leu Ser Phe Thr Asp Ala Val Tyr Ser Thr Val Ile Thr Pro Lys
      65      70      75      80
Met Leu Ala Thr Phe Leu Glu Glu Thr Lys Thr Ile Ser Tyr Val Gly
      85      90      95
Cys Ile Leu Gln Tyr Phe Ser Phe Val Leu Leu Thr Val Arg Glu Cys
      100      105      110
Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Lys
      115      120      125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Lys Ala Val Cys Trp Arg Leu
      130      135      140
Val Lys Gly Leu Tyr Ser Leu Ala Phe Leu Asn Phe Leu Val His Thr
      145      150      155      160
Ser Gly Leu Leu Lys Leu Ser Phe Cys Ser Ser Asn Val Val Asn His
      165      170      175
Phe Phe Cys Asp Asn Ser Pro Leu Phe Gln Ile Ser Ser Ser Ser Thr
      180      185      190
Ala Leu Asn Glu Leu Leu Val Phe Ile Phe Gly Ser Leu Phe Val Met
      195      200      205
Ser Ser Ile Ile Thr Ile Leu Ile Ser Tyr Val Phe Ile Ile Leu Thr
      210      215      220
Val Val Arg Ile Arg Ser Lys Glu Arg Lys Tyr Lys Ala Phe Ser Thr
      225      230      235      240
Cys Thr Ser His Leu Met Ala Val Ser Leu Phe His Gly Thr Ile Val
      245      250      255
Phe Met Tyr Phe Gln Pro Ala Asn Asn Phe Ser Leu Asp Lys Asp Lys
      260      265      270
Ile Met Ser Leu Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
      275      280      285
Ile Tyr Ser Trp Arg Asn Lys Glu Val Lys Asp Ala Leu His Arg Ala

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290 295 300
 Ile Ala Thr Ala Val Leu Phe His
 305 310

<210> 2728
 <211> 162
 <212> PRT
 <213> Unknown (XLORXR1)

<400>2728
 Val Ala Val Cys His Pro Leu Leu Tyr Val Phe His Met Ser Gln Lys
 1 5 10 15
 His Cys Thr Phe Phe Val Ser Ala Ala Trp Ile Ile Gly Phe Leu Asp
 20 25 30
 Pro Thr Ser Tyr Val Val Leu Ile Ser Lys Phe Ser Phe Cys Thr Ser
 35 40 45
 Asn Ile Ile Asp His Phe Phe Cys Asp Leu Ala Pro Leu Leu Lys Leu
 50 55 60
 Ser Cys Ser Asp Thr Phe Gln Ile Glu Val Leu Asn Tyr Val Glu Ser
 65 70 75 80
 Ala Leu Val Thr Leu Asn Ser Phe Val Leu Thr Val Ile Ser Tyr Ile
 85 90 95
 Phe Thr Ile Ser Ala Ile Leu Asn Ile Lys Ser Ala Glu Gly Arg His
 100 105 110
 Lys Ala Phe Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe
 115 120 125
 Tyr Ser Thr Ile Ile Ser Leu Tyr Ile Arg Pro Ile Ser Thr Tyr Ala
 130 135 140
 Pro Lys Gln Asp Gln Phe Phe Ala Leu Leu Tyr Ile Val Leu Ile Pro
 145 150 155 160
 Leu Leu

<210> 2729
 <211> 161
 <212> PRT
 <213> Unknown (XLORXR2)

<400>2729
 Val Ala Ile Cys Tyr Pro Leu His Tyr Ala Leu Arg Met Ser Leu Lys
 1 5 10 15
 His Cys Ala Lys Ile Ile Val Gly Val Trp Val Ala Gly Phe Leu Ala
 20 25 30
 Pro Val Ile His Thr Val Leu Met Thr Asn Leu Ser Phe Cys Ser Ser
 35 40 45
 Asn His Ile Asn His Phe Leu Cys Asp Leu Thr Pro Val Leu Lys Ile
 50 55 60
 Ser Cys Ser Asp Thr Ser Leu Ile Glu Met Ile Thr Tyr Ile Asp Gly
 65 70 75 80
 Val Ile Val Ala Phe Ser Thr Phe Thr Ile Thr Ser Val Ser Tyr Val
 85 90 95
 Phe Ile Leu Phe Lys Ile Leu Lys Ile His Ser Ser Gln Gly Lys Lys
 100 105 110
 Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Cys Val Ile Ile Phe
 115 120 125
 Tyr Gly Ser Ile Ile Cys Leu Tyr Met Arg Pro Thr Lys Ser Ile Ser
 130 135 140
 Pro Asn Gln Asp Val Phe Ala Leu Leu Tyr Ala Val Leu Val Pro Met
 145 150 155 160
 Leu

<210> 2730
 <211> 155
 <212> PRT
 <213> Unknown (XLORXR3)

<400>2730
 Val Ala Ile Cys Met Pro Met Leu Tyr Ser Leu Ile Met Lys Lys Ser
 1 5 10 15
 Ile Cys Ala Leu Leu Ala Ser Val Ser Trp Phe Met Gly Ala Met Asp
 20 25 30
 Ser Phe Met Phe Trp Tyr Leu Val Ser Asn Ser Ser Phe Cys Asp His
 35 40 45
 Gln Glu Ile Asn His Phe Phe Cys Asp Leu Lys Thr Leu Met Lys Leu
 50 55 60
 Ser Cys Arg Gly Ala Glu Thr Ile Lys Ile Val Ile Ile Val Ala Ser
 65 70 75 80
 Ala Val Leu Gly Phe Leu Pro Phe Cys Leu Ile Leu Ile Ser Tyr Ala
 85 90 95
 Asn Ile Ile Ser Ser Val Ser Lys Ile Arg Thr Ala Ala Gly Lys Leu
 100 105 110
 Lys Ile Phe Ser Ser Cys Gly Ser His Leu Thr Val Val Leu Leu Phe
 115 120 125
 Cys Gly Thr Cys Leu Ser Leu Tyr Met Lys Pro Asp Ser Gly Asn Ser
 130 135 140
 Gln Glu Asn Glu Glu Leu Leu Ser Leu Leu Tyr
 145 150 155

<210> 2731
 <211> 162
 <212> PRT
 <213> Unknown (XLORXR5)

<400>2731
 Val Ala Ile Cys Gln Pro Leu Leu Tyr Ala Val Ile Met Asn Arg Lys
 1 5 10 15
 Val Val Ile Ile Phe Val Val Gly Val Tyr Leu Ser Gly Ile Phe Thr
 20 25 30
 Ala Ser Ile His Thr Ala Cys Thr Leu Thr Leu Ser Phe Cys Gly Pro
 35 40 45
 Asn Thr Ile Asn His Phe Tyr Cys Asp Ile Pro Pro Leu Met Glu Leu
 50 55 60
 Ser Cys Ser Asp Thr Tyr Ile His Lys Thr Val Ile Phe Val Val Val
 65 70 75 80
 Phe Cys Leu Gly Leu Phe Asn Val Ala Val Ile Leu Ala Ser Tyr Ser
 85 90 95
 Tyr Ile Phe Phe Thr Ile Ile His Ile Gln Ser Ser Cys Gly Arg His
 100 105 110
 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Cys Val Ser Leu Phe
 115 120 125
 Tyr Gly Thr Val Phe Phe Met Tyr Leu Arg Pro Ala Ser Lys Tyr Ser
 130 135 140
 Val Ser Gln Asp Lys Val Val Ser Val Phe Tyr Thr Met Val Ile Pro
 145 150 155 160
 Met Met

<210> 2732
 <211> 163
 <212> PRT
 <213> Unknown (XLORXR9)

<400>2732

```

Leu Ala Ile Cys Phe Pro Leu Asn Tyr Cys Leu Ile Met Ser Gln Ser
 1           5           10           15
Leu Arg Cys Arg Leu Val Val Val Cys Trp Ala Cys Gly Leu Val Asn
 20           25           30
Ser Leu Val Gln Ala Phe Ser Ile Ser His Leu Asp Phe Cys Gly Pro
 35           40           45
Asn Val Val Asp His Phe Phe Cys Asp Val Thr Pro Leu Phe Lys Leu
 50           55           60
Ser Cys Ser Asp Thr Arg Val Ser Glu Thr Ile Phe Leu Leu Val Val
 65           70           75           80
Ala Val Ala Gly Met Gly Pro Leu Thr Phe Ile Leu Val Thr Tyr Gly
 85           90           95
His Ile Ile Leu Ala Ile Thr Arg Ile Thr Ser Ser His Gly Arg Tyr
 100          105          110
Lys Thr Phe Ser Thr Cys Ala Ser His Phe Thr Val Val Ala Leu Tyr
 115          120          125
Tyr Gly Ser Gly Ile Phe Ser Tyr Ile Trp Pro Thr Ser Thr Tyr Ala
 130          135          140
Met Asn Lys Asp Val Lys Val Val Ala Val Leu Tyr Thr Val Met Thr
 145          150          155          160
Pro Met Leu

```

<210> 2733

<211> 159

<212> PRT

<213> Unknown (XLORXR13)

<400>2733

```

Val Ala Ile Ser Lys Pro Leu Arg Tyr Met Thr Ile Met Asn Trp Lys
 1           5           10           15
Val Cys Ala Val Leu Gly Val Ala Met Trp Thr Ala Gly Thr Val His
 20           25           30
Ser Ile Ser Phe Thr Ser Leu Thr Ile Lys Leu Pro Tyr Cys Gly Pro
 35           40           45
Asp Glu Ile Asp Asn Phe Phe Cys Asp Val Pro Gln Val Ile Glu Leu
 50           55           60
Ala Cys Thr Asp Thr Arg Ile Thr Glu Ile Leu Val Val Ser Asn Ser
 65           70           75           80
Gly Met Ile Ser Met Val Cys Phe Val Ile Ile Val Val Ser Tyr Ala
 85           90           95
Val Ile Leu Val Ser Leu Arg Gln Gln Ile Ser Asp Gly Lys Arg Lys
 100          105          110
Ala Leu Ser Thr Cys Ala Ala His Leu Thr Val Val Thr Leu Phe Leu
 115          120          125
Gly His Cys Ile Phe Ile Tyr Ser Arg Pro Ser Ile Ser Leu Pro Glu
 130          135          140
Asp Lys Ile Val Ser Ala Phe Phe Thr Ala Val Thr Pro Leu Leu
 145          150          155

```

<210> 2734

<211> 162

<212> PRT

<213> Unknown (XLORXR17)

<400>2734

```

Asn Ala Ile Cys Asn Pro Leu Leu Tyr Asn Thr Ile Met Asn Lys Arg
 1           5           10           15
Thr Cys Val Ile Leu Ile Val Gly Ser Trp Leu Ile Ala Ser Ile Asn

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      20      25      30
Ser Leu Ile His Thr Ile Leu Thr Phe Met Leu Pro Phe Cys Gly Ser
      35      40      45
Asn Ala Ile Asp Ser Phe Phe Cys Asp Met Pro Pro Leu Leu Lys Leu
      50      55      60
Ala Cys Thr Asp Thr Leu Val Asn Gln Ile Val Ile Phe Val Thr Gly
      65      70      75      80
Ser Cys Ile Ile Ala Gly Pro Phe Met Leu Thr Val Phe Ser Tyr Val
      85      90      95
Gln Ile Ile Ser Thr Ile Val Ser Ile Arg Ser Ser Ser Arg Lys Lys
      100      105      110
Lys Ala Phe Ser Thr Cys Thr Ser His Ile Thr Ala Val Val Ile Phe
      115      120      125
Tyr Val Pro Ser Ile Cys Ile Tyr Phe Arg Pro Lys Ser Asn Gln Ala
      130      135      140
Met Ile Gln Asp Lys Met Ala Thr Val Ile Cys Ala Val Ile Thr Pro
      145      150      155      160
Leu Leu

```

<210> 2735

<211> 223

<212> PRT

<213> Unknown (XLORXR42)

<400>2735

```

Cys Asn Leu Ser Ser Leu Asp Ile Ala Tyr Thr Ser Val Thr Ala Pro
1      5      10      15
Lys Leu Ile His Ile Phe Ala Val Asn Asn His Arg Ile Ser Phe Trp
      20      25      30
Gln Cys Ile Ala Gln Leu Tyr Phe Phe Ile Ala Phe Gly Ser Thr Glu
      35      40      45
Tyr Leu Leu Leu Thr Leu Met Ser Tyr Asp Arg Tyr Val Ala Val Cys
      50      55      60
Lys Pro Leu His Tyr Arg Val Val Met Ser Pro Met Leu Cys Arg Ala
      65      70      75      80
Gly Ala Ala Gly Thr Trp Ile Gly Gly Leu Leu Ala Ser Ile Pro Thr
      85      90      95
Ala Thr Ala Ala Ala Asn Ile Tyr Tyr Cys Ser Asn Asn Ile Ile Ile
      100      105      110
Asn His Phe Cys Asp Met Met Ala Leu Val Lys Leu Ala Cys Ser
      115      120      125
Asp Thr Thr Met Thr Arg Ala Val Ile Phe Val Glu Gly Met Leu Ile
      130      135      140
Leu Met Thr Cys Phe Leu Leu Thr Val Ile Ser Tyr Ile Cys Ile Leu
      145      150      155      160
Ser Thr Ile Val Arg Ile His Ser Ser Gly Gly Lys Phe Lys Ala Phe
      165      170      175
Ser Thr Cys Ala Ser His Leu Ser Val Val Ser Ile Phe Tyr Val Leu
      180      185      190
Ile Phe Tyr Leu Tyr Leu Lys Pro Lys Ser Glu Ile Ser Leu Ser Gln
      195      200      205
Gly Lys Leu Leu Thr Val Leu Tyr Val Tyr Phe Ile Pro Met Phe
      210      215      220

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<210> 2736

<211> 217

<212> PRT

<213> Unknown (XLORXR46)

<400>2736

```

Leu Leu Phe Asp Thr Ile Thr Thr Pro Lys Ile Ile Ala Lys Tyr Trp
 1           5           10           15
Phe Gly Asp Gly Asn Ile Ser Phe Ser Gly Cys Leu Phe Gln Leu Phe
 20           25           30
Cys Val His Ser Leu Gly Ser Val Asp Ser Phe Ile Leu Met Leu Met
 35           40           45
Ala Ala Asp Arg Tyr Val Ala Ile Leu Gln Pro Leu Arg Tyr Phe Ala
 50           55           60
Ile Ile Thr Lys Lys Leu Thr Ala Ile Phe Cys Ser Cys Phe Trp Val
 65           70           75           80
Leu Ser Val Val Ile Val Ser Val Met Thr Tyr Met Ile Leu Lys Leu
 85           90           95
Pro Phe Cys Gly Pro Asn Asn Ile Thr Gly Cys Phe Cys Ser Ser Ser
 100          105          110
Val Ile Phe Pro Leu Ala Cys Thr Asp Val Thr Tyr Val Arg Gln Val
 115          120          125
Ser Leu Ile Phe Ala Leu Ser Val Leu Leu Ile Pro Leu Ala Phe Ile
 130          135          140
Ile Leu Ser Tyr Ala Leu Ile Val Leu Thr Ile His Ser Met Leu His
 145          150          155          160
Ser Asp Asn Trp Gln Lys Leu Phe Tyr Thr Cys Thr Thr His Leu Leu
 165          170          175
Val Ile Cys Leu Tyr Tyr Ile Pro Arg Val Phe Val Tyr Leu Ala Asn
 180          185          190
Tyr Val Arg Leu Leu Phe Asn Ala Asp Ile Asn Val Leu Ile Leu Tyr
 195          200          205
Met Tyr Thr Phe Leu Pro His Leu Ala
 210          215

```

<210> 2737

<211> 217

<212> PRT

<213> Unknown (XLORXR106)

<400>2737

```

Leu Leu Phe Asp Thr Ile Thr Thr Pro Lys Ile Ile Ala Lys Tyr Trp
 1           5           10           15
Phe Gly Asp Gly Asn Ile Ser Phe Ser Gly Cys Leu Phe Gln Leu Phe
 20           25           30
Cys Val His Ser Leu Gly Ser Val Asp Ser Phe Ile Leu Met Leu Met
 35           40           45
Ala Ala Asp Arg Tyr Ile Ala Ile Leu Gln Pro Leu Arg Tyr Phe Ala
 50           55           60
Ile Ile Thr Lys Lys Leu Thr Thr Ile Phe Cys Ser Cys Phe Trp Val
 65           70           75           80
Leu Ser Val Val Ile Val Ser Val Met Thr Tyr Met Ile Leu Lys Leu
 85           90           95
Pro Phe Cys Gly Pro Asn Asn Ile Thr Gly Cys Phe Cys Ser Ser Ser
 100          105          110
Val Ile Phe Pro Leu Ala Cys Thr Asp Val Thr Tyr Val Arg Gln Val
 115          120          125
Ser Leu Ile Phe Ala Leu Ser Val Leu Leu Ile Pro Leu Ala Phe Ile
 130          135          140
Ile Leu Ser Tyr Ala Leu Ile Val Leu Thr Ile His Ser Met Leu His
 145          150          155          160
Ser Asp Asn Trp Gln Lys Leu Phe Tyr Thr Cys Thr Thr His Leu Leu
 165          170          175
Val Ile Cys Leu Tyr Tyr Ile Pro Arg Val Phe Met Tyr Leu Ala Asn
 180          185          190
Tyr Val Arg Leu Leu Phe Asn Ala Asp Ile Asn Val Leu Ile Leu Tyr
 195          200          205

```

Met Tyr Thr Phe Leu Pro His Leu Ala
 210 215

<210> 2738

<211> 217

<212> PRT

<213> Unknown (XLORXR116)

<400>2738

Leu Leu Phe Asp Thr Ile Thr Leu Pro Lys Ile Ile Ala Lys Tyr Trp
 1 5 10 15
 Phe Gly Ala Arg Ser Ile Ser Phe Tyr Gly Cys Ile Phe Gln Leu Phe
 20 25 30
 Cys Val His Ser Leu Gly Ser Leu Asp Ser Phe Ile Ile Met Leu Met
 35 40 45
 Ala Ile Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu Arg Tyr His Ser
 50 55 60
 Ile Ile Ser Asn Lys Leu Val Thr Leu Leu Cys Tyr Phe Phe Trp Val
 65 70 75 80
 Leu Ala Ala Leu Ile Gly Ser Ile Val Ala Val Ile Ala Gly Gln Leu
 85 90 95
 Pro Tyr Cys Gly Pro Asn Arg Val Arg Asn Cys Phe Cys Val Asn Ser
 100 105 110
 Ala Val Thr Val Leu Ala Cys Val Asp Val Thr Leu Ala Arg Arg Thr
 115 120 125
 Val Phe Thr Leu Ala Met Cys Val Leu Leu Leu Pro Leu Ala Phe Ile
 130 135 140
 Ile Leu Ser Tyr Ile Leu Ile Ile Arg Val Ile His Ser Ser Thr Asn
 145 150 155 160
 Asn Glu Asn Ser Trp Lys Ala Phe Tyr Thr Cys Thr Thr His Leu Met
 165 170 175
 Val Ile Gly Leu Tyr Tyr Ile Pro Arg Val Phe Val Tyr Ser Thr Ser
 180 185 190
 Gln Ile Pro Leu Ile Leu Asp Val Asp Ile Asn Val Leu Leu Leu Cys
 195 200 205
 Leu Tyr Thr Phe Val Pro His Leu Ala
 210 215

<210> 2739

<211> 217

<212> PRT

<213> Unknown (XLORXR117)

<400>2739

Leu Leu Phe Asp Thr Ile Thr Thr Pro Lys Ile Ile Ala Lys Tyr Trp
 1 5 10 15
 Phe Gly Asp Gly Asn Ile Ser Phe Ser Gly Cys Leu Phe Gln Leu Phe
 20 25 30
 Cys Val His Ser Leu Gly Ser Val Asp Ser Phe Ile Leu Met Leu Met
 35 40 45
 Ala Ala Asp Arg Tyr Ile Ala Ile Leu Gln Pro Leu Arg Tyr Phe Ala
 50 55 60
 Ile Ile Thr Lys Lys Leu Thr Thr Ile Phe Cys Ser Cys Phe Trp Val
 65 70 75 80
 Leu Gly Val Val Ile Val Ser Val Met Thr Tyr Met Ile Leu Lys Leu
 85 90 95
 Pro Phe Cys Gly Pro Asn Asn Ile Thr Gly Cys Phe Cys Ser Ser Ser
 100 105 110
 Val Ile Phe Pro Leu Ala Cys Thr Asp Val Thr Tyr Val Arg Gln Val
 115 120 125
 Ser Leu Ile Phe Ala Leu Ser Val Leu Leu Ile Pro Leu Ala Phe Ile

130 135 140
 Ile Leu Ser Tyr Ala Leu Ile Val Leu Thr Ile His Ser Met Leu His
 145 150 155 160
 Ser Asp Asn Trp Gln Lys Pro Phe Tyr Thr Cys Thr Thr His Leu Leu
 165 170 175
 Val Ile Cys Leu Tyr Tyr Ile Pro Arg Val Phe Met Tyr Leu Ala Asn
 180 185 190
 Tyr Val Arg Leu Leu Phe Asn Ala Asp Ile Asn Val Leu Ile Leu Tyr
 195 200 205
 Met Tyr Thr Phe Leu Pro His Leu Ala
 210 215

<210> 2740

<211> 222

<212> PRT

<213> Unknown (XLORXR171)

<400>2740

Gln Gln Leu Ser Val Cys Asp Leu Leu Gln Thr Ala Cys Thr Val Pro
 1 5 10 15
 Leu Leu Leu Trp Thr Ile Ile Asn Asp Gly Thr Thr Ile Ser Val Gly
 20 25 30
 Gly Cys Ile Thr Gln Phe Tyr Phe Phe Asn Ala Ser Glu Ser Val Glu
 35 40 45
 Cys Leu Leu Leu Thr Val Met Ser Phe Asp Arg Tyr Leu Ala Ile Cys
 50 55 60
 Asn Pro Leu Arg Tyr Thr Ser Leu Met Asn Pro Lys Leu Cys Val Lys
 65 70 75 80
 Leu Thr Leu Ile Pro Trp Leu Leu Gly Phe Ser Ile Ile Leu Ile Thr
 85 90 95
 Ala Asn Ala Ile Ala Thr Leu Gln Phe Cys Asn Gln Asn Thr Ile Asn
 100 105 110
 His Tyr Phe Cys Asp Tyr Phe Pro Leu Leu Glu Leu Ser Cys Met Asp
 115 120 125
 Thr Phe Phe Val Gln Thr Glu Ala Ile Leu Gln Ala Val Pro Val Val
 130 135 140
 Phe Ile Pro Ile Ile Leu Ile Ile Ile Ser Tyr Val Phe Ile Ile His
 145 150 155 160
 Thr Leu Leu Lys Ile Val Ser Thr Thr Gly Arg Gln Lys Ala Phe Ser
 165 170 175
 Thr Cys Ser Ser His Leu Ile Val Val Phe Leu Phe Tyr Gly Ser Leu
 180 185 190
 Ile Gly Ile Tyr Val Val Pro Ser Arg Lys Gln Ser Pro Thr Ile Ser
 195 200 205
 Lys Val Phe Ser Leu Leu Tyr Thr Val Val Thr Pro Leu Leu
 210 215 220

<210> 2741

<211> 220

<212> PRT

<213> Unknown (XLORXR181)

<400>2741

Gln Gln Leu Ser Leu Ser Asp Leu Leu Gly Ser Thr Asn Ile Val Pro
 1 5 10 15
 Thr Leu Leu Glu Thr Ile Ile Leu Gly Arg Ala Ser Ile Ser Leu Val
 20 25 30
 Asp Cys Ile Thr Gln Phe Asn Val Phe Gly Gly Ser Glu Thr Phe Val
 35 40 45
 Gly Phe Leu Leu Ala Val Met Ser Asn Asp Arg Tyr Val Ala Ile Cys
 50 55 60

```

Ile Pro Leu Arg Tyr Thr Ser Ile Thr Ser Tyr Asn Ile Cys Asn Lys
65              70              75              80
Leu Ile Leu Val Ser Trp Leu Leu Gly Leu Gly Ala Ile Leu Ile Thr
            85              90              95
Ala Asn Leu Ile*Ala Thr Leu Tyr Phe Cys Asp Gln Asn Ile Ile Asn
            100              105              110
His Phe Phe Cys Asp Phe Phe Pro Leu Leu Gln Leu Ser Cys Ser Asp
            115              120              125
Thr Phe Ile Val Gln Leu Glu Val Ile Leu Leu Ser Ile Pro Val Ile
            130              135              140
Ile Tyr Pro Phe Ile Leu Ile Ile Val Ser Tyr Ile Cys Ile Ala His
145              150              155              160
Ala Ile Leu Lys Ile Val Ser Asn Thr Gly Arg Gln Lys Ala Phe Ser
            165              170              175
Thr Cys Ser Ser His Leu Ala Val Val Ser Ile Phe Tyr Gly Ala Leu
            180              185              190
Thr Ala Val Tyr Val Ala Pro Pro Arg Lys Glu Ser Gln Thr Leu Ser
            195              200              205
Lys Val Phe Ser Leu Leu Tyr Thr Val Met Ile Pro
            210              215              220

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<210> 2742

<211> 220

<212> PRT

<213> Unknown (XLOR185)

<400>2742

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Ser Gln Leu Ser Thr Ser Asp Ile Val Ile Ser Thr Thr Val Cys Pro
1              5              10              15
Asn Leu Leu Tyr Ile Thr Trp Asn Glu Gly Ala Tyr Ile Ser Ile Thr
            20              25              30
Gly Cys Ile Trp Gln Phe Asn Met Phe Ser Val Ser Ser Val Thr Glu
            35              40              45
Cys Phe Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Cys
            50              55              60
Lys Pro Leu His Tyr Ala Ser Ile Met Thr Trp Arg Ser Cys Ile Phe
65              70              75              80
Leu Val Met Ser Cys Trp Ser Leu Gly Phe Leu Leu Ser Met Ile Val
            85              90              95
Thr Val Met Ile His Tyr Leu His Phe Cys Gly Pro Tyr Thr Ile Asp
            100              105              110
His Leu Phe Cys Asp Tyr Thr Pro Leu Met Gln Leu Ser Cys Ser Asp
            115              120              125
Thr Thr Ile Leu Lys Met Thr Val Phe Leu Ile Ala Thr Pro Gly Thr
            130              135              140
Val Leu Gln Pro Phe Phe Ile Ile Ala Thr Tyr Ile Asn Ile Ile Leu
145              150              155              160
Asn Ile Leu Arg Ile Ser Ser Ser Ser Lys Arg Gln Lys Ala Phe Ser
            165              170              175
Thr Cys Ser Ser His Leu Ser Val Val Cys Leu Tyr Tyr Gly Thr Leu
            180              185              190
Ile Ala Thr Tyr Ala Thr Pro Thr Asp Gly Arg Leu Ser Thr Arg Asn
            195              200              205
Lys Leu Leu Ser Leu Ile Tyr Thr Val Gly Thr Pro
            210              215              220

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<210> 2743

<211> 222

<212> PRT

<213> Unknown (XLORXR206)

<400>2743

Gly Asn Leu Ser Phe Val Asp Ile Ser Phe Ile Ser Val Thr Val Pro
 1 5 10 15
 Leu Met Val Ala His Leu Leu Thr Asp Lys Lys Ser Ile Ser Phe Thr
 20 25 30
 Gly Cys Met Thr Gln Leu Phe Phe Ile Trp Ile Ala Val Leu Glu
 35 40 45
 Cys Leu Ile Leu Thr Ile Met Ala Tyr Asp Arg Leu Val Ala Ile Thr
 50 55 60
 Asn Pro Leu Arg Tyr Leu Ser Ile Leu Asp Arg Lys Thr Cys Trp Ser
 65 70 75 80
 Leu Ile Thr Phe Ser Trp Ile Leu Ser Phe Leu His Ser Leu Leu Tyr
 85 90 95
 Ala Ser Thr Ile Ser Ser Leu Asp Tyr Cys Gly Leu Asn Lys Val Asn
 100 105 110
 Glu His Phe Cys Asp Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asn
 115 120 125
 Pro Ala Ser Leu Glu Leu Leu Val Tyr Thr Glu Gly Ser Val Met Ala
 130 135 140
 Met Ser Pro Phe Val Leu Ile Met Val Ser Tyr Leu Arg Ile Ile Lys
 145 150 155 160
 Thr Ile Leu Ser Ile His Ser Ser Ser Gly Arg Tyr Arg Ala Phe Ser
 165 170 175
 Thr Cys Ser Ser His Leu Ile Ser Val Gly Leu Phe Phe Val Thr Ile
 180 185 190
 Phe Val Ser Tyr Leu Gln Pro Ala Ser Ala Gly Ala Val Glu Thr Asn
 195 200 205
 Arg Pro Ile Ala Leu Val Tyr Ser Ile Leu Thr Pro Leu Pro
 210 215 220

<210> 2744

<211> 222

<212> PRT

<213> Unknown (XLORXR214)

<400>2744

Ser Asn Met Ser Phe Leu Glu Ile Arg Tyr Ile Ser Val Thr Leu Pro
 1 5 10 15
 Asn Leu Leu Val Asn Thr Leu Ser Lys Asp Met Ser Ile Ser Leu Ala
 20 25 30
 Gly Cys Met Ala Gln Leu Tyr Phe Phe Ile Ser Leu Met Cys Thr Glu
 35 40 45
 Cys Val Leu Leu Ala Val Met Ala Phe Asp Arg Tyr Ile Ala Val Cys
 50 55 60
 His Pro Leu His Tyr Val Thr Ile Val Ser Asn Lys Leu Cys Ile Gln
 65 70 75 80
 Leu Ala Ala Ala Ser Trp Ile Ala Gly Phe Thr Val Ser Val Ile Lys
 85 90 95
 Val Tyr Phe Ile Ser Arg Leu Ser Phe Cys Gly Pro Asn Ile Ile Asn
 100 105 110
 His Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ala Cys Val Asp
 115 120 125
 Met Ser Leu Ala Glu Phe Val Asp Phe Val Leu Ala Leu Val Ile Leu
 130 135 140
 Leu Thr Pro Leu Phe Val Thr Val Ala Ser Tyr Leu Cys Ile Ile Phe
 145 150 155 160
 Thr Ile Leu Lys Ile Pro Thr Asn Thr Gly Arg Gln Lys Ala Phe Ser
 165 170 175
 Thr Cys Ala Ser His Leu Thr Val Val Thr Ile Phe Phe Ser Thr Thr
 180 185 190
 Leu Phe Met Tyr Ala Arg Pro Lys Lys Ala Lys Ser Leu Asp Tyr Phe

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<210> 2745
<211> 312
<212> PRT
<213> Unknown (HOR5beta3)
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Met 1	Trp	Pro	Asn 5	Ile	Thr	Ala	Ala	Pro	Phe 10	Leu	Leu	Thr	Gly	Phe 15	Pro
Gly	Leu	Glu	Ala 20	Ala	His	His	Trp	Ile 25	Ser	Ile	Pro	Phe	Phe 30	Ala	Val
Tyr	Val	Cys 35	Ile	Leu	Leu	Gly	Asn 40	Gly	Met	Leu	Leu	Tyr 45	Leu	Ile	Lys
His 50	Asp	His	Ser	Leu	His	Glu 55	Pro	Met	Tyr	Tyr	Phe 60	Leu	Thr	Met	Leu
Ala 65	Gly	Thr	Asp	Leu	Met	Val 70	Thr	Leu	Thr	Thr	Met 75	Pro	Thr	Val	Met
Gly	Ile	Leu	Trp 85	Val	Asn	His	Arg	Glu 90	Ile	Ser	Ser	Val	Gly	Cys 95	Phe
Leu	Gln	Ala 100	Tyr	Phe	Ile	His	Ser	Leu 105	Ser	Val	Val	Glu	Ser 110	Gly	Ser
Leu	Leu 115	Ala	Met	Ala	Tyr	Asp	Arg 120	Phe	Ile	Ala	Ile	Arg 125	Asn	Pro	Leu
Arg 130	Tyr	Ala	Ser	Ile	Phe	Thr 135	Asn	Thr	Arg	Val	Ile 140	Ala	Leu	Gly	Val
Gly 145	Val	Phe	Leu	Arg	Gly	Phe 150	Val	Ser	Ile	Leu	Pro 155	Val	Ile	Leu	Arg 160
Leu	Phe	Ser	Phe 165	Ser	Tyr	Cys	Lys	Ser 170	His	Val	Ile	Thr	Arg 175	Ala	Phe
Cys	Leu	His 180	Gln	Glu	Ile	Met	Arg 185	Leu	Ala	Cys	Ala	Asp 190	Ile	Thr	Phe
Asn	Arg 195	Leu	Tyr	Pro	Val	Ile	Leu 200	Ile	Ser	Leu	Thr	Ile 205	Phe	Leu	Asp
Ser 210	Leu	Ile	Ile	Leu	Phe	Ser 215	Tyr	Ile	Leu	Ile	Leu 220	Asn	Thr	Val	Ile
Gly 225	Ile	Ala	Ser	Gly	Glu	Glu 230	Arg	Ala	Lys	Ala	Leu 235	Asn	Thr	Cys 240	Ile
Ser	His	Ile	Ser 245	Cys	Val	Leu	Ile	Phe	Tyr 250	Val	Thr	Val	Met 255	Gly	Leu
Thr	Phe	Ile 260	Tyr	Arg	Phe	Gly	Lys 265	Asn	Val	Pro	Glu	Val 270	Val	His	Ile
Ile	Met 275	Ser	Tyr	Ile	Tyr	Phe	Leu 280	Phe	Pro	Pro	Leu	Met 285	Asn	Pro	Val
Ile 290	Tyr	Ser	Ile	Lys	Thr	Lys 295	Gln	Ile	Gln	Tyr	Gly 300	Ile	Ile	Arg	Leu
Leu 305	Ser	Lys	His	Arg	Phe	Ser	Arg 310								

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<210> 2746
<211> 310
<212> PRT
<213> Unknown (HOR5beta2 (translated via ORDEAL))
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<220>
<221> VARIANT
<222> (1)...(310)
<223> Xaa = Any Amino Acid
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<400>2746

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Thr His Asn Ala Ala Pro Phe Leu Leu Pro Gly Phe Ser Val Leu Glu
 1          5          10          15
Ala Thr Tyr His Ser Ile Ser Ile Pro Phe Phe Ala Val Tyr Val Cys
          20          25          30
Val Leu Leu Gly Asn Gly Lys Leu Leu Tyr Leu Ile Lys His Asp His
          35          40          45
Ser Leu His Glu Pro Met Tyr Cys Phe Leu Ala Thr Leu Arg Gln Asp
          50          55          60
Leu Met Val Lys Leu Thr Met Met Pro Thr Val Met Gly Val Leu Trp
65          70          75          80
Met Asn His Lys Glu Val Ile His Gly Ala Cys Phe Leu Gln Val Tyr
          85          90          95
Ile Ile His Ser His Tyr Pro Leu Ala Glu Ser Gly Ile Leu Leu Ser
          100          105          110
Met Ala Tyr Asp Arg Phe Ile Ile Ile His Met Leu Leu Arg Tyr Asn
          115          120          125
Ser Ile Ser Thr Lys Ser Trp Val Lys Ile Glu Leu Trp Leu Phe Met
          130          135          140
Arg Asp Phe Leu Ser Leu Val Pro Pro Ile Leu Pro Leu His Cys Phe
          145          150          155          160
Pro Tyr Cys His Ser His Val Leu Phe His Thr Phe Phe Leu His Gln
          165          170          175
Asp Val Leu Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn His Leu Tyr
          180          185          190
Pro Ala Ile Leu Val Ala Leu Ile Phe Phe Leu Asp Ala Leu Ile Ile
          195          200          205
Val Phe Ser Tyr Ile Leu Ile Leu Lys Thr Val Ile Gly Ile Ala Ser
          210          215          220
Arg Lys Glu Gln Ala Lys Ala Leu Asn Met Cys Val Ser His Ile Ser
          225          230          235          240
Cys Val Leu Val Phe His Ile Thr Val Ile Ser Glu Thr Phe Ile His
          245          250          255
Arg Phe Gly Lys His Ala Pro His Val Val His Ile Thr Val Ser Xaa
          260          265          270
Xaa Leu Ile Leu Phe Pro Pro Phe Met Asn Pro Ile Ile Tyr Ser Ile
          275          280          285
Lys Pro Ser Arg Ser Lys Glu Ala Leu Xaa Arg Leu Phe Ser Gly His
          290          295          300
Arg Met Ala Xaa Ala Leu
          305          310

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<210> 2747

<211> 310

<212> PRT

<213> Unknown (HOR5beta1)

<400>2747

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Met Trp Tyr Asn Asn Ser Ala Gly Pro Phe Leu Leu Thr Gly Phe Leu
 1          5          10          15
Gly Ser Glu Ala Val His Tyr Arg Ile Ser Met Ser Phe Phe Val Ile
          20          25          30
Tyr Phe Ser Val Leu Phe Gly Asn Gly Thr Leu Leu Val Leu Ile Trp
          35          40          45
Asn Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
          50          55          60
Ala Asp Thr Asp Leu Gly Met Thr Phe Thr Thr Met Pro Thr Val Leu
65          70          75          80
Gly Val Leu Leu Leu Asp Gln Arg Glu Ile Ala His Ala Ala Cys Phe
          85          90          95
Thr Gln Ser Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Ile Leu

```

	100		105		110
Leu Val	Leu Ala Tyr Asp Cys Phe	Ile Ala Ile Arg Thr Pro	Leu Arg		
	115	120	125		
Tyr Asn Cys	Ile Leu Thr Asn Ser Arg Val Met Asn	Ile Gly Leu Gly			
	130	135	140		
Val Leu Met Arg Gly	Phe Met Ser Ile Leu Pro Ile Ile Leu Ser Leu				
145	150	155	160		
Tyr Cys Tyr Pro Tyr Cys Gly Ser Arg Ala Leu Leu His Thr Phe Cys					
	165	170	175		
Leu His Gln Asp Val Ile Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn					
	180	185	190		
His Ile Tyr Pro Ile Ile Gln Thr Ser Leu Thr Val Phe Leu Asp Ala					
	195	200	205		
Leu Ile Ile Ile Phe Ser Tyr Ile Leu Ile Leu Lys Thr Val Met Gly					
	210	215	220		
Ile Ala Ser Gly Gln Glu Ala Lys Ser Leu Asn Thr Cys Val Ser					
225	230	235	240		
His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Met Gly Leu Ser					
	245	250	255		
Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val Pro Ile Thr					
	260	265	270		
Met Ser Tyr Val His Phe Leu Phe Pro Pro Phe Val Asn Pro Ile Ile					
	275	280	285		
Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Ile Arg Leu Phe					
	290	295	300		
Ser Gly Gln Ser Arg Ala					
305	310				

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(21) International Application Number: PCT/US00/27582

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CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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(54) Title: OLFACTORY RECEPTOR SEQUENCES

(57) Abstract: The present invention provides polynucleotide sequences which encode polypeptides involved in olfactory sensation. The present invention also provides the polypeptides encoded by these polynucleotide sequences, vectors comprising these polynucleotide sequences and host cells transfected with these polynucleotide sequences. The present invention further provides for functional variants and homologues of these polynucleotide sequences and the polypeptides encoded by these polynucleotides. Libraries of polypeptides are also provided. Also included in the present invention is the use of these polypeptides and libraries of polypeptides in screening odorant molecules to determine the correspondence (scent representation, scent fingerprint or scent profile) between individual odorant receptors (the polypeptides) and particular odorant molecules. Also encompassed by the present invention is the use of the scent representation, scent fingerprint or scent profile to re-create and edit scents.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/27582

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/705 C12N5/10 G01N33/50 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K C12N C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, SEQUENCE SEARCH, WPI Data, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WETZEL CHRISTIAN H ET AL: "Specificity and sensitivity of a human olfactory receptor functionally expressed in human embryonic kidney 293 cells and Xenopus laevis oocytes." JOURNAL OF NEUROSCIENCE, vol. 19, no. 17, pages 7426-7433, XP002178954 ISSN: 0270-6474 cited in the application the whole document	
A	WO 95 18140 A (YEDA RES & DEV ;RYCUS AVIGAIL (IL); BEN ARIE NISSIM (IL); LANCET D) 6 July 1995 (1995-07-06) pages 3,4,6; Figs 3 + 4 --- -/--	

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document relating to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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Date of the actual completion of the international search

2 October 2001

Date of mailing of the international search report

15. 01. 02

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/27582

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>GLUSMAN GUSTAVO ET AL: "Sequence analysis in the olfactory receptor gene cluster on human chromosome 17: Recombinatorial events affecting receptor diversity." GENOMICS, vol. 37, no. 2, 1996, pages 147-160, XP002178955 ISSN: 0888-7543 the whole document</p>	
A	<p>& DATABASE EMBL SEQUENCE LIBRARY [Online] 22 July 1994 (1994-07-22) CROWE M.L., PERRY B.N., CONNERTON I.F.: "olfactory receptor; OR17-40 gene" abstract</p>	
A	<p>--- BUETTNER JILL A ET AL: "Organization and evolution of olfactory receptor genes on human chromosome 11." GENOMICS, vol. 53, no. 1, 1 October 1998 (1998-10-01), pages 56-68, XP002178956 ISSN: 0888-7543 the whole document</p>	
A	<p>--- TRASK B J ET AL: "Members of the olfactory receptor gene family are contained in large blocks of DNA duplicated polymorphically near the ends of human chromosomes" HUMAN MOLECULAR GENETICS, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 7, no. 1, January 1998 (1998-01), pages 13-26, XP002135641 ISSN: 0964-6906 the whole document</p>	
A	<p>& DATABASE EMBL SEQUENCE LIBRARY [Online] 9 June 1996 (1996-06-09) TRASK, B.J., ET AL.: "Homo sapiens chromosome-19 36.3-kbp cosmid F7501, with 3 regions of similarity to olfactory receptor protein genes" accession no. L78442</p>	
A	<p>--- KRAUTWURST D ET AL: "Identification of ligands for olfactory receptors by functional expression of a receptor library" CELL, CELL PRESS, CAMBRIDGE, MA, US, vol. 95, 25 June 1998 (1998-06-25), pages 917-926, XP002153217 ISSN: 0092-8674 cited in the application</p>	
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/27582

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 98 50081 A (ZHAO HAIQING ;FIRESTEIN STUART J (US)) 12 November 1998 (1998-11-12) cited in the application ---	
P,X	DATABASE EMBL SEQUENCE LIBRARY [Online] 14 June 2000 (2000-06-14) HEILIG R., ET AL.: "Human chromosome 14 DNA sequence BAC R-55G7 of library RPCI-11 from chromosome 14 of Homo sapiens (Human)" XP002178959 accession no. AL359218 ---	1,4
T	GLUSMAN GUSTAVO ET AL: "Sequence, structure, and evolution of a complete human olfactory receptor gene cluster." GENOMICS., vol. 63, no. 2, 15 January 2000 (2000-01-15), pages 227-245, XP002178957 ISSN: 0888-7543 the whole document ---	
T	FUCHS TANIA ET AL: "The human olfactory subgenome: From sequence to structure and evolution." HUMAN GENETICS, vol. 108, no. 1, January 2001 (2001-01), pages 1-13, XP002178958 ISSN: 0340-6717 -----	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/27582

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1-7, 15-19 partially.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claim : 1

Invention 1:

claims 1-7, 15-19 partially

Isolated nucleotide sequence encoding an olfactory receptor as characterized by SEQID1; the recombinant expression of the same in host cells; the translated polypeptide sequence of SEQID1 and a host cell and phage expressing said polypeptide; furthermore, a library of olfactory receptors suitable of determining the interaction pattern of a composition with said receptors comprising the translated expression products of at least two, 50, 100, 200 or 500 polynucleotides encoding olfactory receptors, one of which is characterized by SEQID1.

2. Claim : 2

Invention 2-115:

claims 1-7, 15-19 partially

As invention one but as characterized by SEQIDs 2-73 and 111-152.

3. Claim : 3

Invention 116-1047:

claims 8-10 and 15-19 partially, 31,32,33 completely

Isolated nucleotide sequence encoding an olfactory receptor as characterized by one of the SEQIDs from the group of SEQID153 to SEQID1084; the recombinant expression of the same in a host cell; furthermore, a library of olfactory receptors suitable of determining the interaction pattern of a composition with said receptors comprising the translated expression products of at least two, 50, 100, 200 or 500 polynucleotides encoding olfactory receptors, one of which is characterized by one of the SEQIDs from the group of SEQID153 to SEQID1084; furthermore, a DNA array or a DNA chip comprising a DNA segment derived from one SEQID of the group of SEID153 to SEQID1084, a method determining the differences among individuals with respect to their olfactory faculties,

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

comprising comparing the olfactory DNA of the individual against said DNA array or chip; method to determine a single nucleotide polymorphism in olfactory receptors based on primers designed according to the first and last 25 bases of one of the SEQIDs of the group of SEQID153 to SEQID1084.

4. Claim : 4

Invention 1048-1971:

claims 11-14,20-24,25-30 partially

Isolated olfactory receptor polypeptide
as characterized by one of the SEQIDs from the group of
SEQID1085 to SEQID2008; a recombinant host cell or phage
expressing said polypeptide;
furthermore, a library of olfactory receptors suitable of
determining the interaction pattern of a composition with
said receptors comprising at least two, 50, 100, 200 or 500
olfactory receptor polypeptides, one of which is
characterized by one of the SEQIDs from the group of
SEQID1085 to SEQID2008;
furthermore, a method for determining the binding pattern of
a composition with olfactory receptors, comprising exposing
said library to a composition, further determining whether
the receptor is activated.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/27582

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 9518140	A	06-07-1995	WO	9518140 A1	06-07-1995

WO 9850081	A	12-11-1998	US	5993778 A	30-11-1999
			AU	7372898 A	27-11-1998
			EP	0983506 A2	08-03-2000
			US	6218358 B1	17-04-2001
			WO	9850081 A2	12-11-1998
